

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:49:11 ; Search time 7466 Seconds
(without alignments)
10896.907 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679
Sequence: 1 gttgtccttcagcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1679	100.0	1679	6	CQ768055 Sequence
2	1679	100.0	1679	6	AR528639 Sequence
3	1679	100.0	1679	6	AX358872 Sequence
4	1679	100.0	1679	6	AX362365 Sequence
5	1679	100.0	1679	6	AX403748 Sequence
6	1679	100.0	1679	6	AX454470 Sequence
7	1679	100.0	1679	6	AX464242 Sequence
8	1679	100.0	1679	6	AX490948 Sequence
9	1679	100.0	1679	9	AY358331 Homo sapi
10	1661.4	99.0	1693	6	AX439649 Sequence
11	1432.8	85.3	1839	6	AX665342 Sequence
12	1432.8	85.3	1839	9	AF126426 Homo sapi
13	1032	61.5	1032	6	AX439648 Sequence
14	996.8	59.4	2040	10	RNU16845
15	976.4	58.2	1615	10	BC023307
16	939	55.9	939	6	AR439650 Sequence
17	910.6	54.2	1410	10	AF282980
18	910.4	54.2	1068	6	AX665344 Sequence
19	874.4	52.1	1104	6	AX665346 Sequence

93	272.6	16.2	5582	9	HSM806161	BX538014 Homo sapi	166	108	6.4	172146	2	AC130272	AC130272 Papio anu
94	271	16.1	1119	6	AX675563	AX575563 Sequence	c 167	107.8	6.4	169206	10	AC123550	AC123550 Mus muscu
95	271	16.1	2383	6	AX747470	AX747470 Sequence	c 168	107.8	6.4	277603	2	AC079543	AC079543 Mus muscu
96	271	16.1	2383	9	AK092307	Homo sapi	169	106.2	6.3	229330	2	AC137057	AC137057 Rattus no
97	269.4	16.0	2840	9	AX358132	Homo sapi	c 170	106.2	6.3	238070	2	AC134313	AC134313 Rattus no
98	260.4	15.5	1017	6	AX644995	AX644995 Sequence	c 171	106.2	6.3	242260	2	AC094567	AC094567 Rattus no
99	258.8	15.4	1018	6	AX644993	AX644993 Sequence	c 172	106.2	6.3	225120	2	AC127219	AC127219 Rattus no
100	257.2	15.3	1136	6	AX644997	AX644997 Sequence	c 173	106	6.3	142000	9	AC078813	AC078813 Homo sapi
c 101	256	15.2	257	11	G07361	G07361 human STR	174	105.6	6.3	913	6	AR542162	AR542162 Sequence
102	254.2	15.1	5605	9	BC036771	BC036771 Homo sapi	175	104.4	6.2	237376	2	AC124949	AC124949 Rattus no
103	248.2	14.8	186110	2	AC102204	Mus muscu	c 176	104.4	6.2	277228	2	AC106911	AC106911 Rattus no
104	246	14.7	1169	6	AX644999	AX644999 Sequence	177	102.2	6.1	131490	10	AC122207	AC122207 Mus muscu
105	238.4	14.2	20731	9	AP004721	AP004721 Homo sapi	178	102.2	6.1	177251	10	AC124565	AC124565 Mus muscu
106	238.4	14.2	43087	9	AP005155	AP005155 Homo sapi	179	100	6.0	219	6	AR030583	AR030583 Sequence
c 107	235.6	14.0	203572	9	AC016769	AC016769 Homo sapi	180	99	5.9	219713	2	AC111456	AC111456 Rattus no
c 108	229.2	13.7	251	11	BV199013	BV199013 sqm19956	181	99	5.9	234283	2	AC114113	AC114113 Rattus no
109	223.2	13.3	20750	5	BC080221	BC080221 Danio rer	c 182	99	5.9	250355	2	AC127766	AC127766 Rattus no
110	223.2	13.3	2455	5	AF241637	AF241637 Danio rer	183	99	5.9	263661	2	AC106603	AC106603 Rattus no
111	221.8	13.2	4323	10	AK122576	AK122576 Mus muscu	c 184	99	5.9	319104	2	AC106602	AC106602 Rattus no
c 112	220.4	13.1	197553	2	AC146103	AC146103 Pan trogl	185	98.4	5.9	411	6	CQ731080	CQ731080 Sequence
c 113	217.4	12.9	36000	9	AP003166	AP003166 Homo sapi	186	95.8	5.8	187746	2	CQ87123	CQ87123 Mus muscu
c 114	209.4	12.5	152686	2	AC018913	AC018913 Homo sapi	187	95.2	5.7	219	6	AR030584	AR030584 Sequence
115	207.6	12.4	786	5	GGA132998	AJ132998 Gallus ga	c 188	92.6	5.5	214942	10	AC125214	AC125214 Mus muscu
116	207.2	12.3	168745	2	AC119552	AC119552 Rattus no	189	89.8	5.3	114269	2	AP002341	AP002341 Homo sapi
117	207.2	12.3	248329	2	AC109989	AC109989 Rattus no	190	89.8	5.3	152797	2	AC012134	AC012134 Homo sapi
c 118	205.6	12.2	110000	2	AC102028	Continuation (2 of	c 191	89.8	5.3	159520	9	AC113009	AC113009 Homo sapi
c 119	203.8	12.1	189323	2	AC150620	Callithri	192	89.8	5.3	172128	2	AP000762	AP000762 Homo sapi
120	203.8	12.1	193545	2	AC151029	AC151029 Callithri	193	89.8	5.3	150104	2	AP002831	AP002831 Homo sapi
121	197.4	11.8	189037	2	AC150026	AC150026 Papio anu	194	89.8	5.3	199079	9	AP000844	AP000844 Homo sapi
122	193.6	11.5	352	6	BD026522	BD026522 Sequence	c 195	89	5.3	987	6	CQ734933	CQ734933 Sequence
123	193.6	11.5	352	6	BD026522	BD026522 Sequence	c 196	88	5.3	170006	9	AP005122	AP005122 Homo sapi
124	180.4	10.7	5666	6	AX740565	AX740565 Sequence	197	88	5.2	882	2	CQ732721	CQ732721 Sequence
c 125	177.6	10.6	215743	2	AC148958	AC148958 Otlemur	198	87.2	5.2	163120	5	BX296535	BX296535 Zebrafish
c 126	176.6	10.5	540	6	AX665354	AX665354 Sequence	c 199	87.2	5.2	180842	2	CR536619	CR536619 Danio rer
127	176.6	10.5	116069	2	AP000784	AP000784 Homo sapi	c 200	87	5.2	438	6	AR416888	AR416888 Sequence
c 128	176.6	10.5	123320	9	AP000863	AP000863 Homo sapi	201	87	5.2	438	6	AX977582	AX977582 Sequence
129	176.6	10.5	176676	2	AC012234	AC012234 Homo sapi	202	87	5.2	438	6	BD112441	BD112441 EST and e
130	176.6	10.5	177102	2	AP002808	AP002808 Homo sapi	c 203	86.6	5.2	169582	2	AC102190	AC102190 Mus muscu
131	175	10.4	642	6	CQ732119	CQ732119 Sequence	c 204	86.2	5.1	74368	9	AL391239	AL391239 Human DNA
132	174.4	10.4	182	6	AR413330	AR413330 Sequence	c 205	86.2	5.1	131457	9	AL356600	AL356600 Human DNA
133	174.4	10.4	182	6	AX970164	AX970164 Sequence	c 206	86.2	5.1	153852	2	AC009694	AC009694 Homo sapi
134	174.4	10.4	182	6	BD108883	BD108883 EST and e	c 207	86.2	5.1	315761	2	AL158079	AL158079 Homo sapi
c 135	173.2	10.3	242565	2	AC094728	AC094728 Rattus no	208	85.8	5.1	162247	2	AC102328	AC102328 Mus muscu
136	173.2	10.3	251570	2	AC094463	AC094463 Rattus no	209	85.4	5.1	295	6	CQ732164	CQ732164 Sequence
c 137	172.2	10.3	133989	2	AC149777	AC149777 Bos tauru	210	84.2	5.0	246900	2	AC128465	AC128465 Rattus no
c 138	172.2	10.3	205738	4	AC150499	AC150499 Bos tauru	c 211	83.4	5.0	162717	10	AC127259	AC127259 Mus muscu
139	171.2	10.2	184012	10	AC116523	AC116523 Mus muscu	212	83.4	5.0	258847	2	AC112746	AC112746 Rattus no
140	166.8	9.9	504	6	CQ715694	CQ715694 Sequence	213	83.4	5.0	258847	2	AC104926	AC104926 Mus muscu
141	164.8	9.8	531	6	CQ719449	CQ719449 Sequence	214	81.8	4.9	110000	2	AC110642	Continuation (4 of
142	163.2	9.7	585	6	AX079674	AX079674 Sequence	215	78.6	4.7	420	6	AX665356	AX665356 Sequence
c 143	160	9.5	408	6	AX684132	AX684132 Sequence	c 216	78.6	4.7	113063	2	AC010946	AC010946 Homo sapi
c 144	156	9.3	371	6	CQ731074	CQ731074 Sequence	c 217	78.6	4.7	191204	9	AP000843	AP000843 Homo sapi
145	152.4	9.1	793	5	BX932289	BX932289 Gallus ga	218	78.6	4.6	202505	2	AP000912	AP000912 Homo sapi
c 146	152.2	9.1	168191	2	AC151813	AC151813 Dasyus n	219	77.8	4.6	177	6	AR030585	AR030585 Sequence
147	147.6	8.8	259743	2	AC113965	AC113965 Mus muscu	220	77.8	4.6	177	6	AR030586	AR030586 Sequence
148	146	8.7	200	6	AX898567	AX898567 Sequence	221	76.8	4.6	479	6	AX665358	AX665358 Sequence
c 149	146	8.7	200	6	BD034100	BD034100 Sequence	222	71.4	4.3	480	6	AX665357	AX665357 Sequence
c 150	145	8.6	150308	10	AC098294	AC098294 Rattus no	223	69.2	4.1	62350	9	AC067725	AC067725 Homo sapi
151	145	8.6	225433	2	AC106484	AC106484 Rattus no	224	69	4.1	146352	2	CR548641	Danio rer
152	145	8.6	237199	10	AC094830	AC094830 Rattus no	225	69	4.1	186279	5	AX950870	Zebrafish
153	140.6	8.4	152686	2	AC018913	AC018913 Homo sapi	c 226	69	4.1	191779	2	CR376789	Danio rer
154	135.2	8.1	268	4	AF271984	AF271984 Bos tauru	227	67	4.0	176744	2	AC027631	AC027631 Homo sapi
c 155	135.2	8.1	110000	2	AC102028	AC102028 Mus muscu	228	65.6	3.9	198	6	AR030587	AR030587 Sequence
c 156	135.2	8.1	186110	2	AC102204	AC102204 Mus muscu	c 229	65	3.9	195956	2	AC127626	Rattus no
157	128	7.6	184716	2	AC018368	AC018368 Homo sapi	c 230	65	3.9	249701	2	AC106525	Rattus no
158	113.6	6.8	195993	2	AC134953	AC134953 Pan trogl	c 231	63.4	3.8	198	6	AR030588	AR030588 Sequence
159	113.6	6.8	212752	9	AC063977	AC063977 Homo sapi	232	61.6	3.7	270	6	AX665353	AX665353 Sequence
c 160	112.8	6.7	157263	2	BX957285	BX957285 Danio rer	c 233	60.8	3.6	117951	9	AL359821	AL359821 Human DNA
161	110.6	6.6	292	6	CQ716587	CQ716587 Sequence	c 234	60.8	3.6	199301	2	AC119938	AC119938 Mus muscu
c 162	110.4	6.6	213331	2	AC125960	AC125960 Rattus no	235	60	3.6	60	6	CQ544101	CQ544101 Sequence
163	109.6	6.5	175963	2	AC148913	AC148913 Sus scrof	236	58.6	3.5	2000	6	AX655393	AX655393 Sequence
164	109.4	6.5	134184	2	AC150028	AC150028 Canis fam	237	58.6	3.5	166417	10	AC127685	AC127685 Mus muscu
165	108	6.4	168861	2	AC130786	AC130786 Papio anu	c 238	58	3.5	143672	2	AP001806	AP001806 Homo sapi

239 AX665355 Sequence 3.4 420 6 AX665355
c 240 AP003029 Homo sapi 3.4 142882 9 AP003029
c 241 AC112588 Rattus no 3.3 193180 2 AC112588
242 AC0524931 Sequence 3.6 247 6 AC0524931
243 BX537929 Homo sapi 3.3 4459 9 HSM804634
244 AC008466 Homo sapi 3.3 34930 2 AC008466
245 AC008466 Homo sapi 3.3 1598 9 AC008466
c 246 AC013323 Homo sapi 3.3 6359 6 AC013323
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312 AX665355 Sequence 3.1 8979 6 AX665355
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c 314 AC112588 Rattus no 3.1 8979 6 AX665355
c 315 AC0524931 Sequence 3.1 8979 6 AX665355
316 BX537929 Homo sapi 3.1 8979 6 AX665355
317 AC008466 Homo sapi 3.1 8979 6 AX665355
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AX345686 Sequence
AX348663 Sequence
AX136304 Homo sapi
X61665 N. tabacum p
BX537929 Homo sapi
AC008466 Homo sapi
AL928642 Mouse DNA
AC091549 Homo sapi
CQ516508 Sequence
CQ526778 Sequence
AK116650 Ciona int
BC043572 Homo sapi
BC066857 Mus muscu
BC073932 Homo sapi
BC020211 Homo sapi
BC043583 Homo sapi
AB073429 Ciona sav
BC040407 Mus muscu
AL832393 Homo sapi
BC012147 Homo sapi
BC064466 Mus muscu
AC146464 Salmiri s
BC064270 Xenopus t
BC042196 Homo sapi
BC025349 Homo sapi
AC140335 Mus muscu
BC049625 Mus muscu
CQ078603 Sequence
CQ074687 Xenopus t
BC043584 Homo sapi
BC044232 Homo sapi
BC061098 Mus muscu
BC060504 Mus muscu
BC021410 Mus muscu
BC032495 Homo sapi
BX648018 Homo sapi
AC117731 Mus muscu
AL807787 Mus muscu
AL671901 Mouse DNA
CQ408183 Sequence
BC035323 Mus muscu
BC066725 Danio rer
BC061208 Mus muscu
AX683129 Sequence
S68736 Rattus sp.
AL136787 Homo sapi
CQ493127 Sequence
CQ493522 Sequence
AX279994 Sequence
AX356432 Sequence
AC139387 Rattus no
AC102668 Mus muscu
AC125223 Mus muscu
AC094848 Rattus no
AC094254 Rattus no
AX344556 Sequence
AX187085 Sequence
CQ670102 Sequence
AK174309 Ciona int
AL049466 Homo sapi
BC049725 Mus muscu
BC035292 Homo sapi
BC049565 Mus muscu
BC043747 Mus muscu
BC050385 Homo sapi
BC038597 Homo sapi
BC044242 Homo sapi
AX346598 Sequence
AL929570 Mouse DNA
CQ487162 Sequence
I48979 Sequence 6

C 385	50.2	3.0	383	6	CQ502211	Sequence	C 458	49.8	3.0	8712	6	AX344694	AX344694	Sequence
C 386	50.2	3.0	383	6	CQ511079	Sequence	C 459	49.8	3.0	13758	3	SST558163	AJ558163	Strongylo
C 387	50.2	3.0	384	6	CQ395463	Sequence	C 460	49.8	3.0	84299	5	BX469900	BX469900	Zebrafish
C 388	50.2	3.0	384	6	CQ401799	Sequence	C 461	49.8	3.0	132068	9	AC006965	AC006965	Homo sapi
C 389	50.2	3.0	384	6	CQ487104	Sequence	C 462	49.8	3.0	156254	10	AC129196	AC129196	Homo sapi
C 390	50.2	3.0	448	6	CQ516969	Sequence	C 463	49.8	3.0	183762	2	AC128232	AC128232	Rattus no
C 391	50.2	3.0	861	9	AK026600	Homo sapi	C 464	49.8	3.0	193796	2	AC123600	AC123600	Mus muscu
C 392	50.2	3.0	1090	10	BC049543	BC049543 Mus muscu	C 465	49.8	3.0	198615	10	AC123678	AC123678	Mus muscu
C 393	50.2	3.0	1448	10	BC052344	BC052344 Mus muscu	C 466	49.8	3.0	212604	5	AL805945	AL805945	Zebrafish
C 394	50.2	3.0	1619	9	BC032001	BC032001 Homo sapi	C 467	49.8	3.0	218319	2	AC107863	AC107863	Mus muscu
C 395	50.2	3.0	2078	9	BC042098	BC042098 Homo sapi	C 468	49.8	3.0	251721	2	AC135666	AC135666	Rattus no
C 396	50.2	3.0	2104	9	BC032371	BC032371 Homo sapi	C 469	49.8	3.0	263341	2	AC094581	AC094581	Rattus no
C 397	50.2	3.0	2641	10	BC044860	BC044860 Mus muscu	C 470	49.8	3.0	266869	2	AC123456	AC123456	Rattus no
C 398	50.2	3.0	4064	10	BC072632	BC072632 Mus muscu	C 471	49.8	3.0	289973	2	AC135678	AC135678	Rattus no
C 399	50.2	3.0	6476	6	AX345442	AX345442 Sequence	C 472	49.6	3.0	762	9	BC070287	BC070287	Homo sapi
C 400	50.2	3.0	150751	9	AC092609	AC092609 Homo sapi	C 473	49.6	3.0	793	9	BC018189	BC018189	Homo sapi
C 401	50.2	3.0	168136	2	AC138388	AC138388 Mus muscu	C 474	49.6	3.0	1003	5	BC067645	BC067645	Danio rer
C 402	50.2	3.0	182871	3	AC117176	AC117176 Dictyoste	C 475	49.6	3.0	1044	9	AB019565	AB019565	Homo sapi
C 403	50.2	3.0	189631	2	AC009920	AC009920 Homo sapi	C 476	49.6	3.0	1218	9	BC065742	BC065742	Homo sapi
C 404	50.2	3.0	203114	2	AC011818	AC011818 Homo sapi	C 477	49.6	3.0	1250	9	BC051908	BC051908	Homo sapi
C 405	50.2	3.0	349980	6	AX344553	AX344553 Sequence	C 478	49.6	3.0	1271	9	AF090934	AF090934	Homo sapi
C 406	50	3.0	325	6	CQ527169	Sequence	C 479	49.6	3.0	1340	9	BC073835	BC073835	Homo sapi
C 407	50	3.0	464	6	CQ519083	Sequence	C 480	49.6	3.0	1458	9	BC041443	BC041443	Homo sapi
C 408	50	3.0	471	6	CQ522475	Sequence	C 481	49.6	3.0	1530	9	BC036925	BC036925	Homo sapi
C 409	50	3.0	646	5	BC083988	BC083988 Xenopus 1	C 482	49.6	3.0	1606	10	BC051176	BC051176	Mus muscu
C 410	50	3.0	653	10	BC039566	BC039566 Mus muscu	C 483	49.6	3.0	1657	8	NTACCS	X98492	Nicotiana t
C 411	50	3.0	842	9	BC051899	BC051899 Homo sapi	C 484	49.6	3.0	1787	9	BC046645	BC046645	Homo sapi
C 412	50	3.0	870	6	BD231569	BD231569 31 human	C 485	49.6	3.0	1993	3	AK112520	AK112520	Ciona int
C 413	50	3.0	2240	9	BC062587	BC062587 Homo sapi	C 486	49.6	3.0	2027	9	BC063512	BC063512	Homo sapi
C 414	50	3.0	2556	9	HSN805953	HSN805953 Homo sapi	C 487	49.6	3.0	2081	9	HSN806272	HSN806272	Homo sapi
C 415	50	3.0	2936	5	BC077828	BC077828 Xenopus 1	C 488	49.6	3.0	2135	10	BC017640	BC017640	Mus muscu
C 416	50	3.0	3203	9	BC040341	BC040341 Homo sapi	C 489	49.6	3.0	2161	6	CQ414527	CQ414527	Sequence
C 417	50	3.0	3645	10	BC062916	BC062916 Mus muscu	C 490	49.6	3.0	2350	9	BC063427	BC063427	Homo sapi
C 418	50	3.0	3806	5	AJ720876	AJ720876 Gallus ga	C 491	49.6	3.0	2521	10	BC026021	BC026021	Mus muscu
C 419	50	3.0	4942	9	HSN808887	HSN808887 Homo sapi	C 492	49.6	3.0	2870	9	HSN800882	HSN800882	Homo sapi
C 420	50	3.0	5387	6	AX344633	AX344633 Sequence	C 493	49.6	3.0	3141	10	BC017634	BC017634	Mus muscu
C 421	50	3.0	9747	9	HSN806689	HSN806689 Homo sapi	C 494	49.6	3.0	3232	9	AF090901	AF090901	Homo sapi
C 422	50	3.0	21537	6	AX346901	AX346901 Sequence	C 495	49.6	3.0	3914	9	HSN803724	HSN803724	Homo sapi
C 423	50	3.0	110090	2	PFM413_07	Continuation (8 of	C 496	49.6	3.0	4385	9	HSN806219	HSN806219	Homo sapi
C 424	50	3.0	137697	2	AC126413	AC126419 Mus muscu	C 497	49.6	3.0	5134	9	BC032404	BC032404	Homo sapi
C 425	50	3.0	160706	2	AC137910	AC137910 Canis fam	C 498	49.6	3.0	5355	9	HSN806819	HSN806819	Homo sapi
C 426	50	3.0	173053	10	AL844145	AL844145 Mouse DNA	C 499	49.6	3.0	5520	6	AX345420	AX345420	Sequence
C 427	50	3.0	184057	10	AL928579	AL928579 Mouse DNA	C 500	49.6	3.0	6015	6	AX345579	AX345579	Sequence
C 428	50	3.0	184163	2	AC120245	AC120245 Rattus no	C 501	49.6	3.0	110000	2	AC102349	AC102349	Mus muscu
C 429	50	3.0	189649	2	AC139641	AC139641 Rattus no	C 502	49.6	3.0	142948	9	AC147025	AC147025	Pan trogl
C 430	50	3.0	212996	2	CR548633	CR548633 Danio rer	C 503	49.6	3.0	151802	3	AC114263	AC114263	Dictyoste
C 431	50	3.0	245677	10	AC129162	AC129162 Rattus no	C 504	49.6	3.0	173854	2	AC073047	AC073047	Homo sapi
C 432	50	3.0	249734	2	AC097362	AC097362 Rattus no	C 505	49.6	3.0	187418	10	AL672278	AL672278	Mouse DNA
C 433	49.8	3.0	263	6	CQ663258	CQ663258 Sequence	C 506	49.6	3.0	194398	10	AC135669	AC135669	Mus muscu
C 434	49.8	3.0	270	6	CQ655781	CQ655781 Sequence	C 507	49.6	3.0	214029	2	AC148335	AC148335	Mus muscu
C 435	49.8	3.0	311	6	CQ517391	CQ517391 Sequence	C 508	49.6	3.0	349980	6	AX344563	AX344563	Sequence
C 436	49.8	3.0	376	6	CQ526056	Sequence	C 509	49.4	2.9	408	6	CQ524818	CQ524818	Sequence
C 437	49.8	3.0	381	6	CQ522618	Sequence	C 510	49.4	2.9	438	6	CQ514042	CQ514042	Sequence
C 438	49.8	3.0	543	6	CQ524637	Sequence	C 511	49.4	2.9	481	9	BC070219	BC070219	Homo sapi
C 439	49.8	3.0	545	6	AX185705	AX185705 Sequence	C 512	49.4	2.9	579	6	CQ526842	CQ526842	Sequence
C 440	49.8	3.0	573	11	BY060605	BY060605 S209P6332	C 513	49.4	2.9	622	6	CQ427774	CQ427774	Sequence
C 441	49.8	3.0	726	9	HS4327951	AJ327951 Homo sapi	C 514	49.4	2.9	658	6	BD275413	BD275413	50 Human
C 442	49.8	3.0	815	9	BC070265	BC070265 Homo sapi	C 515	49.4	2.9	781	10	BC028530	BC028530	Mus muscu
C 443	49.8	3.0	854	3	AK174348	AK174348 Ciona int	C 516	49.4	2.9	1081	9	BC043527	BC043527	Homo sapi
C 444	49.8	3.0	894	9	BC044257	BC044257 Homo sapi	C 517	49.4	2.9	1310	9	HSN807559	HSN807559	Homo sapi
C 445	49.8	3.0	1048	6	BD223102	BD223102 98 human	C 518	49.4	2.9	1589	9	BC043543	BC043543	Homo sapi
C 446	49.8	3.0	1048	6	AR243800	AR243800 Sequence	C 519	49.4	2.9	1603	6	CQ490224	CQ490224	Sequence
C 447	49.8	3.0	1073	6	BD190930	BD190930 Secreted	C 520	49.4	2.9	1603	6	CQ491236	CQ491236	Sequence
C 448	49.8	3.0	1824	9	BC018641	BC018641 Homo sapi	C 521	49.4	2.9	1603	6	CQ496086	CQ496086	Sequence
C 449	49.8	3.0	1837	6	AX962574	AX962574 Sequence	C 522	49.4	2.9	1603	6	CQ497104	CQ497104	Sequence
C 450	49.8	3.0	2005	9	BC013372	BC013372 Homo sapi	C 523	49.4	2.9	1647	9	HSN806060	HSN806060	Homo sapi
C 451	49.8	3.0	2012	9	AY125488	AY125488 Homo sapi	C 524	49.4	2.9	2002	9	BC068030	BC068030	Homo sapi
C 452	49.8	3.0	2266	9	BC047898	BC047898 Homo sapi	C 525	49.4	2.9	2395	9	AF090903	AF090903	Homo sapi
C 453	49.8	3.0	2496	6	BD191411	BD191411 Secreted	C 526	49.4	2.9	3475	9	HSN808741	HSN808741	Homo sapi
C 454	49.8	3.0	2539	9	BC041100	BC041100 Homo sapi	C 527	49.4	2.9	4066	10	BC048824	BC048824	Mus muscu
C 455	49.8	3.0	2630	9	BC038222	BC038222 Homo sapi	C 528	49.4	2.9	4744	5	BC066770	BC066770	Xenopus 1
C 456	49.8	3.0	3230	9	BC063118	BC063118 Homo sapi	C 529	49.4	2.9	4782	14	AY744492	AY744492	Tomato sp
C 457	49.8	3.0	7346	6	AX345247	AX345247 Sequence	C 530	49.4	2.9	71532	2	AC023655	AC023655	Homo sapi

C 531	49.4	2.9	84821	10	BX276123	Mouse DNA	604	49	2.9	2700	9	BC064849	BC064849 Homo sapi
C 532	49.4	2.9	110000	3	AC116305	Dictyoste	605	49	2.9	2728	9	BC022218	BC022218 Homo sapi
C 533	49.4	2.9	138604	2	CR847865	Danio rer	606	49	2.9	3020	10	BC055068	BC055068 Mus muscu
C 534	49.4	2.9	169736	2	AC126225	Papio anu	607	49	2.9	3482	9	BSM000550	AL050393 Homo sapi
C 535	49.4	2.9	187024	2	CR759947	Gorilla g	608	49	2.9	3499	10	BC007476	AL050393 Homo sapi
C 536	49.4	2.9	221273	2	AC141526	Rattus no	609	49	2.9	3856	9	BSM005531	AL050393 Homo sapi
C 537	49.4	2.9	335050	3	PF929336	Alu29356	610	49	2.9	3870	9	BSM006049	AL050393 Homo sapi
C 538	49.4	2.9	349980	6	AC344559	Sequence	611	49	2.9	3916	10	BC018439	BC018439 Mus muscu
C 539	49.4	2.9	349980	6	AC344566	Sequence	612	49	2.9	5703	10	BC054080	BC054080 Mus muscu
C 540	49.4	2.9	442	6	CQ526679	Sequence	613	49	2.9	5845	6	AC346564	AC346564 Sequence
C 541	49.2	2.9	539	6	CQ526992	Sequence	614	49	2.9	5930	6	CQ412529	CQ412529 Sequence
C 542	49.2	2.9	544	6	CQ524776	Sequence	615	49	2.9	6012	6	AC346960	AC346960 Sequence
C 543	49.2	2.9	554	6	CQ526772	Sequence	616	49	2.9	6161	6	AC345313	AC345313 Sequence
C 544	49.2	2.9	575	6	CQ526566	Sequence	617	49	2.9	6211	6	AC345708	AC345708 Sequence
C 545	49.2	2.9	621	6	AC187131	Sequence	618	49	2.9	6522	6	AC345952	AC345952 Sequence
C 546	49.2	2.9	650	9	BC034814	Homo sapi	619	49	2.9	6719	9	BSM003507	AL050393 Homo sapi
C 547	49.2	2.9	758	9	BC062750	Homo sapi	620	49	2.9	11416	6	AC251758	AC251758 Sequence
C 548	49.2	2.9	1191	9	BC014547	Homo sapi	621	49	2.9	11416	6	AC345020	AC345020 Sequence
C 549	49.2	2.9	1381	5	BC063358	Xenopus t	622	49	2.9	11416	6	AC348567	AC348567 Sequence
C 550	49.2	2.9	1537	9	BSM003079	AL713709	623	49	2.9	40862	6	AC346974	AC346974 Sequence
C 551	49.2	2.9	1629	10	BC033451	BC033451 Mus muscu	624	49	2.9	135020	9	AF429315	AF429315 Homo sapi
C 552	49.2	2.9	1702	9	BC052393	BC052393 Homo sapi	625	49	2.9	135050	2	AC118536	AC118536 Canis fam
C 553	49.2	2.9	2270	9	BSM06047	BSM06047 Homo sapi	626	49	2.9	160230	10	BSM072552	BSM072552 Mouse DNA
C 554	49.2	2.9	2451	9	BC050636	BC050636 Homo sapi	627	49	2.9	180352	2	AC120550	AC120550 Mus muscu
C 555	49.2	2.9	2501	6	AC599024	AC599024 Sequence	628	49	2.9	198792	2	AC117825	AC117825 Mus muscu
C 556	49.2	2.9	2628	9	BC032691	BC032691 Homo sapi	629	49	2.9	203422	2	AC107857	AC107857 Mus muscu
C 557	49.2	2.9	2661	10	BC026137	BC026137 Mus muscu	630	49	2.9	248353	2	AC106139	AC106139 Rattus no
C 558	49.2	2.9	3030	3	AK116919	Ciona int	631	49	2.9	349980	6	AC344561	AC344561 Sequence
C 559	49.2	2.9	3300	9	BC011656	BC011656 Homo sapi	632	49	2.9	349980	6	AC344565	AC344565 Sequence
C 560	49.2	2.9	3341	9	BC032308	BC032308 Homo sapi	633	49	2.9	299	6	CQ397773	CQ397773 Sequence
C 561	49.2	2.9	3392	3	AF300334	AF300334 Dictyoste	634	49	2.9	299	6	CQ404070	CQ404070 Sequence
C 562	49.2	2.9	3686	10	BC032373	BC032373 Mus muscu	635	49	2.9	308	6	CQ517578	CQ517578 Sequence
C 563	49.2	2.9	3836	9	BC063854	BC063854 Homo sapi	636	49	2.9	313	6	CQ523441	CQ523441 Sequence
C 564	49.2	2.9	4265	9	BSM07603	BSM07603 Homo sapi	637	49	2.9	326	6	CQ472519	CQ472519 Sequence
C 565	49.2	2.9	6644	6	E23356	E23356 Virus vecto	638	49	2.9	445	6	CQ487730	CQ487730 Sequence
C 566	49.2	2.9	7058	6	AC348438	AC348438 Sequence	639	49	2.9	489	6	CQ491815	CQ491815 Sequence
C 567	49.2	2.9	7372	6	E23357	E23357 Virus vecto	640	49	2.9	489	6	CQ497713	CQ497713 Sequence
C 568	49.2	2.9	7797	6	E23355	E23355 Virus vecto	641	49	2.9	510	6	CQ526266	CQ526266 Sequence
C 569	49.2	2.9	7996	6	E23359	E23359 Virus vecto	642	49	2.9	836	6	AX704815	AX704815 Sequence
C 570	49.2	2.9	11394	6	AX233608	AX233608 Sequence	643	49	2.9	844	9	BC009571	BC009571 Homo sapi
C 571	49.2	2.9	35962	6	AX598904	AX598904 Sequence	644	49	2.9	1007	10	BC049692	BC049692 Mus muscu
C 572	49.2	2.9	153064	9	AC011492	AC011492 Homo sapi	645	49	2.9	1345	10	BC048718	BC048718 Mus muscu
C 573	49.2	2.9	162473	9	AC005903	AC005903 Homo sapi	646	49	2.9	1362	9	BC065292	BC065292 Homo sapi
C 574	49.2	2.9	226142	2	AC126422	AC126422 Mus muscu	647	49	2.9	1462	10	BC006018	BC006018 Mus muscu
C 575	49.2	2.9	245117	2	AC111284	AC111284 Rattus no	648	49	2.9	1570	10	BC049624	BC049624 Mus muscu
C 576	49.2	2.9	302156	3	AC116977	AC116977 Dictyoste	649	49	2.9	1770	9	BC025717	BC025717 Homo sapi
C 577	49.2	2.9	349980	6	AC344573	AC344573 Sequence	650	49	2.9	1813	6	AR164089	AR164089 Sequence
C 578	49	2.9	256	6	AX182154	AX182154 Sequence	651	49	2.9	1990	10	BC042668	BC042668 Mus muscu
C 579	49	2.9	347	6	CQ526680	CQ526680 Sequence	652	49	2.9	2064	10	BC053424	BC053424 Mus muscu
C 580	49	2.9	429	6	CQ525532	CQ525532 Sequence	653	49	2.9	2394	5	BC063911	BC063911 Xenopus t
C 581	49	2.9	469	6	CQ524790	CQ524790 Sequence	654	49	2.9	2500	9	BC065207	BC065207 Homo sapi
C 582	49	2.9	472	6	CQ525172	CQ525172 Sequence	655	49	2.9	2735	9	BC046366	BC046366 Homo sapi
C 583	49	2.9	541	6	CQ522598	CQ522598 Sequence	656	49	2.9	2823	9	BC018694	BC018694 Homo sapi
C 584	49	2.9	608	10	BC061544	BC061544 Rattus no	657	49	2.9	2968	9	BC060758	BC060758 Homo sapi
C 585	49	2.9	757	9	BC051791	BC051791 Homo sapi	658	49	2.9	3134	9	BSM005794	BSM005794 Homo sapi
C 586	49	2.9	967	9	BSM080277	BSM080277 Homo sapi	659	49	2.9	3380	9	BSM080723	BSM080723 Homo sapi
C 587	49	2.9	1232	3	BC060554	BC060554 Rattus no	660	49	2.9	4436	10	BSM08961	BSM08961 Homo sapi
C 588	49	2.9	1414	3	AK112149	AK112149 Ciona int	661	49	2.9	4454	9	BSM065344	BSM065344 Mus muscu
C 589	49	2.9	1755	9	BC031825	BC031825 Homo sapi	662	49	2.9	5378	6	AX346781	AX346781 Sequence
C 590	49	2.9	1763	5	AC079192	AC079192 Xenopus t	663	49	2.9	6386	9	BSM003518	BSM003518 Homo sapi
C 591	49	2.9	1850	9	BC040123	BC040123 Homo sapi	664	49	2.9	8339	6	AX458578	AX458578 Sequence
C 592	49	2.9	1853	10	BC052346	BC052346 Mus muscu	665	49	2.9	110000	2	AC10180	Continuation (3 of
C 593	49	2.9	1869	5	BC076804	BC076804 Xenopus 1	666	49	2.9	141914	2	AC108177	AC108177 Felis cat
C 594	49	2.9	1891	9	BSM07589	BSM07589 Homo sapi	667	49	2.9	174495	2	AC101795	AC101795 Mus muscu
C 595	49	2.9	1912	10	BC027060	BC027060 Mus muscu	668	49	2.9	175202	9	AC134684	AC134684 Homo sapi
C 596	49	2.9	1935	5	BC065678	BC065678 Danio rer	669	49	2.9	188884	9	AC130367	AC130367 Homo sapi
C 597	49	2.9	1954	6	BD270057	BD270057 Secreted	670	49	2.9	214132	2	AC124975	AC124975 Mus muscu
C 598	49	2.9	1960	9	BC038806	BC038806 Homo sapi	671	49	2.9	228842	10	AC116130	AC116130 Rattus no
C 599	49	2.9	2045	9	BC047761	BC047761 Homo sapi	672	49	2.9	273978	2	AC130001	AC130001 Rattus no
C 600	49	2.9	2116	9	BC034379	BC034379 Homo sapi	673	49	2.9	274097	2	AC111767	AC111767 Rattus no
C 601	49	2.9	2197	9	BC045177	BC045177 Homo sapi	674	49	2.9	349980	6	AX344564	AX344564 Sequence
C 602	49	2.9	2347	9	BC027875	BC027875 Homo sapi	675	49	2.9	291	6	CQ398062	CQ398062 Sequence
C 603	49	2.9	2553	10	BC061558	BC061558 Rattus no	676	49	2.9	291	6	CQ404353	CQ404353 Sequence

677	48.6	2.9	320	6	CQ517221	Sequence	750	48.4	2.9	3942	10	BC063741	BC063741 Mus muscu
c 678	48.6	2.9	425	6	CQ506214	Sequence	751	48.4	2.9	4073	6	AX269342	AX269342 Sequence
679	48.6	2.9	471	6	CQ515907	Sequence	c 752	48.4	2.9	4316	6	CQ806814	CQ806814 Sequence
680	48.6	2.9	547	9	BC070202	Homo sapi	c 753	48.4	2.9	4316	6	CQ807088	CQ807088 Sequence
681	48.6	2.9	816	6	CQ486089	Sequence	c 754	48.4	2.9	4316	6	AX795752	AX795752 Sequence
682	48.6	2.9	835	9	HSM801514	Sequence	c 755	48.4	2.9	4316	6	AX795868	AX795868 Sequence
683	48.6	2.9	843	10	BC026460	Homo sapi	c 756	48.4	2.9	4316	6	AX822260	AX822260 Sequence
684	48.6	2.9	932	9	BC043537	Homo sapi	c 757	48.4	2.9	4316	6	AX822388	AX822388 Sequence
685	48.6	2.9	1486	9	BC042084	Homo sapi	c 758	48.4	2.9	4316	6	AX825900	AX825900 Sequence
686	48.6	2.9	1569	10	BC083659	Rattus no	c 759	48.4	2.9	4316	6	AX826028	AX826028 Sequence
687	48.6	2.9	1642	5	BC064224	Xenopus t	c 760	48.4	2.9	5195	6	AX345823	AX345823 Sequence
688	48.6	2.9	1781	9	BC043529	Homo sapi	c 761	48.4	2.9	6070	6	AX281468	AX281468 Sequence
689	48.6	2.9	1808	6	AX535019	Sequence	c 762	48.4	2.9	6070	6	AX346581	AX346581 Sequence
690	48.6	2.9	1959	9	BC043548	Homo sapi	c 763	48.4	2.9	6070	6	AX348804	AX348804 Sequence
691	48.6	2.9	1994	3	AK116078	Ciona int	c 764	48.4	2.9	6070	6	AX458614	AX458614 Sequence
692	48.6	2.9	2009	9	BC050391	Homo sapi	c 765	48.4	2.9	6577	6	AX251920	AX251920 Sequence
693	48.6	2.9	2034	6	AX127529	Sequence	c 766	48.4	2.9	6577	6	AX346258	AX346258 Sequence
694	48.6	2.9	2034	6	AX675184	Sequence	c 767	48.4	2.9	6577	6	AX348993	AX348993 Sequence
695	48.6	2.9	2390	9	AF090900	Homo sapi	c 768	48.4	2.9	6690	9	HSM803755	HSM803755 Sequence
696	48.6	2.9	3000	9	BC036812	Homo sapi	c 769	48.4	2.9	6849	10	BS324169	BS324169 Mouse DNA
c 697	48.6	2.9	5532	6	AX345680	Sequence	c 770	48.4	2.9	6944	6	AX347467	AX347467 Sequence
c 698	48.6	2.9	8946	6	AX345813	Sequence	c 771	48.4	2.9	6944	6	AX349188	AX349188 Sequence
c 699	48.6	2.9	14615	6	AX251461	Sequence	c 772	48.4	2.9	6944	6	AX657867	AX657867 Sequence
700	48.6	2.9	68222	9	AL391904	Human DNA	c 773	48.4	2.9	7467	6	AX659141	AX659141 Sequence
c 701	48.6	2.9	111865	2	AL355883	Homo sapi	c 774	48.4	2.9	7467	6	AX828406	AX828406 Sequence
c 702	48.6	2.9	139772	2	AC068270	Homo sapi	c 775	48.4	2.9	8546	6	AX828406	AX828406 Sequence
c 703	48.6	2.9	151736	2	AC138596	Mus muscu	c 776	48.4	2.9	8546	6	AX828406	AX828406 Sequence
c 704	48.6	2.9	157311	10	AC132236	Mus muscu	c 777	48.4	2.9	9117	6	AX345970	AX345970 Sequence
705	48.6	2.9	167489	5	BX664600	Zebrafish	c 778	48.4	2.9	11097	6	AX828972	AX828972 Sequence
706	48.6	2.9	167728	2	AC115889	Mus muscu	c 779	48.4	2.9	11097	6	AX828974	AX828974 Sequence
707	48.6	2.9	177083	10	AC126805	Mus muscu	780	48.4	2.9	18207	9	AX828384	AX828384 Sequence
708	48.6	2.9	181226	10	AC147111	Mus muscu	781	48.4	2.9	18207	9	AF156100	AF156100 Homo sapi
709	48.6	2.9	182229	2	AC145600	Mus muscu	782	48.4	2.9	26459	9	AL390854	AL390854 Human DNA
c 710	48.6	2.9	184736	10	AL808128	Mouse DNA	783	48.4	2.9	42839	2	AC027282	AC027282 Homo sapi
c 711	48.6	2.9	185291	2	AC123147	Rattus no	c 784	48.4	2.9	73778	6	AX344575	AX344575 Sequence
c 712	48.6	2.9	206324	10	AL807786	Mouse DNA	c 785	48.4	2.9	145275	9	AF189745	AF189745 Homo sapi
713	48.6	2.9	210233	2	AC073684	Sequence	c 786	48.4	2.9	149813	2	AX942840	AX942840 Danio rer
714	48.6	2.9	210269	2	AX927280	Danio rer	c 787	48.4	2.9	165146	2	AP002415	AP002415 Homo sapi
c 715	48.6	2.9	212557	2	AC120134	Mus muscu	c 788	48.4	2.9	167671	2	AC142166	AC142166 Mus muscu
c 716	48.6	2.9	212908	2	CR847533	Danio rer	c 789	48.4	2.9	176929	9	AC004887	AC004887 Homo sapi
c 717	48.6	2.9	221023	10	AL844487	Mouse DNA	c 790	48.4	2.9	182871	3	AC117176	AC117176 Dictyoste
718	48.6	2.9	231447	2	AC121422	Rattus no	c 791	48.4	2.9	183648	3	C1117081	C1117081 Dictyoste
c 719	48.6	2.9	269576	2	AC073684	Sequence	c 792	48.4	2.9	188555	10	AC122417	AC122417 Mus muscu
720	48.4	2.9	147	6	AR418886	Sequence	c 793	48.4	2.9	198377	2	CR792437	CR792437 Danio rer
721	48.4	2.9	147	6	AX979580	Sequence	c 794	48.4	2.9	199472	9	AC022267	AC022267 Homo sapi
722	48.4	2.9	147	6	BD114439	BST and e	c 795	48.4	2.9	204278	10	AC124507	AC124507 Mus muscu
723	48.4	2.9	186	6	CQ677473	Sequence	c 796	48.4	2.9	208921	2	AP001911	AP001911 Homo sapi
c 724	48.4	2.9	388	6	CQ410454	Sequence	c 797	48.4	2.9	215676	2	AC131299	AC131299 Mus muscu
725	48.4	2.9	432	6	CQ524989	Sequence	c 798	48.4	2.9	221944	2	AC119914	AC119914 Mus muscu
726	48.4	2.9	451	6	CQ524930	Sequence	c 799	48.4	2.9	228178	2	AC101866	AC101866 Mus muscu
727	48.4	2.9	661	10	BC051629	Mus muscu	c 800	48.4	2.9	232304	2	AC103201	AC103201 Rattus no
728	48.4	2.9	1078	9	BC035314	Homo sapi	c 801	48.4	2.9	258658	3	AE014832	AE014832 Plasmodi
729	48.4	2.9	1117	6	AR123345	Sequence	c 802	48.4	2.9	349980	6	AX344558	AX344558 Sequence
730	48.4	2.9	1175	5	BC049447	Danio rer	c 803	48.4	2.9	349980	6	AX344570	AX344570 Sequence
731	48.4	2.9	1445	9	BC063345	Homo sapi	c 804	48.2	2.9	268	6	AX340795	AX340795 Sequence
732	48.4	2.9	1550	9	BC063432	Homo sapi	c 805	48.2	2.9	268	6	AX185659	AX185659 Sequence
733	48.4	2.9	1586	9	BC027982	Homo sapi	c 806	48.2	2.9	317	6	CQ526915	CQ526915 Sequence
734	48.4	2.9	1727	10	BC050800	Mus muscu	c 807	48.2	2.9	359	6	CQ431130	CQ431130 Sequence
735	48.4	2.9	1872	9	BC038952	Homo sapi	c 808	48.2	2.9	385	6	CQ398297	CQ398297 Sequence
736	48.4	2.9	1978	9	BC012750	Homo sapi	c 809	48.2	2.9	385	6	CQ404584	CQ404584 Sequence
737	48.4	2.9	2065	5	BC066376	Danio rer	c 810	48.2	2.9	430	9	BC062435	BC062435 Homo sapi
738	48.4	2.9	2138	5	AB060903	Macaca fa	c 811	48.2	2.9	453	6	CQ517526	CQ517526 Sequence
739	48.4	2.9	2284	5	BC063964	Danio rer	c 812	48.2	2.9	504	6	CQ525672	CQ525672 Sequence
740	48.4	2.9	2265	9	BC063477	Homo sapi	c 813	48.2	2.9	527	10	BC049658	BC049658 Mus muscu
741	48.4	2.9	2402	5	BC077592	Xenopus l	c 814	48.2	2.9	633	10	BC059147	BC059147 Rattus no
742	48.4	2.9	2652	3	AK174388	Ciona int	c 815	48.2	2.9	724	10	BC049721	BC049721 Mus muscu
743	48.4	2.9	2679	10	BC006021	Mus muscu	c 816	48.2	2.9	745	10	BC049606	BC049606 Mus muscu
744	48.4	2.9	3270	9	BC050552	Homo sapi	c 817	48.2	2.9	1119	10	BC021629	BC021629 Mus muscu
745	48.4	2.9	3422	9	HSM805920	Sequence	c 818	48.2	2.9	1561	9	BC040443	BC040443 Homo sapi
746	48.4	2.9	3454	9	HSM802993	Homo sapi	c 819	48.2	2.9	1608	10	BC057455	BC057455 Mus muscu
747	48.4	2.9	3498	5	BC065888	Danio rer	c 820	48.2	2.9	1725	5	BC080409	BC080409 Xenopus l
748	48.4	2.9	3521	9	BC027712	Homo sapi	c 821	48.2	2.9	1770	10	BC060519	BC060519 Rattus no
749	48.4	2.9	3810	9	HSM803390	Homo sapi	c 822	48.2	2.9	1942	10	BC062081	BC062081 Rattus no

823	48.2	2.9	2038	6	AX573129	Sequence	896	48	2.9	1985	9	AY358500	AY358500 Homo sapi
824	48.2	2.9	2096	10	BC034131	BC034131 Mus muscu	897	48	2.9	2003	9	BC051760	BC051760 Homo sapi
825	48.2	2.9	2137	9	AB062938	Macaca fa	898	48	2.9	2081	10	BC043712	BC043712 Mus muscu
826	48.2	2.9	2406	9	BC017107	Homo sapi	899	48	2.9	2155	9	BC075814	BC075814 Homo sapi
827	48.2	2.9	4765	5	BC068982	Danio rer	900	48	2.9	2202	10	BC052362	BC052362 Mus muscu
828	48.2	2.9	7037	6	AX346553	Sequence	901	48	2.9	2209	9	BC063878	BC063878 Homo sapi
829	48.2	2.9	7238	6	AX343550	Sequence	902	48	2.9	2248	5	BC068963	BC068963 Xenopus l
830	48.2	2.9	8895	6	AX345234	Sequence	903	48	2.9	2590	9	BC064421	BC064421 Homo sapi
831	48.2	2.9	11996	6	AX281381	Sequence	904	48	2.9	2632	9	BC030698	BC030698 Homo sapi
832	48.2	2.9	110000	2	AL954350	Continuation (5 of	905	48	2.9	2777	5	BC063344	BC063344 Xenopus t
833	48.2	2.9	157996	10	AL772203	Mouse DNA	906	48	2.9	2905	3	AK174395	AK174395 Ciona int
834	48.2	2.9	161297	10	AC139135	Mus muscu	907	48	2.9	2915	10	BC061479	BC061479 Mus muscu
835	48.2	2.9	167418	10	AC133944	Mus muscu	908	48	2.9	3223	6	CQ806938	CQ806938 Sequence
836	48.2	2.9	172928	10	AC123735	Mus muscu	909	48	2.9	3223	6	CQ807212	CQ807212 Sequence
837	48.2	2.9	179206	2	AC113199	Mus muscu	910	48	2.9	3723	9	BSM80835	BSM80835 Sequence
838	48.2	2.9	185634	2	AC119930	Mus muscu	911	48	2.9	3880	10	BC048229	BC048229 Mus muscu
839	48.2	2.9	195888	10	AC114604	Mus muscu	912	48	2.9	3973	6	AX345073	AX345073 Sequence
840	48.2	2.9	218297	2	AC126035	Mus muscu	913	48	2.9	3983	9	BSM803572	BSM803572 Sequence
841	48.2	2.9	219106	10	AC123640	Mus muscu	914	48	2.9	4306	10	BC059824	BC059824 Homo sapi
842	48.2	2.9	22725	2	AC110732	Mus muscu	915	48	2.9	4389	10	BC058345	BC058345 Mus muscu
843	48.2	2.9	257700	2	AC147391	Pan trogl	916	48	2.9	5070	6	AX345703	AX345703 Sequence
844	48	2.9	312	6	CQ699683	Sequence	917	48	2.9	5338	9	BSM808825	BSM808825 Sequence
845	48	2.9	323	6	CQ524910	Sequence	918	48	2.9	5774	10	BC060122	BC060122 Mus muscu
846	48	2.9	452	6	CQ527434	Sequence	919	48	2.9	6145	6	AX345875	AX345875 Sequence
847	48	2.9	515	6	CQ526571	Sequence	920	48	2.9	6192	6	AX251440	AX251440 Sequence
848	48	2.9	533	6	CQ525634	Sequence	921	48	2.9	12669	6	AX252150	AX252150 Sequence
849	48	2.9	540	6	CQ526524	Sequence	922	48	2.9	12669	6	AX344518	AX344518 Sequence
850	48	2.9	580	10	BC006049	Mus muscu	923	48	2.9	12669	6	AX348921	AX348921 Sequence
851	48	2.9	583	11	HUMUT5097	Human SPS U	924	48	2.9	18281	6	AX345864	AX345864 Sequence
852	48	2.9	585	6	CQ526237	Sequence	925	48	2.9	193342	5	EX465846	EX465846 Zebrafish
853	48	2.9	602	9	BC008488	Homo sapi	926	48	2.9	170496	2	AC140472	AC140472 Mus muscu
854	48	2.9	606	6	CQ503221	Sequence	927	48	2.9	184039	10	AC139376	AC139376 Mus muscu
855	48	2.9	606	6	CQ512068	Sequence	928	48	2.9	184365	2	AC079639	AC079639 Mus muscu
856	48	2.9	721	9	AK026526	Homo sapi	929	48	2.9	187028	10	BX119956	BX119956 Mouse DNA
857	48	2.9	760	9	BC032326	Homo sapi	930	48	2.9	194180	2	AC069140	AC069140 Homo sapi
858	48	2.9	836	10	BC049716	Mus muscu	931	48	2.9	200510	2	AC097048	AC097048 Rattus no
859	48	2.9	869	10	BC054421	Mus muscu	932	48	2.9	213401	2	AC124940	AC124940 Rattus no
860	48	2.9	927	10	BC047927	Mus muscu	933	48	2.9	224630	2	AC101853	AC101853 Mus muscu
861	48	2.9	988	5	BC055636	Danio rer	934	48	2.9	232080	2	AC145374	AC145374 Mus muscu
862	48	2.9	1248	5	BC071085	Xenopus l	935	48	2.9	232234	2	AC108634	AC108634 Rattus no
863	48	2.9	1277	5	BC084489	Xenopus t	936	48	2.9	239189	10	AC133208	AC133208 Mus muscu
864	48	2.9	1352	3	AX115954	Ciona int	937	48	2.9	247650	2	AC094213	AC094213 Rattus no
865	48	2.9	1391	5	BC074604	Xenopus t	938	48	2.9	257109	3	AC116963	AC116963 Dictyoste
866	48	2.9	1409	5	BC064261	Xenopus t	939	48	2.9	309805	2	AC026340	AC026340 Homo sapi
867	48	2.9	1409	10	BC040771	Mus muscu	940	48	2.9	321708	2	AC087142	AC087142 Mus muscu
868	48	2.9	1415	10	BC020016	Mus muscu	941	48	2.9	349980	6	AX344554	AX344554 Sequence
869	48	2.9	1426	5	BC054250	Xenopus l	942	48	2.9	349980	6	AX344555	AX344555 Sequence
870	48	2.9	1483	9	AK026528	Homo sapi	943	48	2.9	349980	6	AX344571	AX344571 Sequence
871	48	2.9	1526	5	BC084459	Xenopus t	944	47.8	2.8	212	6	CQ677317	CQ677317 Sequence
872	48	2.9	1608	9	AX358187	Homo sapi	945	47.8	2.8	233	6	CQ516563	CQ516563 Sequence
873	48	2.9	1622	9	BC043524	Homo sapi	946	47.8	2.8	309	6	CQ513146	CQ513146 Sequence
874	48	2.9	1632	5	BC068370	Danio rer	947	47.8	2.8	327	6	CQ408014	CQ408014 Sequence
875	48	2.9	1637	6	AX460089	Sequence	948	47.8	2.8	441	6	AR344256	AR344256 Sequence
876	48	2.9	1643	10	BC024405	Mus muscu	949	47.8	2.8	441	6	AX019230	AX019230 Sequence
877	48	2.9	1646	9	BC051812	Homo sapi	950	47.8	2.8	441	6	BD130456	BD130456 Expressio
878	48	2.9	1690	6	E32442	Mammal-Deri	951	47.8	2.8	497	6	CQ526425	CQ526425 Sequence
879	48	2.9	1720	10	BC046603	Mus muscu	952	47.8	2.8	498	6	CQ481059	CQ481059 Sequence
880	48	2.9	1727	5	BC071446	Danio rer	953	47.8	2.8	503	6	CQ524887	CQ524887 Sequence
881	48	2.9	1860	9	BC058897	Homo sapi	954	47.8	2.8	503	10	BC054554	BC054554 Mus muscu
882	48	2.9	1985	6	BD172402	Secreted	955	47.8	2.8	515	6	CQ522671	CQ522671 Sequence
883	48	2.9	1985	6	BD172721	Secreted	956	47.8	2.8	535	6	CQ471891	CQ471891 Sequence
884	48	2.9	1985	6	BD173040	Secreted	957	47.8	2.8	543	11	BV064080	BV064080 S208P6631
885	48	2.9	1985	6	BD173359	Secreted	958	47.8	2.8	548	6	CQ516864	CQ516864 Sequence
886	48	2.9	1985	6	BD175393	Secretory	959	47.8	2.8	574	6	CQ525654	CQ525654 Sequence
887	48	2.9	1985	6	CQ881212	Sequence	960	47.8	2.8	639	6	CQ399100	CQ399100 Sequence
888	48	2.9	1985	6	AR410771	Sequence	961	47.8	2.8	639	6	CQ405378	CQ405378 Sequence
889	48	2.9	1985	6	AR439135	Sequence	962	47.8	2.8	711	6	CQ422915	CQ422915 Sequence
890	48	2.9	1985	6	AR473155	Sequence	963	47.8	2.8	756	3	AK174008	AK174008 Ciona int
891	48	2.9	1985	6	AR527141	Sequence	964	47.8	2.8	791	9	BC038970	BC038970 Homo sapi
892	48	2.9	1985	6	AR566174	Sequence	965	47.8	2.8	798	10	BC005501	BC005501 Mus muscu
893	48	2.9	1985	6	AX375960	Sequence	966	47.8	2.8	872	6	AX068322	AX068322 Sequence
894	48	2.9	1985	6	AX697621	Sequence	967	47.8	2.8	885	3	AK174656	AK174656 Ciona int
895	48	2.9	1985	6	BD075542	Secretory	968	47.8	2.8	980	10	BC063173	BC063173 Rattus no

969	47.8	2.8	990	9	BC070127	BC070127 Homo sapi	c1042	47.8	2.8	113515	6	AX347077	AX347077 Sequence
970	47.8	2.8	995	9	BC043534	BC043534 Homo sapi	1043	47.8	2.8	114897	2	AP003624	AP003624 Oryza sat
971	47.8	2.8	1004	9	BC043536	BC043536 Homo sapi	1044	47.8	2.8	124048	10	AC134526	AC134526 Mus muscu
972	47.8	2.8	1035	10	BC055104	BC055104 Mus muscu	1045	47.8	2.8	133276	2	AC087147	AC087147 Mus muscu
c 973	47.8	2.8	1052	8	AB840524	AB840524 Arabidops	1046	47.8	2.8	143226	9	ALJ533802	ALJ533802 Human DNA
974	47.8	2.8	1080	9	HSN805509	AL834421 Homo sapi	c1047	47.8	2.8	167181	2	AC131701	AC131701 Mus muscu
975	47.8	2.8	1110	9	BC040953	BC040953 Homo sapi	c1048	47.8	2.8	168025	10	AC117778	AC117778 Mus muscu
976	47.8	2.8	1115	10	BC049575	BC049575 Mus muscu	c1049	47.8	2.8	175107	10	AC119911	AC119911 Mus muscu
977	47.8	2.8	1264	6	BD227246	BD227246 Secretd	c1050	47.8	2.8	198965	10	AC145606	AC145606 Mus muscu
978	47.8	2.8	1279	9	BC062634	BC062634 Homo sapi	1051	47.8	2.8	199101	10	MMAS000665	AE000665 Mus muscu
979	47.8	2.8	1345	9	BC073861	BC073861 Homo sapi	c1052	47.8	2.8	201293	2	AC118780	AC118780 Rattus no
980	47.8	2.8	1368	10	BC083654	BC083654 Rattus no	1053	47.8	2.8	204437	10	AC117678	AC117678 Mus muscu
981	47.8	2.8	1375	9	BC043554	BC043554 Homo sapi	c1054	47.8	2.8	205939	10	AC145469	AC145469 Mus muscu
982	47.8	2.8	1488	10	BC055456	BC055456 Mus muscu	c1055	47.8	2.8	209947	2	AC121454	AC121454 Rattus no
983	47.8	2.8	1500	5	BC065586	BC065586 Danio rer	1056	47.8	2.8	214331	2	AC141645	AC141645 Mus muscu
984	47.8	2.8	1580	5	BC067146	BC067146 Danio rer	c1057	47.8	2.8	216799	10	AC125382	AC125382 Mus muscu
985	47.8	2.8	1728	9	AB070110	AB070110 Macaca fa	1058	47.8	2.8	225000	2	AC123674	AC123674 Rattus no
986	47.8	2.8	1743	10	BC051150	BC051150 Mus muscu	1059	47.8	2.8	228302	2	AC109973	AC109973 Rattus no
987	47.8	2.8	1767	9	HSN800099	AL049314 Homo sapi	c1060	47.8	2.8	233887	2	AC133687	AC133687 Rattus no
988	47.8	2.8	1788	5	BC084147	BC084147 Xenopus t	1061	47.8	2.8	247796	2	AC094539	AC094539 Rattus no
989	47.8	2.8	1819	9	BC073865	BC073865 Homo sapi	c1062	47.8	2.8	252504	2	AC073815	AC073815 Mus muscu
990	47.8	2.8	1863	10	BC083817	BC083817 Rattus no	1063	47.8	2.8	252504	2	AC123658	AC123658 Rattus no
991	47.8	2.8	2076	5	BC053185	BC053185 Danio rer	c1064	47.8	2.8	256391	2	AC107557	AC107557 Rattus no
992	47.8	2.8	2158	9	AB070046	AB070046 Macaca fa	c1065	47.8	2.8	257501	2	AC097734	AC097734 Rattus no
993	47.8	2.8	2172	9	AB096591	AB096591 Macaca fa	1066	47.8	2.8	258819	2	AC118292	AC118292 Rattus no
994	47.8	2.8	2173	10	BC048927	BC048927 Mus muscu	1067	47.8	2.8	333321	3	AC116986	AC116986 Dictyoste
995	47.8	2.8	2208	10	BC052921	BC052921 Mus muscu	1068	47.6	2.8	333321	3	AC116986	AC116986 Dictyoste
996	47.8	2.8	2407	10	BC058192	BC058192 Mus muscu	1069	47.6	2.8	147	6	AR418757	AR418757 Sequence
997	47.8	2.8	2556	9	AF125948	AF125948 Homo sapi	1070	47.6	2.8	147	6	AX979451	AX979451 Sequence
998	47.8	2.8	3020	6	CQ491158	CQ491158 Sequence	1071	47.6	2.8	291	6	BD114310	BD114310 EST and e
999	47.8	2.8	3020	6	CQ497023	CQ497023 Sequence	c1072	47.6	2.8	345	6	CQ517629	CQ517629 Sequence
1000	47.8	2.8	3178	9	HSN803719	AL832411 Homo sapi	1073	47.6	2.8	358	6	CQ671266	CQ671266 Sequence
1001	47.8	2.8	3310	9	BC054816	BC054816 Homo sapi	1074	47.6	2.8	368	10	BC049735	BC049735 Mus muscu
1002	47.8	2.8	3430	9	BC065520	BC065520 Homo sapi	1075	47.6	2.8	376	6	CQ521729	CQ521729 Sequence
1003	47.8	2.8	3574	6	CQ412010	CQ412010 Sequence	1076	47.6	2.8	391	6	CQ524976	CQ524976 Sequence
1004	47.8	2.8	4057	10	BC067005	BC067005 Mus muscu	1077	47.6	2.8	394	6	CQ527287	CQ527287 Sequence
1005	47.8	2.8	4121	6	AR344255	AR344255 Sequence	1078	47.6	2.8	410	6	CQ522484	CQ522484 Sequence
1006	47.8	2.8	4121	6	AR344255	AR344255 Sequence	c1079	47.6	2.8	465	11	BV155767	BV155767 RPAMSGEQ
1007	47.8	2.8	4121	6	BD130455	BD130455 Expressio	1080	47.6	2.8	470	6	CQ516232	CQ516232 Sequence
1008	47.8	2.8	4213	5	BC084298	BC084298 Xenopus l	1081	47.6	2.8	479	6	CQ522457	CQ522457 Sequence
1009	47.8	2.8	4298	6	AX780085	AX780085 Sequence	1082	47.6	2.8	480	10	BC028543	BC028543 Mus muscu
1010	47.8	2.8	4562	9	HSN805779	BS537704 Homo sapi	1083	47.6	2.8	514	6	CQ522634	CQ522634 Sequence
1011	47.8	2.8	4536	10	BC057352	BC057352 Mus muscu	1084	47.6	2.8	520	6	CQ523964	CQ523964 Sequence
1012	47.8	2.8	4818	9	HSN807492	BK647348 Homo sapi	1085	47.6	2.8	529	5	BC053827	BC053827 Xenopus l
c1013	47.8	2.8	6486	6	AX458534	AX458534 Sequence	1086	47.6	2.8	631	10	MMU296942	AJ296942 Mus muscu
c1014	47.8	2.8	8079	6	AX356488	AX356488 Sequence	1087	47.6	2.8	732	5	AY522586	AY522586 Oreochrom
c1015	47.8	2.8	8298	6	AX344783	AX344783 Sequence	1088	47.6	2.8	873	6	AX780227	AX780227 Sequence
c1016	47.8	2.8	8913	6	AX599017	AX599017 Sequence	1089	47.6	2.8	889	10	BC049685	BC049685 Mus muscu
c1017	47.8	2.8	9021	6	AX347134	AX347134 Sequence	1090	47.6	2.8	959	9	BC031674	BC031674 Homo sapi
c1018	47.8	2.8	9021	6	AX347426	AX347426 Sequence	1091	47.6	2.8	1000	9	BSM806624	BS571748 Homo sapi
c1019	47.8	2.8	9021	6	AX348462	AX348462 Sequence	1092	47.6	2.8	1001	10	BC049605	BC049605 Mus muscu
c1020	47.8	2.8	9021	6	AX349147	AX349147 Sequence	1093	47.6	2.8	1130	10	BC043698	BC043698 Mus muscu
c1021	47.8	2.8	9021	6	AX657808	AX657808 Sequence	1094	47.6	2.8	1157	9	BC013883	BC013883 Homo sapi
c1022	47.8	2.8	9021	6	AX659082	AX659082 Sequence	1095	47.6	2.8	1314	5	BC054577	BC054577 Danio rer
c1023	47.8	2.8	11913	6	CQ787442	CQ787442 Sequence	1096	47.6	2.8	1343	10	BC061103	BC061103 Mus muscu
c1024	47.8	2.8	11913	6	CQ807085	CQ807085 Sequence	1097	47.6	2.8	1383	9	BC032432	BC032432 Homo sapi
c1025	47.8	2.8	11913	6	AX795865	AX795865 Sequence	1098	47.6	2.8	1408	10	BC048693	BC048693 Mus muscu
c1026	47.8	2.8	11913	6	AX822385	AX822385 Sequence	1099	47.6	2.8	1411	10	BC049571	BC049571 Mus muscu
c1027	47.8	2.8	11913	6	AX826025	AX826025 Sequence	1100	47.6	2.8	1412	3	AF083228	AF083228 Caenorhab
c1028	47.8	2.8	13606	6	AX251315	AX251315 Sequence	1101	47.6	2.8	1457	6	BD231695	BD231695 31 human
c1029	47.8	2.8	13606	6	AX278002	AX278002 Sequence	1102	47.6	2.8	1694	9	BC012597	BC012597 Homo sapi
c1030	47.8	2.8	13606	6	AX323699	AX323699 Sequence	1103	47.6	2.8	1744	8	BF009253	BF009253 Triticum
c1031	47.8	2.8	13606	6	AX346712	AX346712 Sequence	1104	47.6	2.8	1805	9	AB070053	AB070053 Macaca fa
c1032	47.8	2.8	15832	6	AX277943	AX277943 Sequence	1105	47.6	2.8	1820	5	BC066434	BC066434 Danio rer
c1033	47.8	2.8	15832	6	AX323630	AX323630 Sequence	1106	47.6	2.8	1836	10	BC034256	BC034256 Mus muscu
c1034	47.8	2.8	15832	6	AX346245	AX346245 Sequence	1107	47.6	2.8	1880	9	AB060863	AB060863 Macaca fa
1035	47.8	2.8	16156	2	AC149363	AC149363 Phakopsor	1108	47.6	2.8	2019	10	BC063758	BC063758 Mus muscu
c1036	47.8	2.8	56153	3	AC115682	AC115682 Dictyoste	1109	47.6	2.8	2085	5	BC077186	BC077186 Xenopus l
c1037	47.8	2.8	57538	3	AC101648	AC101648 Homo sapi	1110	47.6	2.8	2165	5	BC054602	BC054602 Danio rer
c1038	47.8	2.8	71021	2	AC101648	AC101648 Homo sapi	1111	47.6	2.8	2198	6	BD270040	BD270040 Secreted
c1039	47.8	2.8	99930	9	AC068640	AC068640 Homo sapi	1112	47.6	2.8	2284	9	AB055303	AB055303 Macaca fa
1040	47.8	2.8	104992	2	AC005504	AC005504 Plasmodiu	1113	47.6	2.8	2369	9	AK074384	AK074384 Homo sapi
c1041	47.8	2.8	110000	3	PFMAL1P2_0	AL0311745 Plasmodiu	1114	47.6	2.8	2420	5	BC066695	BC066695 Danio rer

1115	47.6	2.8	2447	6	AR079032	Sequence	AR079032	Sequence	47.6	2.8	187545	10	AC127550	Mus muscu
1116	47.6	2.8	2447	6	BD190886	Secreted	BD190886	Secreted	47.6	2.8	188823	2	AC101690	Homo sapi
1117	47.6	2.8	2447	6	BC027927	Homo sapi	BC027927	Homo sapi	47.6	2.8	194760	9	CNS01690	Human chr
1118	47.6	2.8	2501	6	AX598878	Sequence	AX598878	Sequence	47.6	2.8	199537	10	AL837510	Mouse DNA
1119	47.6	2.8	2607	5	BC054610	Danio rer	BC054610	Danio rer	47.6	2.8	202640	2	AC113851	Rattus no
1120	47.6	2.8	2610	10	BC063267	Mus muscu	BC063267	Mus muscu	47.6	2.8	211371	2	CR450764	Danio rer
1121	47.6	2.8	2621	10	MUS8RED	Mus muscu	L31396	Mus muscu	47.6	2.8	213397	2	AC125027	Mus muscu
1122	47.6	2.8	2674	6	AR183261	Sequence	AR183261	Sequence	47.6	2.8	213558	2	AC149587	Mus muscu
1123	47.6	2.8	2674	6	AR456323	Sequence	AR456323	Sequence	47.6	2.8	217740	2	AC139949	Rattus no
1124	47.6	2.8	2752	9	HSMB06735	Homo sapi	BS641046	Homo sapi	47.6	2.8	226256	2	AC130087	Rattus no
1125	47.6	2.8	2770	9	HSMB07752	Homo sapi	BS647606	Homo sapi	47.6	2.8	226734	2	AC103431	Rattus no
1126	47.6	2.8	2782	9	HSMB03706	Homo sapi	AL832398	Homo sapi	47.6	2.8	232319	2	AC113253	Rattus no
1127	47.6	2.8	2804	9	HSMB07489	Homo sapi	BS647345	Homo sapi	47.6	2.8	235660	2	AC128377	Rattus no
1128	47.6	2.8	2840	10	BC052769	Mus muscu	BC052769	Mus muscu	47.6	2.8	241394	2	AC131549	Rattus no
1129	47.6	2.8	3448	10	BC034679	Mus muscu	BC034679	Mus muscu	47.6	2.8	248214	2	AL138811	Homo sapi
1130	47.6	2.8	3582	10	BC053927	Mus muscu	BC053927	Mus muscu	47.6	2.8	257700	2	AC147391	Pan trogl
1131	47.6	2.8	3924	10	MUS8RED	Mus muscu	L31397	Mus muscu	47.6	2.8	258818	2	AC135265	Rattus no
1132	47.6	2.8	4001	6	AX347363	Sequence	AX347363	Sequence	47.6	2.8	264350	2	AC127094	Rattus no
1133	47.6	2.8	4001	6	AX349084	Sequence	AX349084	Sequence	47.6	2.8	301536	2	AC134158	Rattus no
1134	47.6	2.8	4001	6	AX657851	Sequence	AX657851	Sequence	47.6	2.8	315790	3	AE003484	Drosophil
1135	47.6	2.8	4001	6	AX659125	Sequence	AX659125	Sequence	47.6	2.8	334028	2	AC116537	Drosophil
1136	47.6	2.8	4004	9	BC041086	Homo sapi	BC041086	Homo sapi	47.6	2.8	343980	6	AX344552	Sequence
1137	47.6	2.8	4418	9	BC006195	Homo sapi	BC006195	Homo sapi	47.6	2.8	349980	6	AX344572	Sequence
1138	47.6	2.8	4421	10	BC042512	Mus muscu	BC042512	Mus muscu	47.6	2.8	267	6	CQ525163	Sequence
1139	47.6	2.8	4447	9	HSMB08517	Homo sapi	BS648369	Homo sapi	47.6	2.8	268	6	CQ526263	Sequence
1140	47.6	2.8	4675	9	HSMB03445	Homo sapi	AL832138	Homo sapi	47.6	2.8	291	6	CQ399019	Sequence
1141	47.6	2.8	5306	6	AX345413	Sequence	AX345413	Sequence	47.6	2.8	291	6	CQ405298	Sequence
1142	47.6	2.8	6134	6	AX458624	Sequence	AX458624	Sequence	47.6	2.8	301	6	CQ516510	Sequence
1143	47.6	2.8	6436	6	AX345583	Sequence	AX345583	Sequence	47.6	2.8	376	6	CQ517117	Sequence
1144	47.6	2.8	6436	6	AX345583	Sequence	AX345583	Sequence	47.6	2.8	406	6	CQ517355	Sequence
1145	47.6	2.8	6775	6	AX458643	Sequence	AX458643	Sequence	47.6	2.8	407	6	CQ522526	Sequence
1146	47.6	2.8	6802	6	AX346133	Sequence	AX346133	Sequence	47.6	2.8	439	6	CQ518358	Sequence
1147	47.6	2.8	7416	6	CQ574115	Sequence	CQ574115	Sequence	47.6	2.8	453	6	CQ477688	Sequence
1148	47.6	2.8	7967	3	AF222717	Plasmodiu	AF222717	Plasmodiu	47.6	2.8	467	3	AF156168	Butus ma
1149	47.6	2.8	8900	6	CQ806977	Sequence	CQ806977	Sequence	47.6	2.8	472	6	CQ518059	Sequence
1150	47.6	2.8	8900	6	CQ807251	Sequence	CQ807251	Sequence	47.6	2.8	484	6	CQ526160	Sequence
1151	47.6	2.8	8910	6	AX344725	Sequence	AX344725	Sequence	47.6	2.8	506	6	CQ518031	Sequence
1152	47.6	2.8	9483	6	AX251786	Sequence	AX251786	Sequence	47.6	2.8	516	6	CQ524041	Sequence
1153	47.6	2.8	9483	6	AX345278	Sequence	AX345278	Sequence	47.6	2.8	546	6	AX186746	Sequence
1154	47.6	2.8	9483	6	AX348947	Sequence	AX348947	Sequence	47.6	2.8	589	10	BC049706	Mus muscu
1155	47.6	2.8	9666	6	AX281420	Sequence	AX281420	Sequence	47.6	2.8	631	10	BC049570	Mus muscu
1156	47.6	2.8	9666	6	AX345987	Sequence	AX345987	Sequence	47.6	2.8	643	6	CQ423476	Sequence
1157	47.6	2.8	9666	6	AX348688	Sequence	AX348688	Sequence	47.6	2.8	671	5	BC082915	Xenopus l
1158	47.6	2.8	11700	2	AC013911	Drosophil	AC013911	Drosophil	47.6	2.8	682	10	BC049545	Mus muscu
1159	47.6	2.8	17848	6	AX277865	Sequence	AX277865	Sequence	47.6	2.8	685	10	BC049720	Mus muscu
1160	47.6	2.8	17848	6	AX323550	Sequence	AX323550	Sequence	47.6	2.8	685	11	CNS06EJ4	T3 end of
1161	47.6	2.8	17848	6	AX348363	Sequence	AX348363	Sequence	47.6	2.8	686	10	BC060302	Mus muscu
1162	47.6	2.8	17848	6	AX598758	Sequence	AX598758	Sequence	47.6	2.8	688	6	CQ422987	Sequence
1163	47.6	2.8	63585	2	AC026983	Homo sapi	AC026983	Homo sapi	47.6	2.8	690	9	BC040927	Homo sapi
1164	47.6	2.8	77322	2	AC021334	Homo sapi	AC021334	Homo sapi	47.6	2.8	705	9	HSMB00237	Homo sapi
1165	47.6	2.8	84492	2	AC021676	Homo sapi	AC021676	Homo sapi	47.6	2.8	805	10	BC063183	Rattus no
1166	47.6	2.8	95026	3	AC0215292	Drosophil	AC125292	Drosophil	47.6	2.8	811	11	BV073335	S212P6813
1167	47.6	2.8	110000	2	AC110244	Mus muscu	AC110244	Mus muscu	47.6	2.8	824	9	BC070291	Homo sapi
1168	47.6	2.8	110000	2	PFMAL13_11	Continuation (12 o	Continuation (12 o	Continuation (12 o	47.6	2.8	843	10	BC038641	Mus muscu
1169	47.6	2.8	110000	3	PFMAL13P2_2	Continuation (3 of	Continuation (3 of	Continuation (3 of	47.6	2.8	883	9	BC049726	Mus muscu
1170	47.6	2.8	110000	3	PFMAL1P2_0	Continuation (3 of	Continuation (3 of	Continuation (3 of	47.6	2.8	887	9	AB125184	Macaca fa
1171	47.6	2.8	113027	9	AC090669	Homo sapi	AC090669	Homo sapi	47.6	2.8	902	10	BC048724	Mus muscu
1172	47.6	2.8	120211	10	AL773515	Mouse DNA	AL773515	Mouse DNA	47.6	2.8	935	10	BC049693	Mus muscu
1173	47.6	2.8	127580	9	HSBJ74J1	Human DNA	AL049692	Human DNA	47.6	2.8	942	5	BC049498	Danio rer
1174	47.6	2.8	151501	9	BS000215	Pan trogl	BS000215	Pan trogl	47.6	2.8	971	10	BC030946	Mus muscu
1175	47.6	2.8	155320	2	AC135762	Rattus no	AC135762	Rattus no	47.6	2.8	989	10	BC051033	Mus muscu
1176	47.6	2.8	155646	9	AC146044	Pan trogl	AC146044	Pan trogl	47.6	2.8	997	9	BC047943	Homo sapi
1177	47.6	2.8	156459	10	AC147155	Mus muscu	AC147155	Mus muscu	47.6	2.8	1068	9	BC071641	Homo sapi
1178	47.6	2.8	158803	2	AC117771	Mus muscu	AC117771	Mus muscu	47.6	2.8	1071	9	BC073941	Homo sapi
1179	47.6	2.8	16025	10	AL844493	Mouse DNA	AL844493	Mouse DNA	47.6	2.8	1107	3	AX173973	Ciona int
1180	47.6	2.8	16292	10	AC123049	Mus muscu	AC123049	Mus muscu	47.6	2.8	1113	9	BC030277	Homo sapi
1181	47.6	2.8	168439	10	AC131803	Mus muscu	AC131803	Mus muscu	47.6	2.8	1222	9	BC035237	Homo sapi
1182	47.6	2.8	173585	2	AC021113	Homo sapi	AC021113	Homo sapi	47.6	2.8	1240	9	BC055418	Homo sapi
1183	47.6	2.8	174893	5	BX004876	Zebrafish	BX004876	Zebrafish	47.6	2.8	1281	5	BC083538	Danio rer
1184	47.6	2.8	175106	2	AC148984	Mus muscu	AC148984	Mus muscu	47.6	2.8	1299	10	BC021404	Mus muscu
1185	47.6	2.8	176261	5	BSX27252	Zebrafish	BSX27252	Zebrafish	47.6	2.8	1332	10	BC060992	Mus muscu
1186	47.6	2.8	179312	3	AC023745	Drosophil	AC023745	Drosophil	47.6	2.8	1348	9	BC070154	Homo sapi
1187	47.6	2.8	185195	10	AC134565	Mus muscu	AC134565	Mus muscu	47.6	2.8	1425	9	BC036851	Homo sapi

c1188	47.6	2.8	187545	10	AC127550	Mus muscu	AC127550	Mus muscu	47.6	2.8	187545	10	AC127550	Mus muscu
c1189	47.6	2.8	188823	2	AC016990	Homo sapi	AC016990	Homo sapi	47.6	2.8	188823	2	AC016990	Homo sapi
c1190	47.6	2.8	194760	9	CNS01697	Human chr	CNS01697	Human chr	47.6	2.8	194760	9	CNS01697	Human chr
c1191	47.6	2.8	199537	10	AL837510	Mouse DNA	AL837510	Mouse DNA	47.6	2.8	199537	10	AL837510	Mouse DNA
c1192	47.6	2.8	202640	2	AC113851	Rattus no	AC113851	Rattus no	47.6	2.8	202640	2	AC113851	Rattus no
c1193	47.6	2.8	211371	2	CR450764	Danio rer	CR450764	Danio rer	47.6	2.8	211371	2	CR450764	Danio rer
c1194	47.6	2.8	213397	2	AC125027	Mus muscu	AC125027	Mus muscu	47.6	2.8	213397	2	AC125027	Mus muscu
c1195	47.6	2.8	213558	2	AC149587	Mus muscu	AC149587	Mus muscu	47.6	2.8	213558	2	AC149587	Mus muscu
c1196	47.6	2.8	217740	2	AC139949	Rattus no	AC139949	Rattus no	47.6	2.8	217740	2	AC139949	Rattus no
c1197	47.6	2.8	226256	2	AC130087	Rattus no	AC130087	Rattus no	47.6	2.8	226256	2	AC130087	Rattus no
c1198	47.6	2.8	226734	2	AC103431	Rattus no	AC103431	Rattus no	47.6	2.8	226734	2	AC103431	Rattus no
c1199	47.6	2.8	232319	2	AC113253	Rattus no	AC113253	Rattus no	47.6	2.8	232319	2	AC113253	Rattus no
c1200	47.6	2.8	235660	2	AC128377	Rattus no	AC128377	Rattus no	47.6	2.8	235660	2	AC128377	Rattus no
c1201	47.6	2.8	241394	2	AC131549	Rattus no	AC131549	Rattus no	47.6	2.8	241394	2	AC131549	Rattus no
c1202	47.6	2.8	248214	2	AL138811	Homo sapi	AL138811	Homo sapi	47.6	2.8	248214	2	AL138811	Homo sapi
c1203	47.6	2.8	257700	2	AC147391	Pan trogl	AC147391	Pan trogl	47.6	2.8	257700	2	AC147391	Pan trogl
c1204	47.6	2.8	258818	2	AC135265	Rattus no	AC135265	Rattus no	47.6	2.8	258818	2	AC135265	Rattus no
c1205	47.6	2.8	264350	2	AC127094	Rattus no	AC127094	Rattus no	47.6	2.8	264350	2	AC127094	Rattus no
c1206	47.6	2.8	301536	2	AC134158	Rattus no	AC134158	Rattus no	47.6	2.8	301536	2	AC134158	Rattus no
c1207	47.6	2.8	315790	3	AE003484	Drosophill	AE003484	Drosophill	47.6	2.8	315790	3	AE003484	Drosophill
c1208	47.6	2.8	334028	2	AC116537	Sequence	AC116537	Sequence	47.6	2.8	334028	2	AC116537	Sequence
c1209	47.6	2.8	349980	6	AX344552	Sequence	AX344552	Sequence	47.6	2.8	349980	6	AX344552	Sequence
c1210	47.6	2.8	349980	6	AX344572	Sequence	AX344572	Sequence	47.6	2.8	349980	6	AX344572	Sequence
c1211	47.4	2.8	267	6	CQ525163	Sequence	CQ525163	Sequence	47.4	2.8	267	6	CQ525163	Sequence
c1212	47.4	2.8	268	6	CQ526263	Sequence	CQ526263	Sequence	47.4	2.8	268	6	CQ526263	Sequence
c1213	47.4	2.8	291	6	CQ399019	Sequence	CQ399019	Sequence	47.4	2.8	291	6	CQ399019	Sequence
c1214	47.4	2.8	291	6	CQ405298	Sequence	CQ405298	Sequence	47.4	2.8	291	6	CQ405298	Sequence
c1215	47.4	2.8	301	6	CQ516510	Sequence	CQ516510	Sequence	47.4	2.8	301	6	CQ516510	Sequence
c1216	47.4	2.8	376	6	CQ517117	Sequence	CQ517117	Sequence	47.4	2.8	376	6	CQ517117	Sequence
c1217	47.4	2.8	406	6	CQ517355	Sequence	CQ517355	Sequence	47.4	2.8	406	6	CQ517355	Sequence
c1218	47.4	2.8	407	6	CQ522526	Sequence	CQ522526	Sequence	47.4	2.8	407	6	CQ522526	Sequence
c1219	47.4	2.8	439	6	CQ518358	Sequence	CQ518358	Sequence	47.4	2.8	439	6	CQ518358	Sequence
c1220	47.4	2.8	453	6	CQ477688	Sequence	CQ477688	Sequence	47.4	2.8	453	6	CQ477688	Sequence
c1221	47.4	2.8	467	3	AF156168	Buthus ma	AF156168	Buthus ma	47.4	2.8	467	3	AF156168	Buthus ma
c1222	47.4	2.8	472	6	CQ518059	Sequence	CQ518059	Sequence	47.4	2.8	472	6	CQ518059	Sequence
c1223	47.4	2.8	484	6	CQ526160	Sequence	CQ526160	Sequence	47.4	2.8	484	6	CQ526160	Sequence
c1224	47.4	2.8	506	6	CQ518031	Sequence	CQ518031	Sequence	47.4	2.8	506	6	CQ518031	Sequence
c1225	47.4	2.8	516	6	CQ524041	Sequence	CQ524041	Sequence	47.4	2.8	516	6	CQ524041	Sequence
c1226	47.4	2.8	546	6	AX186746	Sequence	AX186746	Sequence	47.4	2.8	546	6	AX186746	Sequence
c1227	47.4	2.8	589	10	BC049706	Mus muscu	BC049706	Mus muscu	47.4	2.8	589	10	BC049706	Mus muscu
c1228	47.4	2.8	631	10	BC049570	Mus muscu	BC049570	Mus muscu	47.4	2.8	631	10	BC049570	Mus muscu
c1229	47.4	2.8	643	6	CQ423476	Sequence	CQ423476	Sequence	47.4	2.8	643	6	CQ423476	Sequence
c1230	47.4	2.8	671	5	BC082915	Xenopus l	BC082915	Xenopus l	47.4	2.8	671	5	BC082915	Xenopus l
c1231	47.4	2.8	682	10	BC049545	Mus muscu	BC049545	Mus muscu	47.4	2.8	682	10	BC049545	Mus muscu
c1232	47.4	2.8	685	10	BC049720	Mus muscu	BC049720	Mus muscu	47.4	2.8	685	10	BC049720	Mus muscu
c1233	47.4	2.8	685	11	CNS068374	T3 end of	AL395174	T3 end of	47.4	2.8	685	11	CNS068374	T3 end of
c1234	47.4	2.8	686	10	BC060302	Mus muscu	BC060302	Mus muscu	47.4	2.8	686	10	BC060302	Mus muscu
c1235	47.4	2.8	688	6	CQ422987	Sequence	CQ422987	Sequence	47.4	2.8	688	6	CQ422987	Sequence
c1236	47.4	2.8	690	9	BC040927	Homo sapi	BC040927	Homo sapi	47.4	2.8	690	9	BC040927	Homo sapi
c1237	47.4	2.8	705	9	HSM800237	Homo sapi	AL049452	Homo sapi	47.4	2.8	705	9	HSM800237	Homo sapi
c1238	47.4	2.8	805	10	BC063183	Rattus no	BC063183	Rattus no	47.4	2.8	805	10	BC063183	Rattus no
c1239	47.4	2.8	811	11	BV073335	Sequence	BV073335	Sequence	47.4	2.8	811	11	BV073335	Sequence
c1240	47.4	2.8	824	9	BC070231	Homo sapi	BC070231	Homo sapi	47.4	2.8	824	9	BC070231	Homo sapi
c1241	47.4	2.8	843	10	BC038641	Mus muscu	BC038641	Mus muscu	47.4	2.8	843	10	BC038641	Mus muscu
c1242	47.4	2.8	883	10	BC049726	Macaca fa	AB125184	Macaca fa	47.4	2.8	883	10	BC049726	Macaca fa
c1243	47.4	2.8	887	9	AB125184	Mus muscu	BC048724	Mus muscu	47.4	2.8	887	9	AB125184	Mus muscu
c1244	47.4	2.8	902	10	BC048724	Mus muscu	BC048724	Mus muscu	47.4	2.8	902	10	BC048724	Mus muscu
c1245	47.4	2.8	935	10	BC049693	Mus muscu	BC049693	Mus muscu	47.4	2.8	935	10	BC049693	Mus muscu
c1246	47.4	2.8	942	5	BC049498	Danio rer	BC049498	Danio rer	47.4	2.8	942	5	BC049498	Danio rer
c1247	47.4	2.8	971	10	BC030346	Mus muscu	BC030346	Mus muscu	47.4	2.8	971	10	BC030346	Mus muscu
c1248	47.4	2.8	989	10	BC051033	Mus muscu	BC051033	Mus muscu	47.4	2.8	989	10	BC051033	Mus muscu
c1249	47.4	2.8	997	9	BC047943	Homo sapi	BC047943	Homo sapi	47.4	2.8	997	9	BC047943	Homo sapi
c1250	47.4	2.8	1068	9	BC071641	Homo sapi	BC071641	Homo sapi	47.4	2.8	1068	9	BC071641	Homo sapi
c1251	47.4	2.8	1107	9	BC073941	Homo sapi	BC073941	Homo sapi	47.4	2.8	1107	9	BC073941	Homo sapi
c1252	47.4	2.8	1107	3	AC130277	Homo sapi	AC130277	Homo sapi	47.4	2.8	1107	3	AC130277	Homo sapi
c1253	47.4	2.8	1113	9	BC035237	Homo sapi	BC035237	Homo sapi	47.4	2.8	1113	9	BC035237	Homo sapi
c1254	47.4	2.8	1222	9	BC055418	Homo sapi	BC055418	Homo sapi	47.4	2.8	1222	9	BC055418	Homo sapi
c1255	47.4	2.8	1240	9	BC055418	Homo sapi	BC055418	Homo sapi	47.4	2.8	1240	9	BC055418	Homo sapi
c1256	47.4	2.8	1281	5	BC083538	Danio rer	BC083538	Danio rer	47.4	2.8	1281	5	BC083538	Danio rer
c1257	47.4	2.8	1299	10	BC021404	Mus muscu	BC021404	Mus muscu	47.4	2.8	1299	10	BC021404	Mus muscu
c1258	47.4	2.8	1332	10	BC060992	Mus muscu	BC060992	Mus muscu	47.4	2.8	1332	10	BC060992	Mus muscu
c1259	47.4	2.8	1348	9	BC070154	Homo sapi	BC070154	Homo sapi	47.4	2.8	1348	9	BC070154	Homo sapi
c1260	47.4	2.8	1425	9	BC036851	Homo sapi	BC036851	Homo sapi	47.4	2.8	1425	9	BC036851	Homo sapi

1261	47.4	2.8	1433	5	BC082836	BC082836 Xenopus l	c1334	47.4	2.8	14006	6	AX346860	AX346860 Sequence
1262	47.4	2.8	1445	10	BC071177	BC071177 Rattus no	c1335	47.4	2.8	14798	6	AX345934	AX345934 Sequence
1263	47.4	2.8	1463	6	CQ491467	CQ491467 Sequence	c1336	47.4	2.8	17721	6	AX346631	AX346631 Sequence
1264	47.4	2.8	1463	6	CQ497350	CQ497350 Sequence	c1337	47.4	2.8	19289	2	AC090926	AC090926 Homo sapi
1265	47.4	2.8	1493	9	HS0805897	BS58346 Homo sapi	c1338	47.4	2.8	40324	6	AX458633	AX458633 Sequence
1266	47.4	2.8	1500	3	AX174058	AK174058 Ciona int	1339	47.4	2.8	57538	3	AC115682	AC115682 Dictyosae
1267	47.4	2.8	1591	9	HS0807298	BX647154 Homo sapi	c1340	47.4	2.8	67374	2	AC118933	AC118933 Mus muscu
1268	47.4	2.8	1653	10	BC083548	BC083548 Rattus no	c1341	47.4	2.8	72981	10	BX511117	BX511117 Mouse DNA
1269	47.4	2.8	1661	6	BC025753	BC025753 Homo sapi	c1342	47.4	2.8	73778	6	AX344562	AX344562 Sequence
1270	47.4	2.8	1696	6	AR256293	AR256293 Sequence	c1343	47.4	2.8	82771	2	AC011953	AC011953 Homo sapi
1271	47.4	2.8	1719	10	BC045148	BC045148 Mus muscu	1344	47.4	2.8	85916	3	AC117080	AC117080 Dictyosae
1272	47.4	2.8	1738	6	AR560934	AR560934 Sequence	c1345	47.4	2.8	110000	2	AC113129_2	Continuation (3 of
1273	47.4	2.8	1738	8	BT009079	BT009079 Triticum	c1346	47.4	2.8	110000	2	AC114623_1	Continuation (2 of
1274	47.4	2.8	1744	9	BC019265	BC019265 Homo sapi	c1347	47.4	2.8	110000	10	AE014180_1	Continuation (2 of
1275	47.4	2.8	1750	9	BC048294	BC048294 Homo sapi	1348	47.4	2.8	120653	5	BX649590	BX649590 Zebrafish
1276	47.4	2.8	1825	9	BC050524	BC050524 Homo sapi	1349	47.4	2.8	121554	2	AC142244	AC142244 Mus muscu
1277	47.4	2.8	1939	5	BC079974	BC079974 Xenopus l	c1350	47.4	2.8	142324	5	EX005420	EX005420 Zebrafish
1278	47.4	2.8	1980	10	BC027199	BC027199 Mus muscu	c1351	47.4	2.8	148053	2	CR352222	CR352222 Danio rer
1279	47.4	2.8	1999	9	BC020684	BC020684 Homo sapi	c1352	47.4	2.8	152506	10	AC145589	AC145589 Mus muscu
1280	47.4	2.8	2161	9	AB063084	AB063084 Macaca fa	1353	47.4	2.8	156060	2	AC004153	AC004153 Plasmodi
1281	47.4	2.8	2224	6	BD189940	BD189940 Tumor ant	c1354	47.4	2.8	162646	2	AC112977	AC112977 Mus muscu
1282	47.4	2.8	2224	9	AB062292	AB062292 Homo sapi	1355	47.4	2.8	163035	2	AC142822	AC142822 Macaca mu
1283	47.4	2.8	2237	3	AK112710	AK112710 Ciona int	1356	47.4	2.8	164520	2	AC020738	AC020738 Homo sapi
1284	47.4	2.8	2245	9	BC037547	BC037547 Homo sapi	c1357	47.4	2.8	166529	10	AC147621	AC147621 Mus muscu
1285	47.4	2.8	2307	5	BC081197	BC081197 Xenopus l	1358	47.4	2.8	179253	5	AL928870	AL928870 Zebrafish
1286	47.4	2.8	2320	10	BC046962	BC046962 Mus muscu	1359	47.4	2.8	181571	10	AC108949	AC108949 Mus muscu
1287	47.4	2.8	2335	5	BC068409	BC068409 Danio rer	c1360	47.4	2.8	191119	2	CR749163	CR749163 Danio rer
1288	47.4	2.8	2372	9	BC042652	BC042652 Homo sapi	c1361	47.4	2.8	194362	10	AC124716	AC124716 Mus muscu
1289	47.4	2.8	2403	9	HS0808752	BX648601 Homo sapi	1362	47.4	2.8	195972	10	AC117567	AC117567 Mus muscu
1290	47.4	2.8	2477	9	BC034692	BC034692 Homo sapi	1363	47.4	2.8	198590	10	AC113983	AC113983 Mus muscu
1291	47.4	2.8	2539	10	BC046284	BC046284 Mus muscu	1364	47.4	2.8	199274	2	AC123626	AC123626 Mus muscu
1292	47.4	2.8	2593	9	HS0807470	BX647326 Homo sapi	1365	47.4	2.8	200934	10	AC123850	AC123850 Mus muscu
1293	47.4	2.8	2601	5	BC072034	BC072034 Xenopus l	c1366	47.4	2.8	205878	2	CR392366	CR392366 Danio rer
1294	47.4	2.8	2765	3	AK115430	AK115430 Ciona int	1367	47.4	2.8	212144	2	AC140356	AC140356 Mus muscu
1295	47.4	2.8	2783	10	BC058527	BC058527 Mus muscu	1368	47.4	2.8	215427	2	AC130980	AC130980 Rattus no
1296	47.4	2.8	2789	3	AK114441	AK114441 Ciona int	1369	47.4	2.8	219491	2	AC092256	AC092256 Mus muscu
1297	47.4	2.8	2824	5	BC042665	BC042665 Homo sapi	1370	47.4	2.8	221068	2	AC102378	AC102378 Mus muscu
1298	47.4	2.8	2980	6	BD270060	BD270060 Secreted	c1371	47.4	2.8	229332	2	AC137869	AC137869 Mus muscu
1299	47.4	2.8	3149	10	BC040763	BC040763 Mus muscu	c1372	47.4	2.8	233869	2	AC119834	AC119834 Mus muscu
1300	47.4	2.8	3186	5	BC068331	BC068331 Danio rer	1373	47.4	2.8	227395	10	AL512346	AL512346 Mouse DNA
1301	47.4	2.8	3446	9	HS0803955	AL713742 Homo sapi	1374	47.4	2.8	230184	10	AC138679	AC138679 Mus muscu
1302	47.4	2.8	3492	5	BC078645	BC078645 Danio rer	1375	47.4	2.8	235664	2	AC126522	AC126522 Rattus no
1303	47.4	2.8	3502	9	HS0807726	BX647580 Homo sapi	1376	47.4	2.8	238781	10	AC127351	AC127351 Mus muscu
1304	47.4	2.8	3664	6	AX598782	AX598782 Sequence	c1377	47.4	2.8	240185	2	AC115132	AC115132 Rattus no
1305	47.4	2.8	3664	6	AX598928	AX598928 Sequence	1378	47.4	2.8	240931	2	AC107097	AC107097 Rattus no
1306	47.4	2.8	3664	6	AX705378	AX705378 Sequence	c1379	47.4	2.8	240931	2	AC107097	AC107097 Rattus no
1307	47.4	2.8	3664	6	AX705400	AX705400 Sequence	c1380	47.4	2.8	244656	10	AC031278	AC031278 Mus muscu
1308	47.4	2.8	3930	9	BC027963	BC027963 Homo sapi	c1381	47.4	2.8	245859	2	AC099418	AC099418 Rattus no
1309	47.4	2.8	3964	5	BC077739	BC077739 Xenopus l	c1382	47.4	2.8	252632	3	AE014818	AE014818 Plasmodi
1310	47.4	2.8	3997	6	AX086658	AX086658 Sequence	c1383	47.4	2.8	253441	2	AC135668	AC135668 Mus muscu
1311	47.4	2.8	4154	9	HS0803629	AL832322 Homo sapi	c1384	47.4	2.8	255189	2	AC106391	AC106391 Rattus no
1312	47.4	2.8	4180	10	BC042645	BC042645 Mus muscu	1385	47.4	2.8	258938	2	AC099416	AC099416 Mus muscu
1313	47.4	2.8	4237	6	BD057918	BD057918 Secreted	c1386	47.4	2.8	262640	2	AC139057	AC139057 Mus muscu
1314	47.4	2.8	4550	10	AB015672	AB015672 Mus muscu	c1387	47.4	2.8	267140	2	AC097568	AC097568 Rattus no
1315	47.4	2.8	4679	9	HS0808418	BX648270 Homo sapi	1388	47.4	2.8	275156	2	AC105868	AC105868 Rattus no
1316	47.4	2.8	5182	6	AX252007	AX252007 Sequence	c1389	47.4	2.8	302489	2	AC100742	AC100742 Mus muscu
1317	47.4	2.8	5182	6	AX348780	AX348780 Sequence	1390	47.2	2.8	203	6	CQ524826	CQ524826 Sequence
1318	47.4	2.8	5349	6	AX345242	AX345242 Sequence	1391	47.2	2.8	240	6	CQ663206	CQ663206 Sequence
1319	47.4	2.8	5437	6	AX346644	AX346644 Sequence	c1392	47.2	2.8	281	6	CQ410312	CQ410312 Sequence
1320	47.4	2.8	5893	6	AX345761	AX345761 Sequence	1393	47.2	2.8	348	6	CQ524785	CQ524785 Sequence
1321	47.4	2.8	6664	6	AX252071	AX252071 Sequence	1394	47.2	2.8	396	6	CQ525748	CQ525748 Sequence
1322	47.4	2.8	6664	6	AX822358	AX822358 Sequence	1395	47.2	2.8	504	6	CQ526419	CQ526419 Sequence
1323	47.4	2.8	6664	6	AX822486	AX822486 Sequence	1396	47.2	2.8	539	10	BC031454	BC031454 Mus muscu
1324	47.4	2.8	6664	6	AX825998	AX825998 Sequence	1397	47.2	2.8	623	9	BC043516	BC043516 Homo sapi
1325	47.4	2.8	6664	6	AX826126	AX826126 Sequence	1398	47.2	2.8	625	10	BC059134	BC059134 Rattus no
1326	47.4	2.8	6898	6	AX344814	AX344814 Sequence	1399	47.2	2.8	656	6	CQ487057	CQ487057 Sequence
1327	47.4	2.8	8059	5	BC076779	BC076779 Xenopus l	1400	47.2	2.8	675	10	BC059112	BC059112 Rattus no
1328	47.4	2.8	8305	6	AX346470	AX346470 Sequence	1401	47.2	2.8	720	3	AK174023	AK174023 Ciona int
1329	47.4	2.8	8607	6	AR453095	AR453095 Sequence	1402	47.2	2.8	749	9	BC008417	BC008417 Homo sapi
1330	47.4	2.8	8607	6	AX281207	AX281207 Sequence	c1403	47.2	2.8	756	6	CQ399155	CQ399155 Sequence
1331	47.4	2.8	8607	6	AX356478	AX356478 Sequence	c1404	47.2	2.8	756	6	CQ405433	CQ405433 Sequence
1332	47.4	2.8	12138	6	AX346530	AX346530 Sequence	1405	47.2	2.8	760	9	BC040885	BC040885 Homo sapi
1333	47.4	2.8	12138	6	AX348420	AX348420 Sequence	c1406	47.2	2.8	780	8	CNS019TW	AL112092 Botrytis

1407	47.2	2.8	859	9	AK026608 Homo sapi	AK026608 Homo sapi	47.2	2.8	182870	2	AC015653	AC015653 Homo sapi
1408	47.2	2.8	891	14	TMO308687	AJ308687 Tobacco m	47.2	2.8	186155	2	AC099708	AC099708 Mus muscu
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1411	47.2	2.8	1117	8	AF243375	Glycine m	47.2	2.8	195580	10	AC148982	AC148982 Mus muscu
1412	47.2	2.8	1155	9	BC036792	Homo sapi	47.2	2.8	198318	2	BX957253	BX957253 Danio rer
1413	47.2	2.8	1285	9	BSM801947	Homo sapi	47.2	2.8	198582	9	AC005291	AC005291 Homo sapi
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1415	47.2	2.8	1352	9	BC043573	Homo sapi	47.2	2.8	203657	2	BX927302	BX927302 Danio rer
1416	47.2	2.8	1368	5	BC064278	Homo sapi	47.2	2.8	204210	2	AC115583	AC115583 Mus muscu
1417	47.2	2.8	1464	9	IR2005397	Xenopus t	47.2	2.8	204724	10	AC131912	AC131912 Mus muscu
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ALIGNMENTS

LOCUS

CO768055

Sequence 522 from Patent EP1386931.

ACCESSION

CO768055

VERSION

CO768055.1

GI:45108887

KEYWORDS

Homo sapiens (human)

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1

WOOD, W.I., GODDARD, A., GURNEY, A., YUAN, J., BAKER, K.P. and CHEN, J.

AUTHORS

HUMAN NEUROTRIMIN HOMOLOGUE

TITLE

PATENT: EP 1386931-A 522 04-FEB-2004;

JOURNAL

Genentech, Inc. (US)

FEATURES

Location/Qualifiers

source

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/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match

Best Local Similarity

Matches 1679; Conservative

100.0%; Score 1679; DB 6; Length 1679;

100.0%; Pred. No. 0;

0; Mismatches 0; Indels 0; Gaps 0;

QY

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60

DB

1

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QY

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DB

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LOCUS Sequence 375 from patent US 6725730.
DEFINITION AR528639
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Bollinger, C.L. Jr.
TITLE Crane test weight assembly and method
JOURNAL Patent: US 6725730-A 375 27-APR-2004;
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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX358872 Sequence 125 from Patent WO0193983.
DEFINITION AX358872
ACCESSION AX358872.1 GI:18675337
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc.(US)
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Best Local Similarity 100.0%; Pred. No. 0;
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AX362365 1679 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 125 from Patent WO0208288.
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
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AX403748 1679 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 103 from Patent WO0077037.
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Ashkenazi, A., Baker, K., Botstein, D., Desnoyers, L., Eaton, D.L.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, W.E.,
Goddard, A., Godowski, P., Gurney, A., Kijavini, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS Sequence 55 from Patent WO0208284.
DEFINITION AX454470
ACCESSION AX454470
VERSION AX454470.1 GI:21713859
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.
TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
JOURNAL Patent: WO 0208284-A 55 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)
FEATURES
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Matches 1679; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AX464242 1679 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 375 from Patent WO0140466.
DEFINITION AX464242
ACCESSION AX464242
VERSION AX464242.1 GI:21899137
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS Baker, K.P., Bersini, M., Deforge, L., Desnoyers, L., Filvaroff, E.,
Gao, W.Q., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
same
JOURNAL Patent: WO 0140466-A 375 07-JUN-2001;
Genentech Inc. (US)
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DEFINITION Sequence 55 from Patent WO0200690.

ACCESSION AX490948

VERSION AX490948.1 GI:22323811

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoi,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 55 03-JAN-2002; Genentech, Inc. (US)

FEATURES

Location/Qualifiers

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ACCESSION AY358331
VERSION AY358331.1 GI:37181786
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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AUTHORS Clark, H. F., Gurney, A. L., Abaya, E., Baker, K., Baldwin, D., Brush, J., Chen, J., Chow, B., Chui, C., Crowley, C., Currell, B., Deuel, B., Dowd, P., Eaton, D., Foster, J., Grimaldi, C., Gu, Q., Haas, P. E., Heldens, S., Huang, A., Kim, H. S., Klimowski, L., Jin, Y., Johnson, S., Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W. I. and Godowski, P.
TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark, H. F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
FEATURES
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REFERENCE 1
AUTHORS Sellar,G.C. and Gabra,H.
TITLE Cancer
JOURNAL Patent: WO 03002765-A 100 09-JAN-2003;
Cancer Research Technology Limited (GB)
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Db 1545 GGAAGAACACAGCACACCGGCTTTGACCCACTGCAAGCTGCACTGCAACCTCTTTGG 1604
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Qy 1587 -----CTTCCGGCCCAAGCGTGGGGCTGCGGGCACTTTGGTAGACTGTGCA 1633
Db 1725 CCCAAGCGTGGCGCTTCCGGCCCAAGCGTGGGGCTGCGGGCACTTTGGTAGACTGTGCA 1784
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Db 1785 CCACGCGGTGTGTGTGAACGTGAAATATAAAGAGCAAAAAA 1830
RESULT 12
AF126426 Homo sapiens neurotrophin (HNT) mRNA, complete cds. PRI 10-JUN-2002
DEFINITION
ACCESSION
AF126426
VERSION
AF126426.1 GI:7158997
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1839)
AUTHORS
Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE
Cloning and identification of human neurotrophin full length cDNA
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 1839)
AUTHORS
Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.
TITLE
Direct Submission
JOURNAL
Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical
Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China
FEATURES
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Best Local Similarity 98.5%; Pred. No. 0;
Matches 1464; Conservative 0; Mismatches 2; Indels 20; Gaps 1;
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Qy 274 CCGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACCGGGTCACCCGGGTGGC 333
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LOCUS	Sequence 1	1032 bp	DNA linear PAT 20-FEB-2004
DEFINITION	Sequence 1 from patent US 6664383.		
ACCESSION	AR439648		
VERSION	AR439648.1	GI:42665572	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1032)		
AUTHORS	Fukushima,D., Shibayama,S. and Tada,H.		
TITLE	Polypeptides, cDNA encoding the same and utilization thereof		
JOURNAL	Patent: US 6664383-A 1 16-DEC-2003;		
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Matches 1032;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	254	GCTATGGACAACTGACCGTCCGGCAGGGGGAGAGGGCCACCTCAGGTGCACATTATGAC	313
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Qy	314	AACCGGCTCACCCGGGTGGCTTAAACCCGACGACCATCTCTATGCTGGGAATGAC	373
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Qy	374	AAAGTGTGCTGGATCTCTCGCGTGTCTTCTTGAGCAACACCCAAACGAGTACAGCATC	433
Db	241	AAAGTGTGCTGGATCTCTCGCGTGTCTTCTTGAGCAACACCCAAACGAGTACAGCATC	300
Qy	434	GAGATCCAGAACTGTGATGACGAGGGGCTTACACCTGCTCGGTGCAGACAGAC	493
Db	301	GAGATCCAGAACTGTGATGACGAGGGGCTTACACCTGCTCGGTGCAGACAGAC	360
Qy	494	AACCAACCCAAAGACCTCTAGGGTCCAACCTTATGTGCAAGTATCTCCCAAAATTTGTAGAG	553
Db	361	AACCAACCCAAAGACCTCTAGGGTCCAACCTTATGTGCAAGTATCTCCCAAAATTTGTAGAG	420
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Db	421	ATTTCTTTCAGATATCTCCATTTAATGAAGGAAACAATATTATAGCCTCACTGCAATAGCAACT	480
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Db	481	GGTAGACACAGCGCTACGGTTACTTGGAGACACATCTCTCTCCCAAGCGGTGGCTTTGTG	540
Qy	674	AGTGAAGACGAATACTTTGGAAATTTAGGGGCATCACCCGGGAGCAGTCAAGGGGACTACGAG	733
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794 TATCCACCATACATTTAGAAAGCCAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853
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1034 CTGGGCCACACCAATGCGAGCATCATGCTATTTGGTCCAGCGCGGTGAGCGAGGTGAGC 1093
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1154 CTTCTCAAAATTT 1165
Db |||||||
1021 CTTCTCAAAATTT 1032
RESULT 14
RNU16845 2040 bp mRNA linear ROD 26-MAY-1995
LOCUS Rattus norvegicus neurotrophin mRNA, complete cds.
DEFINITION U16845
ACCESSION U16845
VERSION U16845.1 GI:755184
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 2040)
Struyk,A.F., Canoll,P.D., Wolfgang,M.J., Rosen,C.L., D'Eustachio,P.
and Salzer,J.L.
Cloning of neurotrophin defines a new subfamily of differentially
expressed neural cell adhesion molecules
J. Neurosci. 15 (3 Pt 2), 2141-2156 (1995)
95198094
7891157
REFERENCE 2 (bases 1 to 2040)
Salzer,J.L.
Direct Submision
Submitted (02-NOV-1994) James L. Salzer, Cell Biology, NYU Medical
Center, 550 First Avenue, New York, NY 10016, USA
Location/Qualifiers
1. -2040
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ORIGIN
Query Match 59.4%; Score 996.8; DB 10; Length 2040;
Best Local Similarity 84.3%; Pred. No. 4.2e-253;
Matches 1249; Conservative 0; Mismatches 202; Indels 31; Gaps 10;
Qy 214 AGGAGTGCCTGCGGAGCGGAGATGCCACCTCTCCCAAAAGCTATGGACAAACGTGACCGGT 273
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RESULT 15
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LOCUS Mus musculus neurotrimin, mRNA (cDNA clone MGC:30504
DEFINITION IMAGE:4480983), complete cds.
ACCESSION BC023307
VERSION BC023307.1 GI:23958300
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1615)
Strausberg,R.B., Feingold,B.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Abramson,R.D., Prange,C., Raha,S., Loquellano,N.A., Peters,G.J.,
Cramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Touchman,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywicki,M.I., Skalek,U., Smaluk,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
JOURNAL 22388257
MEDLINE 12477932
PUBMED
REFERENCE 2 (bases 1 to 1615)
AUTHORS Strausberg,R.
TITLE Direct Submission

JOURNAL

REMARK
COMMENT

Submitted (05-FEB-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 41 Row: h Column: 10
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 26986610.

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173. 442
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/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"
485. 664
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740. 973
/gene="Hnt-pending"
/note="IG; Region: Immunoglobulin"
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misc_feature

173. 442
/gene="Hnt-pending"
/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"
485. 664
/gene="Hnt-pending"
/note="IGc2; Region: Immunoglobulin C-2 Type"
/db_xref="CDD:smart00408"
740. 973
/gene="Hnt-pending"
/note="IG; Region: Immunoglobulin"
/db_xref="CDD:smart00409"

ORIGIN

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Qy 214 AGGAGTCCCTGCGCAGCGGAGATGCCACCTTCCCAAGCTATGGACACGTCACGGT 273
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Db 124 AGGAGTCCGGTGGCTAGCGGAGATGCCACCTTTCCCAAAGCTATGGACAAACGTGACGGT 183
 Qy 274 CCGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGACCCGGGTGGC 333
 Db 184 CAGGACGGGAGAGCGCCACCTCAGGTGCACTATTGACAAACGGGTGACCCGGGTGGC 243
 Qy 334 CTGGTAAACCGCAGCACCCTCTATGCTGGGAAATGACAAGTGGTGGCTTGGATCTCTCG 393
 Db 244 CTGGCTAAACCGCAGTACCACTCTATGCTGGGAAATGACAAGTGGTGGCTTGGATCTCTCG 303
 Qy 394 CGTGTCTCTTGAGCAACAACCCAAACCCAGTACAGCATCAGATCCAGAAACGTGGATGT 453
 Db 304 TGTGTCTCTCTGAGTAAACCCAGCACCAGTACAGCATCAGATCCAGAAATGTGGATGT 363
 Qy 454 GTATGACGAGGGCCCTTACACTGCTCGGTGAGACAGACAAACCCAAAGACCTCTAG 513
 Db 364 GTACGATGAGGGCCCTTATACCTGCTCGGTGAGACAGACAAACCCAAAGACCTCTAG 423
 Qy 514 GGTCCACCTCATTTGTCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATATCTCCAT 573
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 Db 484 TAATGAAGGGAAACAATATTAGCTCACTGATAGCAACTCGGTAGACAGAGCCCTACAGT 543
 Qy 634 TACTTGGAGACACATCTCTCCCAAAGCGTTGGCTTTGTGAGTGNAGCAATACTTGA 693
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 Db 604 GATCCAGGGCATCACTCGGGAAACAGTCAGGGGACTACAGGTGACGTGCTCCAATGACGT 663
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 Db 1024 AGGCTGCGTCTGGCTGCTGCTCTTTCTGGTCTTGCACTGCTCTTCAAAATTTGATGTGA 1083
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Qy 1349 TAAAAA---GAATTCGAAATTTGCCCTTGCAGATATTTAGTCAATGCGAGTTTCTTT- 1404
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 Qy 1464 ACCTCTTTGGTCCAGTGTGGGCAAGGGCTCAGCCTCTCTGCCAC-AGAGTGGCCCCAC 1522
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Search completed: October 30, 2005, 11:25:01
 Job time : 7608 secs

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DE Human PRO337 cDNA sequence SEQ ID NO:55.				
PN W0200200690-A2.				
PD 03-JAN-2002.				
PA (GETH) GENENTECH INC.				
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RESULT 7				
ID ABL95588 standard; cDNA; 1679 BP.				
DE Human angiogenesis related cDNA PRO337 SEQ ID NO: 55.				
PN W0200208284-A2.				
PD 31-JAN-2002.				
PA (GETH) GENENTECH INC.				
PA (BAKE/) BAKER K P.				
PA (FERR/) FERRARA N.				
PA (GERB/) GERBER H.				
PA (GERE/) GERRITSEN M E.				
PA (GODD/) GODDARD A.				
PA (GODO/) GODOWSKI P J.				
PA (GURN/) GURNEY A L.				
PA (HILL/) HILLAN K J.				
PA (MARS/) MARSTERS S A.				
PA (PANJ/) PAN J.				
PA (PAON/) PAONI N F.				
PA (STEP/) STEPHAN J F.				
PA (WATA/) WATANABE C K.				
PA (WILL/) WILLIAMS P M.				
PA (WOOD/) WOOD W I.				
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PN US2002192706-A1.				
PD 19-DEC-2002.				
PA (GETH) GENENTECH INC.				
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Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 9				
ID ACA03790 standard; cDNA; 1679 BP.				
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PN US2003036180-A1.				
PD 20-FEB-2003.				
PA (GETH) GENENTECH INC.				
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Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 10				
ID ACA04996 standard; cDNA; 1679 BP.				
DE Novel human secreted and transmembrane protein PRO337 cDNA.				
PN US2003032063-A1.				
PD 13-FEB-2003.				
PA (GETH) GENENTECH INC.				
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Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 11				
ID ACA72056 standard; cDNA; 1679 BP.				
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.				
PN US2002177553-A1.				
PD 28-NOV-2002.				
PA (GETH) GENENTECH INC.				
Query Match	100.0%;	Score 1679;	DB 8;	Length 1679;
Best Local Similarity	100.0%;	Pred. No. 0;		
RESULT 12				
ID ABX89328 standard; cDNA; 1679 BP.				
DE DNA encoding novel secreted and transmembrane protein PRO337.				
PN US2003017563-A1.				
PD 23-JAN-2003.				
PA (GETH) GENENTECH INC.				
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Best Local Similarity	100.0%;	Pred. No. 0;		

RESULT 13
ID ABX92696 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 14
ID ACD41982 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 15
ID ACA60526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
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RESULT 16
ID ACA04516 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 17
ID ACA66437 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 18
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200308063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 19
ID ACA04211 standard; cDNA; 1679 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 8; Length 1679;
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RESULT 20
ID ACA65657 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 21
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200302328-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 22

ID ADA76325 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 23
ID ABT44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 24
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
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RESULT 25
ID ADA61598 standard; cDNA; 1679 BP.
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PD 13-MAR-2003.
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DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 27
ID ADB27924 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
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DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 29
ID ADB15967 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
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ID ADA47753 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
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ID ADA67548 standard; cDNA; 1679 BP.

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DE Human PRO polynucleotide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
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  PD 10-APR-2003.
  PA (GETH ) GENENTECH INC.
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  PN US2003082693-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  ID ADA97063 standard; cDNA; 1679 BP.
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  PN US2003082705-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  DE Human PRO polynucleotide #188.
  PN US2003082763-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  DE Human PRO polynucleotide #188.
  PN US2003087349-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
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  PA (GETH ) GENENTECH INC.
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  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
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  PD 24-APR-2003.
  PA (GETH ) GENENTECH INC.
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  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PN US2003082710-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
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  PD 06-MAR-2003.
  PA (GETH ) GENENTECH INC.
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  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
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  PD 20-MAR-2003.
  PA (GETH ) GENENTECH INC.
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  PN US2003068798-A1.
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PD 10-APR-2003.
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PN US200307713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
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DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
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PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 53
ID ADA85229 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 54
ID ADA84747 standard; cDNA; 1679 BP.
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PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 55
ID ADB30003 standard; cDNA; 1679 BP.
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PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 56
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DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
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PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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PD 17-APR-2003.
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PD 24-APR-2003.
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PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
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ID ADB31107 standard; cDNA; 1679 BP.
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PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 63
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 64
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 65
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 66
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 67
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
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Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 68
ID ADA95959 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 69
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 70
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 71
ID ACB82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 72
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 73
ID ADA77532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 74
ID ADB18272 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 75
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 76
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 77
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 78
ID ADB28476 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 79
ID ADB29028 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 80
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 81
ID ADA88610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 82
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 83
ID ADB27372 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 84
ID ADB23305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 85
ID ACD30273 standard; cDNA; 1679 BP.
DE Human cDNA encoding Pro337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 86
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.

PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 87
ID ADA66996 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 88
ID ADB22857 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 89
ID ADB23630 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 90
ID ADA92352 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 91
ID ADB15415 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 92
ID ADB83615 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 93
ID ADB80721 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 94
ID ADB73262 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 95
ID ADB38667 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082766-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 96
ID ADB78344 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 97
ID ADB38115 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 98
ID ADB66587 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 9; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 99
ID ADB84992 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 100
ID ADB89667 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 101
ID ADB90399 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 102
ID ADB39500 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 103
ID ADB78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 104
ID ADB74028 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003045462-A1.
PD 06-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 105
ID ADB87164 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 106
ID ADB84746 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
FN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 107
ID ADB47123 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 108
ID ADB83861 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 109
ID ADB86730 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 110
ID ADB73016 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 111
ID ADB76744 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
FN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 112
ID ADB77335 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 113
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 114
ID ADB35596 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 115
ID ADB33940 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 116
ID ADB35044 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 117
ID ADB36148 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
FN US2003077720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 118
ID ADB46543 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 119
ID ADC44170 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 120
ID ADC61930 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 121
ID ADC63894 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 122
ID ADC66994 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;

Best Local Similarity 100.0%; Pred. No. 0;
RESULT 123
ID ADC69118 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 124
ID ADC63178 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 125
ID ADC68243 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 126
ID ADC41563 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 127
ID ADC67618 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 128
ID ADC62554 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 129
ID ADC36854 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003088065-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 130
ID ADC42187 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 131
ID ADC21844 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 132
ID ADC50416 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 133
ID ADC71963 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 134
ID ADC59942 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 135
ID ADC49875 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 136
ID ADC49074 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 137
ID ADC49591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 138
ID ADC47452 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 139
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 140
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 141

ID ADC60494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 142
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 143
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 144
ID ADC54594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 145
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 146
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 147
ID ADC55956 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 148
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 149
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 150
ID ADD03200 standard; cDNA; 1679 BP.

DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 151
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 152
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 153
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 154
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 155
ID ADC78072 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 156
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 157
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 158
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 159
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 160
ID ADD10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 161
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 162
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200308066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 163
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 164
ID ADD11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 165
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 166
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 167
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 168
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.

PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 169
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 170
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 171
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 172
ID ADD37097 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 173
ID ADD51777 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 174
ID ADD02576 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 175
ID ADD50516 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 176
ID ADD02010 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 177
ID ADD54192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 178
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 179
ID ADE51281 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 180
ID ADE49556 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 181
ID ADE92509 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 182
ID ADE91405 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 183
ID ADE04019 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 184
ID ADE32316 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 185
ID ADE22248 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 186
ID ADE79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 187
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 188
ID ADE16724 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 189
ID ADE73339 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 190
ID ADE42008 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 191
ID ADE17825 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 192
ID ADE91957 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 193
ID ADE33420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 194
ID ADE33972 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 195
ID ADE80024 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;

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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 196
ID ADP93061 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 197
ID ADD72697 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 198
ID ADE19481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 199
ID ADE18929 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 200
ID ADE43125 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 201
ID ADP95914 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 202
ID ADE22800 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 203
ID ADD78918 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 204
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 205
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 206
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 207
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 208
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 209
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 210
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 211
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 212
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 213
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 214
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ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 215
ID ADF97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 216
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 217
ID ADG53119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 218
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 219
ID ADG80013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
FN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 220
ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
FN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 221
ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 222
ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 223
ID ADI61199 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.
FN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 224
ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 225
ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 226
ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 227
ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 228
ID ADH81386 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 229
ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 230
ID ACA6903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
FN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 231
ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
FN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 232
ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 233
ID AC68655 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 234
ID AC67181 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 10; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 235
ID ADM2555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 236
ID ADNI5954 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 237
ID ADNI6583 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 238
ID ADNI5402 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 239
ID ADNI4850 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 11; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 240
ID ADC4828 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 241
ID ADC8112 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092115-A1.

PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 242
ID ADE20999 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 243
ID ADE05843 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 244
ID ADD76560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 245
ID ADD75072 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 246
ID ADD75818 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 247
ID ADD85050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 248
ID ADD86876 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 249
ID ADE20753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 250
ID ADE39050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200309362-A1.
PD 22-MAY-2003.

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PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 251
ID ADE21245 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 252
ID ADE87924 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 253
ID ADE86328 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 254
ID ADE05597 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 255
ID ADE73582 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 256
ID ADE75776 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 257
ID ADE48856 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 258
ID ADE78422 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 259
ID ADE41305 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 260
ID ADE21245 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 261
ID ADE77360 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 262
ID ADE20507 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 263
ID ADE75572 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 264
ID ADE74088 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 265
ID ADE74334 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 266
ID ADE76064 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 267
ID ADE85556 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 268
ID ADE23904 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 269
ID ADE24547 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 270
ID ADD87372 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 271
ID ADE05105 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 272
ID ADD75318 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 273
ID ADD76862 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 274
ID ADD86630 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 275
ID ADE69238 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 276
ID ADE41198 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 277
ID ADD78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 278
ID ADE18377 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 279
ID ADE88686 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 280
ID ADE89957 standard; cDNA; 1679 BP.
DE Human CDNA encoding secreted/transmembrane protein, PRO337.
PN US200310181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHENNAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 281
ID ADD77606 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 282
ID ADD77852 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
RESULT 283
ID ADD85310 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
Pred. No. 0;
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Best Local Similarity 100.0%; Pred. No. 0;
RESULT 284
ID ADE94706 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 285
ID ADE91117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 286
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 287
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 288
ID ADE24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 289
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 290
ID ADF61597 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 291
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 292
ID ADF40289 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 293
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 294
ID ADE91117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 295
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 296
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 297
ID ADE24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 298
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 299
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 300
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 301
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 303
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 304
ID ADF2264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 305
ID ADF90565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 306
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 307
ID ADF33216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 308
ID ADF25582 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 309
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 310
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 311
ID ADF46709 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 312
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 313
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 314
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 315
ID ADG02291 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 316
ID ADG22077 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 317
ID ADG20147 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 318
ID ADF98053 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 319
ID ADG24270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 320
ID ADF98624 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 321
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 322
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 323
ID ADG16761 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 324
ID ADG05220 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 325
ID ADG19487 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 326
ID ADG11255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 327
ID ADG13324 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 328
ID ADG08381 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 329
ID ADG15551 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003219885-A1.

PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 330
ID ADG12034 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 331
ID ADF96949 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 332
ID ADG06134 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207374-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 333
ID ADG23718 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 334
ID ADG04007 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 335
ID ADG24908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 336
ID ADF94591 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 337
ID ADG07205 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1679; DB 12; Length 1679;
RESULT 338
ID ADG07757 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 339
ID ADG06687 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 340
ID ADG55252 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 341
ID ADG60916 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 342
ID ADG262020 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 343
ID ADG82221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 344
ID ADG57460 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 345
ID ADG56908 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 346
ID ADG55804 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 347
ID ADG58564 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 348
ID ADG70930 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 349
ID ADH39031 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 350
ID ADG58012 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 351
ID ADG53596 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 352
ID ADG71482 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 353
ID ADG50695 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 354
ID ADG81669 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 355
ID ADH30631 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 356
ID ADG63633 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;

RESULT 357
ID ADH1198 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 358
ID ADG50071 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 359
ID ADG51943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 360
ID ADG52420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 361
ID ADG54148 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 362
ID ADG49447 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 363
ID ADG81117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 364
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 365
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 366

ID ADG48823 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 367
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 368
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 369
ID ADG54700 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 370
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 371
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 372
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 373
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 374
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 375
ID ADG62719 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 376
ID ADI181164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 377
ID ADI33591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 378
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 379
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 380
ID ADG09907 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 381
ID ADI15378 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 382
ID ADG09255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 383
ID ADI14710 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 384
ID ADI29846 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.

PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 385
ID ADI18305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 386
ID ADM27243 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 387
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 388
ID ADJ77481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 389
ID ADK82833 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 390
ID ADK66601 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 391
ID ADJ65603 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 392
ID ADM27739 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 393
ID ADM17521 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004048332-A1.

PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 394
ID ADL07355 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
FN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 395
ID ADM42463 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 396
ID ADM28325 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 12; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 397
ID AD195807 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
FN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 398
ID AD196359 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
FN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1679; DB 13; Length 1679;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 399
ID AA247893 standard; cDNA; 1693 BP.
DE Human protein encoding cDNA SEQ ID NO:3.
FN WO958668-A1.
PD 18-NOV-1999.
PA (ONOY) ONO PHARM CO LTD.
Query Match 99.0%; Score 1661.4; DB 3; Length 1693;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 400
ID AAA88791 standard; cDNA; 2012 BP.
DE Human SECX cDNA Clone 11753149.0.37.
FN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 97.9%; Score 1643.4; DB 3; Length 2012;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 401
ID ADD18290 standard; DNA; 2012 BP.
DE Human molecule (MOL) protein MOL11 DNA sequence.
FN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 97.9%; Score 1643.4; DB 10; Length 2012;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 402
ID AA88790 standard; cDNA; 1603 BP.
DE Human SECX cDNA Clone 11753149.0.6.
FN WO200061754-A2.
PD 19-OCT-2000.

PA (CURA-) CURAGEN CORP.
Query Match 95.4%; Score 1601.4; DB 3; Length 1603;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 403
ID ADD18288 standard; DNA; 1603 BP.
DE Human molecule (MOL) protein MOL10 DNA sequence.
FN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Query Match 95.4%; Score 1601.4; DB 10; Length 1603;
Best Local Similarity 99.9%; Pred. No. 0;
RESULT 404
ID ABK49272 standard; cDNA; 1873 BP.
DE Human Kruppel associated DNA binding protein 42 cDNA.
FN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 89.9%; Score 1509.8; DB 6; Length 1873;
Best Local Similarity 93.1%; Pred. No. 0;
RESULT 405
ID AAI57869 standard; cDNA; 1678 BP.
DE Human polynucleotide SEQ ID NO 72.
FN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 86.8%; Score 1457; DB 4; Length 1678;
Best Local Similarity 100.0%; Pred. No. 0;
RESULT 406
ID ADQ22984 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;
Best Local Similarity 98.9%; Pred. No. 0;
RESULT 407
ID ADQ24601 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 85.7%; Score 1438.4; DB 12; Length 3987;
Best Local Similarity 98.9%; Pred. No. 0;
RESULT 408
ID ABT17390 standard; DNA; 1839 BP.
DE Human IG gene related nucleic acid SEQ ID No 16.
FN WO20029040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 409
ID ABX76448 standard; DNA; 1839 BP.
DE Lung cancer-associated polynucleotide #312.
FN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 85.3%; Score 1432.8; DB 8; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 410
ID ADG63208 standard; DNA; 1839 BP.
DE Human neurotrophin DNA.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 85.3%; Score 1432.8; DB 10; Length 1839;
Best Local Similarity 98.5%; Pred. No. 0;
RESULT 411
ID ADN39137 standard; cDNA; 1839 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
FN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.

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Query Match
Best Local Similarity 85.3%; Score 1432.8; DB 11; Length 1839;
RESULT 412
ID ADT121817 standard; cDNA; 2884 BP.
DE Novel human protein cDNA #76.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 85.3%; Score 1432.8; DB 10; Length 2884;
RESULT 413
ID ADT35771 standard; DNA; 2129 BP.
DE Human neurotrophin DNA.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 84.5%; Score 1418.2; DB 10; Length 2129;
RESULT 414
ID AA159655 standard; cDNA; 1690 BP.
DE Human polynucleotide SEQ ID NO 3644.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 78.3%; Score 1315; DB 4; Length 1690;
RESULT 415
ID ADT121360 standard; cDNA; 1690 BP.
DE Novel human expressed sequence tag, EST #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 78.3%; Score 1315; DB 10; Length 1690;
RESULT 416
ID AA247892 standard; cDNA; 1032 BP.
DE Human protein encoding cDNA SEQ ID NO:2.
PN WO958668-A1.
PD 18-NOV-1999.
PA (ONOF) ONO PHARM CO LTD.
Query Match
Best Local Similarity 61.5%; Score 1032; DB 3; Length 1032;
RESULT 417
ID ABT17393 standard; DNA; 1061 BP.
DE Human IG gene related nucleic acid SEQ ID No 19.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 58.0%; Score 974; DB 8; Length 1061;
RESULT 418
ID AA247894 standard; cDNA; 939 BP.
DE Human protein encoding cDNA SEQ ID NO:5.
PN WO958668-A1.
PD 18-NOV-1999.
PA (ONOF) ONO PHARM CO LTD.
Query Match
Best Local Similarity 55.9%; Score 939; DB 3; Length 939;
RESULT 419
ID ABT17391 standard; DNA; 1094 BP.
DE Human IG gene related nucleic acid SEQ ID No 17.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 55.4%; Score 931; DB 8; Length 1094;
RESULT 420
ID ADG63210 standard; DNA; 1068 BP.
DE Human neurotrophin DNA +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 54.2%; Score 910.4; DB 10; Length 1068;
Query Match
Best Local Similarity 85.3%; Score 1432.8; DB 11; Length 1839;
RESULT 421
ID ABT17392 standard; DNA; 1130 BP.
DE Human IG gene related nucleic acid SEQ ID No 18.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 53.1%; Score 891.8; DB 8; Length 1130;
RESULT 422
ID ADG63212 standard; DNA; 1104 BP.
DE Human neurotrophin DNA +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 52.1%; Score 874.4; DB 10; Length 1104;
RESULT 423
ID ADG63214 standard; DNA; 1140 BP.
DE Human neurotrophin DNA +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match
Best Local Similarity 50.7%; Score 851.8; DB 10; Length 1140;
RESULT 424
ID AA44536 standard; cDNA; 832 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1111.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 47.9%; Score 803.8; DB 3; Length 832;
RESULT 425
ID ADE07017 standard; DNA; 3298 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 33.6%; Score 564.2; DB 10; Length 3298;
RESULT 426
ID AAQ51015 standard; cDNA; 3069 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN) LEE N M.
PA (LOHH) LOH H H.
PA (LIPP) LIPPMAN D.
Query Match
Best Local Similarity 32.2%; Score 540.8; DB 2; Length 3069;
RESULT 427
ID ABT17409 standard; DNA; 1478 BP.
DE Human IG gene related nucleic acid SEQ ID No 35.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 32.1%; Score 539.2; DB 8; Length 1478;
RESULT 428
ID ABT17406 standard; DNA; 3110 BP.
DE Human IG gene related nucleic acid SEQ ID No 32.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 32.1%; Score 539.2; DB 8; Length 3110;
RESULT 429
ID ADG63206 standard; DNA; 3110 BP.
DE Opioid-binding protein/cell adhesion molecule-like DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
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Query Match      32.1%; Score 539.2; DB 10; Length 3110;
Best Local Similarity 73.0%; Pred. No. 1.1e-131;
RESULT 430
ID ABT17408 standard; DNA; 1071 BP.
DE Human IG gene related nucleic acid SEQ ID No 34.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match      32.0%; Score 537.6; DB 8; Length 1071;
Best Local Similarity 72.9%; Pred. No. 1.7e-131;
RESULT 431
ID ABT17407 standard; DNA; 1080 BP.
DE Human IG gene related nucleic acid SEQ ID No 33.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match      32.0%; Score 537.6; DB 8; Length 1080;
Best Local Similarity 72.9%; Pred. No. 1.7e-131;
RESULT 432
ID AAQ51017 standard; cDNA; 2179 BP.
DE Rat opioid receptor gene.
FN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match      31.1%; Score 523; DB 2; Length 2179;
Best Local Similarity 72.2%; Pred. No. 1.7e-127;
RESULT 433
ID AAQ51016 standard; cDNA; 2337 BP.
DE Rat opioid receptor gene.
FN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Query Match      31.1%; Score 523; DB 2; Length 2337;
Best Local Similarity 72.2%; Pred. No. 1.8e-127;
RESULT 434
ID AAQ51016 standard; cDNA; 2337 BP.
DE Human EST DNA42301.
FN WO9946281-A2.
PD 16-SEP-1999.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 2; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 435
ID AAC78591 standard; cDNA; 503 BP.
DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
FN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 3; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 436
ID ACA63893 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein DNA42301.
FN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 437
ID ACA72057 standard; DNA; 503 BP.
DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
FN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 438
ID ABX92697 standard; cDNA; 503 BP.
DE Human PRO337 EST polynucleotide sequence.
PN US2002169284-A1.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 439
ID ACA66438 standard; cDNA; 503 BP.
DE Human secreted/transmembrane protein EST DNA42301.
FN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 8; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 440
ID ADA25063 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
FN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 441
ID ACD30039 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
FN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 442
ID ADA12724 standard; cDNA; 503 BP.
DE Human secreted/transmembrane polypeptide PRO337 EST.
FN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 443
ID ACD29454 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #134.
FN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 9; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 444
ID ADB74030 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
FN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 445
ID ADB76746 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
FN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 446
ID ADC41172 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match      30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 447
ID ADC61932 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
FN US2003049684-A1.
PD 13-MAR-2003.
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PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 448
ID ADE63896 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 449
ID ADE66996 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 450
ID ADE69120 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 451
ID ADE63180 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 452
ID ADE68245 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 453
ID ADE641565 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 454
ID ADE67620 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 455
ID ADE62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 456
ID ADC42189 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 457
ID ADE49558 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 458
ID ADE35612 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 459
ID ADE16726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 460
ID ADE73341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 461
ID ADD72699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 462
ID ADE17350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 463
ID ADF47364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 464
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 465
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 466
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO3337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 466
ID AD161201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 467
ID ACD42858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050339-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 10; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 468
ID ADE48858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 469
ID ADE89959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 470
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 471
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 472
ID ADF46087 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 473
ID ADF24483 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 474
ID ADF40915 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 475
ID ADF23859 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 476
ID ADF33842 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 477
ID ADF27309 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 478
ID ADF27945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 479
ID ADF41539 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 480
ID ADF33218 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;

Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 481
ID ADP25584 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 482
ID ADP26685 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 483
ID ADP34474 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 484
ID ADP46711 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 485
ID ADG50697 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 486
ID ADG50073 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 487
ID ADG51945 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 488
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 489
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;

RESULT 490
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 491
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 492
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 493
ID ADH25746 standard; cDNA; 503 BP.
DE Human DNA42301 expressed sequence tag (EST) SEQ ID NO:524.
PN EPI386931-A1.
PD 04-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 494
ID ADM17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 495
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 30.0%; Score 503; DB 12; Length 503;
Best Local Similarity 100.0%; Pred. No. 1.6e-122;
RESULT 496
ID AAC91321 standard; cDNA; 537 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN WO200073509-A2.
PD 07-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 29.3%; Score 491.2; DB 4; Length 537;
Best Local Similarity 98.6%; Pred. No. 2.2e-119;
RESULT 497
ID ADM47274 standard; DNA; 617 BP.
DE Oestrogen regulated protein like NOVX 25b gene.
PN WO2003083039-A2.
PD 09-OCT-2003.
PA (CURA-) CURAGEN CORP.
Query Match 26.8%; Score 449.4; DB 11; Length 617;
Best Local Similarity 97.6%; Pred. No. 2.8e-108;
RESULT 498
ID AAF93346 standard; cDNA; 452 BP.
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Query Match 26.3%; Score 441.2; DB 5; Length 452;
Best Local Similarity 99.1%; Pred. No. 3.5e-106;
RESULT 499

ID ACH15238 standard; cDNA; 437 BP.
DE Human adult brain cDNA #2450.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.
PA (DICK//) DICKSON M C.
PA (JONE//) JONES L W.
Query Match 24.1%; Score 404; DB 9; Length 437;
Best Local Similarity 97.4%; Pred. No. 2.4e-96;
RESULT 500
ID AAS78035 standard; cDNA; 484 BP.
DE Human encoding novel human diagnostic protein #13839.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 23.6%; Score 396; DB 5; Length 484;
Best Local Similarity 92.3%; Pred. No. 3.4e-94;
RESULT 501
ID ACH46276 standard; cDNA; 409 BP.
DE Human infant brain cDNA #339.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA//) DRMANAC R T.
PA (LABA//) LABAT I.
PA (STAC//) STACHE-CRAIN B.
PA (DICK//) DICKSON M C.
PA (JONE//) JONES L W.
Query Match 21.1%; Score 353.8; DB 9; Length 409;
Best Local Similarity 98.1%; Pred. No. 4.6e-83;
RESULT 502
ID AAL50356 standard; cDNA; 1411 BP.
DE Human limbic system associated membrane protein 36-85 coding sequence.
FN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
Query Match 20.5%; Score 343.8; DB 6; Length 1411;
Best Local Similarity 62.1%; Pred. No. 3.8e-80;
RESULT 503
ID AAT42080 standard; cDNA to mRNA; 1238 BP.
DE Rat LAMP coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.4%; Score 343; DB 2; Length 1238;
Best Local Similarity 62.0%; Pred. No. 5.8e-80;
RESULT 504
ID ABX63560 standard; cDNA; 1195 BP.
DE Human cDNA #560 differentially expressed in activated vascular tissue.
FN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND//) BANDMAN O.
Query Match 20.3%; Score 341.6; DB 8; Length 1195;
Best Local Similarity 60.1%; Pred. No. 1.3e-79;
RESULT 505
ID ADI12674 standard; cDNA; 1195 BP.
DE Human steroid-induced C3A liver cell cDNA #403.
FN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 20.3%; Score 341.6; DB 12; Length 1195;
Best Local Similarity 60.1%; Pred. No. 1.3e-79;
RESULT 506
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 2.2e-79;
RESULT 507
ID AAT42079 standard; cDNA to mRNA; 977 BP.
DE Human LAMP residues 8-332 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 977;
Best Local Similarity 63.3%; Pred. No. 2.2e-79;
RESULT 508
ID AAT42081 standard; cDNA to mRNA; 1014 BP.
DE Rat LAMP coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 2.3e-79;
RESULT 509
ID ABT17402 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 28.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 20.3%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2.3e-79;
RESULT 510
ID ABT17404 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 30.
FN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 20.3%; Score 340.6; DB 8; Length 1017;
Best Local Similarity 63.3%; Pred. No. 2.3e-79;
RESULT 511
ID AAT42086 standard; cDNA to mRNA; 861 BP.
DE Human LAMP residues 29-315 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.2%; Score 338.6; DB 2; Length 861;
Best Local Similarity 63.7%; Pred. No. 7.1e-79;
RESULT 512
ID AAT42082 standard; cDNA to mRNA; 912 BP.
DE Human mature LAMP coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.2%; Score 338.6; DB 2; Length 912;
Best Local Similarity 63.7%; Pred. No. 7.3e-79;
RESULT 513
ID AAT42085 standard; cDNA to mRNA; 945 BP.
DE Rat LAMP residues 1-315 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.1%; Score 337.4; DB 8; Length 945;
Best Local Similarity 63.1%; Pred. No. 1.5e-78;
RESULT 514
ID ABZ72624 standard; cDNA; 1757 BP.
DE Human GENSET cDNA clone name SLAMP.
FN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST-) GENSET SA.
Query Match 20.1%; Score 337.4; DB 8; Length 1757;
Best Local Similarity 63.8%; Pred. No. 2.1e-78;
RESULT 515
ID AAT42083 standard; cDNA to mRNA; 930 BP.
DE Rat mature LAMP coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 20.1%; Score 337; DB 2; Length 930;
Best Local Similarity 62.1%; Pred. No. 2e-78;
RESULT 516
ID ABT17403 standard; DNA; 1075 BP.
DE Human IG gene related nucleic acid SEQ ID No 29.

PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 20.0%; Score 335; DB 8; Length 1075;
Best Local Similarity 63.5%; Pred. No. 7.1e-78;
RESULT 517
ID AAT42087 standard; cDNA to mRNA; 861 BP.
DE Rat LAMP residues 29-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 19.9%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 1.3e-77;
RESULT 518
ID AAT42116 standard; cDNA to mRNA; 1307 BP.
DE Rat LAMP clone 6c coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 19.8%; Score 331.8; DB 2; Length 1307;
Best Local Similarity 63.3%; Pred. No. 5.5e-77;
RESULT 519
ID AAT43425 standard; cDNA; 1153 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 19.4%; Score 325.2; DB 4; Length 1153;
Best Local Similarity 62.7%; Pred. No. 2.9e-75;
RESULT 520
ID AAC19214 standard; cDNA; 333 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23289.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST-) GENSET.
Query Match 18.8%; Score 316.2; DB 3; Length 333;
Best Local Similarity 97.0%; Pred. No. 3.7e-73;
RESULT 521
ID ABT17405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID No 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 18.7%; Score 314.6; DB 8; Length 898;
Best Local Similarity 61.6%; Pred. No. 1.6e-72;
RESULT 522
ID AAT42094 standard; cDNA to mRNA; 756 BP.
DE Human LAMP residues 46-294 coding sequence.
PN WO9630052 A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 18.1%; Score 303.6; DB 2; Length 756;
Best Local Similarity 63.5%; Pred. No. 1.2e-69;
RESULT 523
ID AAT42095 standard; cDNA to mRNA; 756 BP.
DE Rat LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 17.8%; Score 298.2; DB 2; Length 756;
Best Local Similarity 63.0%; Pred. No. 3.3e-68;
RESULT 524
ID AAT78034 standard; cDNA; 443 BP.
DE DNA encoding novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 17.7%; Score 296.8; DB 5; Length 443;
Best Local Similarity 89.6%; Pred. No. 5.9e-68;
RESULT 525
ID ABT17401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID No 27.
PN WO200299040-A2.

PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 16.6%; Score 279; DB 8; Length 1809;
Best Local Similarity 57.8%; Pred. No. 6.2e-63;
RESULT 526
ID ADS82049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS) LG LIFE SCI LTD.
Query Match 16.3%; Score 274.2; DB 13; Length 4891;
Best Local Similarity 58.6%; Pred. No. 1.9e-61;
RESULT 527
ID ABQ82338 standard; cDNA; 1165 BP.
DE Human NOV12b encoding cDNA SEQ ID NO:25.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.2%; Score 272.6; DB 6; Length 1165;
Best Local Similarity 58.4%; Pred. No. 2.4e-61;
RESULT 528
ID ADI28059 standard; cDNA; 1327 BP.
DE ECMAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 16.2%; Score 272.6; DB 6; Length 1327;
Best Local Similarity 58.4%; Pred. No. 2.6e-61;
RESULT 529
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 4; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 530
ID ABK3536 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 6; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 531
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 532
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 533
ID ACA04534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 8; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 534
ID ACA68497 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.


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Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 553
ID ADC21720 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 554
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308064-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 555
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308070-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 556
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308071-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 557
ID . ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308072-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 558
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 559
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 560
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 561
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200308066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 562
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 563
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 564
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 565
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 566
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 567
ID ADG63810 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 568
ID ACA66841 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO polypeptide #1.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 569
ID ACD42405 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 570
ID ACD68593 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 10; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 571
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ID ADC48704 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 572
ID ADE20875 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 573
ID ADE05719 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 574
ID ADD74948 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 575
ID ADD75694 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 576
ID ADB84926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 577
ID ADD86752 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 578
ID ADE20629 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 579
ID ADE38926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 580
ID ADE05473 standard; cDNA; 4834 BP.

DE Human PRO polynucleotide #1.
FN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 581
ID ADD73458 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 582
ID ADD78298 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 583
ID ADE21121 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 584
ID ADD7236 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 585
ID ADE20383 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 586
ID ADD75448 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 587
ID ADD73964 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 588
ID ADD74210 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 589
ID ADD75940 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 590
ID ADD85432 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 591
ID ADE04981 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 592
ID ADD75194 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 593
ID ADD76738 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 594
ID ADD86506 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 595
ID ADE41224 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 596
ID ADD77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 597
ID ADD77482 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 598
ID ADD77728 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100730-A1.

PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 599
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 600
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 601
ID ADD74456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 602
ID ADD76984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 603
ID ADD85678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 604
ID ADE05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 605
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 606
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 607
ID ADG27068 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096962-A1.
PD 22-MAY-2003.

PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 608
ID ADG1131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 609
ID ADG1131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 610
ID ADF9467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 611
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 612
ID ADH38907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 613
ID ADG63658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
FN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 614
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 615
ID ADI33467 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 616
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH) GENENTECH INC.

Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 617
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 618
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
FN US200404179-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 619
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
FN US200404180-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.2%; Score 272.6; DB 12; Length 4834;
Best Local Similarity 58.4%; Pred. No. 5e-61;
RESULT 620
ID ABO82337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
FN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.2%; Score 272.2; DB 6; Length 1196;
Best Local Similarity 58.3%; Pred. No. 3.2e-61;
RESULT 621
ID AEN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
FN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 271; DB 6; Length 1119;
Best Local Similarity 58.3%; Pred. No. 6.3e-61;
RESULT 622
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBF20110210.
FN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 16.1%; Score 271; DB 10; Length 2383;
Best Local Similarity 58.3%; Pred. No. 9.3e-61;
RESULT 623
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
FN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 3; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 624
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
FN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 8; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 625
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
FN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH) GENENTECH INC.

ID ADC42276 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 645
ID AD849645 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 646
ID AD835699 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 647
ID AD816813 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 648
ID AD873428 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 649
ID AD872786 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 650
ID AD817437 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 651
ID ADF47451 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 652
ID AD853208 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003216361-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 653
ID ADG60528 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 654
ID AD161288 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003077700-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 655
ID ACD42944 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
FN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 10; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 656
ID AD848945 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 657
ID ADE90046 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 658
ID ADF61686 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
FN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 659

ID ADF40378 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 660
ID ADF46174 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 661
ID ADF24570 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 662
ID ADF41002 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 663
ID ADF23946 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 664
ID ADF33929 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 665
ID ADF27396 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 666
ID ADF28032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 667
ID ADF41626 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 668
ID ADF33305 standard; cDNA; 2840 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 669
ID ADF25671 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 670
ID ADF26772 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 671
ID ADF34561 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 672
ID ADF46798 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 673
ID ADF50784 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 674
ID ADF50160 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 675
ID ADF52032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 676
ID ADF49536 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 677
ID ADF48912 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.

PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 678
ID ADG51408 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 679
ID ADG59352 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 680
ID ADG62808 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 681
ID ADM17610 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 682
ID ADL07444 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Query Match 16.0%; Score 269.4; DB 12; Length 2840;
Best Local Similarity 58.2%; Pred. No. 2.7e-60;
RESULT 683
ID ADP28685 standard; DNA; 834 BP.
DE Human secreted protein encoding sequence SEQ ID #683.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 15.5%; Score 260.4; DB 12; Length 834;
Best Local Similarity 59.5%; Pred. No. 3.5e-58;
RESULT 684
ID ADH71401 standard; DNA; 926 BP.
DE Human gene of the invention NOV111 SEQ ID NO:297.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 926;
Best Local Similarity 59.5%; Pred. No. 3.7e-58;
RESULT 685
ID ADH71405 standard; DNA; 927 BP.
DE Human gene of the invention NOV11k SEQ ID NO:301.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 927;
Best Local Similarity 59.5%; Pred. No. 3.7e-58;
RESULT 686
ID ADH71409 standard; DNA; 946 BP.
DE Human gene of the invention NOV11m SEQ ID NO:305.
PN WO2003102155-A2.

PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 946;
Best Local Similarity 59.5%; Pred. No. 3.7e-58;
RESULT 687
ID ADH71393 standard; DNA; 946 BP.
DE Human gene of the invention NOV11e SEQ ID NO:289.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 946;
Best Local Similarity 59.5%; Pred. No. 3.7e-58;
RESULT 688
ID ADH71395 standard; DNA; 976 BP.
DE Human gene of the invention NOV11f SEQ ID NO:291.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 3.8e-58;
RESULT 689
ID ADH71415 standard; DNA; 976 BP.
DE Human gene of the invention NOV11p SEQ ID NO:311.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 3.8e-58;
RESULT 690
ID ADH71389 standard; DNA; 976 BP.
DE Human gene of the invention NOV11c SEQ ID NO:285.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 3.8e-58;
RESULT 691
ID ADH71397 standard; DNA; 976 BP.
DE Human gene of the invention NOV11g SEQ ID NO:293.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 976;
Best Local Similarity 59.5%; Pred. No. 3.8e-58;
RESULT 692
ID ABS71699 standard; DNA; 1017 BP.
DE DNA encoding human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1017;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 693
ID ADL35978 standard; cDNA; 1017 BP.
DE Human NOVX cDNA #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Query Match 15.5%; Score 260.4; DB 11; Length 1017;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 694
ID ADH71417 standard; DNA; 1030 BP.

DE Human gene of the invention NOV11q SEQ ID NO:313.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1030;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 695
ID ADH71411 standard; DNA; 1033 BP.
DE Human gene of the invention NOV11n SEQ ID NO:307.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 696
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV11b SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1033;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 697
ID ADH71413 standard; DNA; 1035 BP.
DE Human gene of the invention NOV11o SEQ ID NO:309.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.5%; Score 260.4; DB 12; Length 1035;
Best Local Similarity 59.5%; Pred. No. 3.9e-58;
RESULT 698
ID ABS76364 standard; DNA; 1427 BP.
DE DNA encoding human immunoglobulin superfamily protein IGSFP-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 15.5%; Score 260.4; DB 6; Length 1427;
Best Local Similarity 59.5%; Pred. No. 4.6e-58;
RESULT 699
ID AAD47371 standard; DNA; 2653 BP.
DE Human LP289 DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 15.5%; Score 260.4; DB 8; Length 2653;
Best Local Similarity 59.5%; Pred. No. 6.3e-58;
RESULT 700
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.4%; Score 258.8; DB 6; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;
RESULT 701
ID ADL35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY) MALYANKAR U M.
PA (SHEN) SHENOY S G.
PA (SPYT) SPYTEK K A.
PA (ZERH) ZERHUSEN B D.
PA (PATT) PATTURAJAN M.
PA (GUOX) GUO X.
PA (KEKU) KEKUDA R.
PA (GANG) GANGOLLI E A.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (LILL) LI L.
PA (PADI) PADIGARU M.
Query Match 15.4%; Score 258.8; DB 11; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;

RESULT 702
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV11h SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.4%; Score 258.8; DB 12; Length 1018;
Best Local Similarity 59.4%; Pred. No. 1e-57;
RESULT 703
ID ABS71700 standard; DNA; 1136 BP.
DE DNA encoding human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 6; Length 1136;
Best Local Similarity 59.3%; Pred. No. 2.9e-57;
RESULT 704
ID ADH71403 standard; DNA; 1171 BP.
DE Human gene of the invention NOV11f SEQ ID NO:299.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1171;
Best Local Similarity 59.3%; Pred. No. 2.9e-57;
RESULT 705
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11a SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 3e-57;
RESULT 706
ID ADH71421 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11s SEQ ID NO:317.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.3%; Score 257.2; DB 12; Length 1271;
Best Local Similarity 59.3%; Pred. No. 3e-57;
RESULT 707
ID ADH71419 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11r SEQ ID NO:315.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 15.2%; Score 255.6; DB 12; Length 1271;
Best Local Similarity 59.1%; Pred. No. 8.1e-57;
RESULT 708
ID AAH87585 standard; DNA; 255 BP.
DE Human single nucleotide polymorphism containing DNA sequence #2442.
PN WO9953095-A2.
PD 21-OCT-1999.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 15.2%; Score 255; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.2e-57;
RESULT 709
ID AAX10694 standard; DNA; 251 BP.
DE Human biallelic polymorphic DNA fragment WI-9617.
PN WO9820165-A2.
PD 14-MAY-1998.
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
Query Match 14.9%; Score 250.6; DB 2; Length 251;
Best Local Similarity 99.6%; Pred. No. 7.5e-56;
RESULT 710
ID ABK35606 standard; DNA; 1011 BP.
DE Gene encoding novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 14.7%; Score 246; DB 6; Length 1011;
Best Local Similarity 99.6%; Pred. No. 7.5e-56;

Best Local Similarity 58.4%; Pred. No. 2.5e-54;
RESULT 711
ID ABS71701 standard; DNA; 1169 BP.
DE DNA encoding human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 14.7%; Score 246; DB 6; Length 1169;
Best Local Similarity 58.4%; Pred. No. 2.7e-54;
RESULT 712
ID ADH71407 standard; DNA; 1169 BP.
DE Human gene of the invention NOV111 SEQ ID NO:303.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.7%; Score 246; DB 12; Length 1169;
Best Local Similarity 58.4%; Pred. No. 2.7e-54;
RESULT 713
ID ABA06475 standard; cDNA; 2813 BP.
DE Human cDNA SEQ ID NO: 141.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 14.3%; Score 240.8; DB 4; Length 2813;
Best Local Similarity 58.3%; Pred. No. 1e-52;
RESULT 714
ID ABV83812 standard; cDNA; 2813 BP.
DE Human polynucleotide SEQ ID NO 141.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 14.3%; Score 240.8; DB 6; Length 2813;
Best Local Similarity 58.3%; Pred. No. 1e-52;
RESULT 715
ID ADH71391 standard; DNA; 760 BP.
DE Human gene of the invention NOV11d SEQ ID NO:287.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 14.1%; Score 236.6; DB 12; Length 760;
Best Local Similarity 59.9%; Pred. No. 6.7e-52;
RESULT 716
ID AAD47374 standard; DNA; 2601 BP.
DE Human LP319b DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 13.9%; Score 234; DB 8; Length 2601;
Best Local Similarity 58.3%; Pred. No. 6.1e-51;
RESULT 717
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 13.8%; Score 232; DB 6; Length 1056;
Best Local Similarity 58.1%; Pred. No. 1.3e-50;
RESULT 718
ID ADL35982 standard; cDNA; 1168 BP.
DE Human NOVX cDNA #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
Query Match 13.8%; Score 231.2; DB 11; Length 1168;
Best Local Similarity 58.1%; Pred. No. 2.2e-50;
RESULT 719
ID ADL35980 standard; cDNA; 1133 BP.
DE Human NOVX cDNA #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
Query Match 13.4%; Score 224.8; DB 11; Length 1133;
Best Local Similarity 59.3%; Pred. No. 1.1e-48;
RESULT 720
ID AAS28811 standard; cDNA; 4656 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.
PN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 220.6; DB 4; Length 4656;
Best Local Similarity 57.5%; Pred. No. 2.9e-47;
RESULT 721
ID ADB31536 standard; cDNA; 4656 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 57.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 13.1%; Score 220.6; DB 10; Length 4656;
Best Local Similarity 57.5%; Pred. No. 2.9e-47;
RESULT 722
ID AAS78003 standard; cDNA; 2883 BP.
DE DNA encoding novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 217.8; DB 5; Length 2883;
Best Local Similarity 71.1%; Pred. No. 1.2e-46;
RESULT 723
ID ADE08816 standard; DNA; 2883 BP.
DE Novel DNA-related contig nucleotide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 13.0%; Score 217.8; DB 10; Length 2883;
Best Local Similarity 71.1%; Pred. No. 1.2e-46;
RESULT 724
ID AAD47372 standard; DNA; 754 BP.
DE Human LP289 splice variant (LP343) DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Query Match 12.6%; Score 211.4; DB 8; Length 754;
Best Local Similarity 61.1%; Pred. No. 3.1e-45;
RESULT 725
ID ADP28686 standard; DNA; 666 BP.
DE Human secreted protein encoding sequence SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match 12.5%; Score 210; DB 12; Length 666;

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Best Local Similarity 60.2%; Pred. No. 6.9e-45;
RESULT 726
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL ) LILLY & CO ELI.
Query Match 12.4%; Score 208.6; DB 8; Length 2597;
Best Local Similarity 58.1%; Pred. No. 3.2e-44;
RESULT 727
ID AAC02777 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2775.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (G8ST ) GENSET.
Query Match 11.5%; Score 193.6; DB 3; Length 352;
Best Local Similarity 82.5%; Pred. No. 1.1e-40;
RESULT 728
ID AB199899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
PN WO200220756-A2.
PD 14-MAR-2002.
PA (INCYL ) INCYTE GENOMICS INC.
Query Match 10.7%; Score 180.4; DB 6; Length 5666;
Best Local Similarity 56.1%; Pred. No. 1.4e-36;
RESULT 729
ID ADG63283 standard; DNA; 540 BP.
DE Human OBCAM gene exon 2.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 10.5%; Score 176.6; DB 10; Length 540;
Best Local Similarity 74.9%; Pred. No. 4.3e-36;
RESULT 730
ID AQ083739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (GETH ) GENENTECH INC.
PA (WUTD ) WU T D.
PA (ZHOU ) ZHOU Y.
Query Match 10.4%; Score 175; DB 12; Length 919;
Best Local Similarity 58.0%; Pred. No. 1.5e-35;
RESULT 731
ID AAS78037 standard; cDNA; 767 BP.
DE DNA encoding novel human diagnostic protein #13841.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 10.1%; Score 170.2; DB 5; Length 767;
Best Local Similarity 95.6%; Pred. No. 2.5e-34;
RESULT 732
ID AAF93597 standard; cDNA; 595 BP.
DE Umbilical vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH ) GENENTECH INC.
Query Match 9.7%; Score 163.2; DB 5; Length 595;
Best Local Similarity 62.0%; Pred. No. 1.6e-32;
RESULT 733
ID ABS52769 standard; cDNA; 408 BP.
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
PN WO200246475-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Query Match 9.5%; Score 160; DB 6; Length 408;
Best Local Similarity 63.7%; Pred. No. 9.2e-32;
RESULT 734
ID AAC10355 standard; cDNA; 20C BP.
DE Human secreted protein 5' EST, SEQ ID NO: 14430.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST ) GENSET.

Query Match 8.7%; Score 146; DB 3; Length 200;
Best Local Similarity 100.0%; Pred. No. 3.3e-28;
RESULT 735
ID AAS78038 standard; cDNA; 693 BP.
DE DNA encoding novel human diagnostic protein #13842.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 8.2%; Score 137.2; DB 5; Length 693;
Best Local Similarity 97.9%; Pred. No. 1.3e-25;
RESULT 736
ID AQ021981 standard; DNA; 125 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4801.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.6%; Score 110.8; DB 12; Length 125;
Best Local Similarity 97.6%; Pred. No. 5.3e-19;
RESULT 737
ID AAS78592 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #14396.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 738
ID AAS71904 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #7708.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 739
ID AAS78036 standard; cDNA; 1275 BP.
DE DNA encoding novel human diagnostic protein #13840.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.4%; Score 107; DB 5; Length 1275;
Best Local Similarity 100.0%; Pred. No. 1.8e-17;
RESULT 740
ID ABX71182 standard; cDNA; 913 BP.
DE Novel human cDNA sequence #407.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
PA (GOOD/) GOODRICH R W.
Query Match 6.3%; Score 105.6; DB 8; Length 913;
Best Local Similarity 61.1%; Pred. No. 3.5e-17;
RESULT 741
ID ADQ54463 standard; DNA; 351 BP.
DE Novel canine microarray-related DNA sequence SeqID5765.
PN WO2004063324-A2.
PD 29-JUL-2004.
PA (GENE-) GENE LOGIC INC.
PA (PFIZ ) PFIZER PROD INC.
Query Match 6.2%; Score 104.6; DB 13; Length 351;
Best Local Similarity 60.8%; Pred. No. 3.9e-17;
RESULT 742
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 6.0%; Score 100; DB 2; Length 219;
Best Local Similarity 67.0%; Pred. No. 5.1e-16;
RESULT 743
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
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PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 5.7%; Score 95.2; DB 2; Length 219;
Best Local Similarity 65.6%; Pred. No. 9.6e-15;
RESULT 744
ID AAS67246 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #3050.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 5.5e-14;
RESULT 745
ID AAS71723 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #7527.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 2678;
Best Local Similarity 57.1%; Pred. No. 5.5e-14;
RESULT 746
ID AAS64445 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #249.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 6e-14;
RESULT 747
ID AAS64798 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #602.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.6%; Score 94.4; DB 5; Length 3131;
Best Local Similarity 57.1%; Pred. No. 6e-14;
RESULT 748
ID ADM18382 standard; DNA; 2026 BP.
DE Human chromosome 11qtel subtelomeric DNA probe SEQ ID NO:6.
FN WO2004029283-A2.
PD 08-APR-2004.
PA (CHIL-) CHILDREN'S MERCY HOSPITAL.
Query Match 5.3%; Score 89; DB 12; Length 2026;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
RESULT 749
ID ADG63285 standard; DNA; 420 BP.
DE Human OBCAM gene exon 4.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 4.7%; Score 78.6; DB 10; Length 420;
Best Local Similarity 70.5%; Pred. No. 3.3e-10;
RESULT 750
ID AAT42090 standard; cDNA to mRNA; 177 BP.
DE Human LAMP residues 156-204 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 4.6%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 3.5e-10;
RESULT 751
ID AAT42091 standard; cDNA to mRNA; 177 BP.
DE Rat LAMP residues 156-204 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 4.6%; Score 77.8; DB 2; Length 177;
Best Local Similarity 65.0%; Pred. No. 3.5e-10;
RESULT 752
ID ADG63287 standard; DNA; 480 BP.
DE Human OBCAM gene exon 6.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.

Query Match 4.6%; Score 76.8; DB 10; Length 480;
Best Local Similarity 70.8%; Pred. No. 1.1e-09;
RESULT 753
ID AAS28866 standard; cDNA; 293 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 112.
FN WO200155315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 754
ID ABA06681 standard; cDNA; 293 BP.
DE Human cDNA SEQ ID NO: 347.
FN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 4; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 755
ID ABV84018 standard; cDNA; 293 BP.
DE Human polynucleotide SEQ ID NO 347.
FN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 4.3%; Score 73; DB 6; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 756
ID ADB31591 standard; cDNA; 293 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 112.
FN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 4.3%; Score 73; DB 10; Length 293;
Best Local Similarity 62.9%; Pred. No. 8.3e-09;
RESULT 757
ID ADG63286 standard; DNA; 480 BP.
DE Human OBCAM gene exon 5.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 4.3%; Score 71.4; DB 10; Length 480;
Best Local Similarity 74.4%; Pred. No. 2.8e-08;
RESULT 758
ID AAT42092 standard; cDNA to mRNA; 198 BP.
DE Human LAMP residues 232-297 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 3.8%; Score 64.6; DB 2; Length 198;
Best Local Similarity 61.3%; Pred. No. 1.1e-06;
RESULT 759
ID AAT42093 standard; cDNA to mRNA; 198 BP.
DE Rat LAMP residues 232-297 coding sequence.
FN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Query Match 3.8%; Score 63.4; DB 2; Length 198;
Best Local Similarity 60.7%; Pred. No. 2.4e-06;
RESULT 760
ID ADG63282 standard; DNA; 270 BP.
DE Human OBCAM gene exon 1.
FN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR-) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 3.7%; Score 61.6; DB 10; Length 270;
Best Local Similarity 88.6%; Pred. No. 8.3e-06;
RESULT 761
ID ABN40988 standard; DNA; 60 BP.
DE Human spliced transcript detection oligonucleotide SEQ ID NO:13736.
FN WO200210449-A2.
PD 07-FEB-2002.

PA (COMP-) COMPUGEN INC.
Query Match 3.6%; Score 60; DB 6; Length 60;
Best Local Similarity 100.0%; Pred. No. 1e-05;
RESULT 762
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.5%; Score 58.6; DB 8; Length 2000;
Best Local Similarity 9.5%; Pred. No. 0.00014;
RESULT 763
ID ADG63284 standard; DNA; 420 BP.
DE Human OBCAM gene exon 3.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Query Match 3.4%; Score 57.6; DB 10; Length 420;
Best Local Similarity 65.6%; Pred. No. 0.00012;
RESULT 764
ID ACN55172 standard; cDNA; 248 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-030-Q6-K6-C8, SEQ:9953.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.4%; Score 57.2; DB 13; Length 248;
Best Local Similarity 58.0%; Pred. No. 0.00012;
RESULT 765
ID ABX47608 standard; cDNA; 399 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12773.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.4%; Score 56.6; DB 8; Length 399;
Best Local Similarity 57.7%; Pred. No. 0.00021;
RESULT 766
ID ABV56779 standard; cDNA; 247 BP.
DE Human prostate expression marker cDNA 56770.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.3%; Score 55.6; DB 5; Length 247;
Best Local Similarity 54.4%; Pred. No. 0.00031;
RESULT 767
ID ABK39945 standard; DNA; 6359 BP.
DE Human chemically pretreated gene sequence #13 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.3%; Score 55; DB 6; Length 6359;
Best Local Similarity 66.4%; Pred. No. 0.0023;
RESULT 768
ID ACH15235 standard; cDNA; 514 BP.
DE Human adult brain cDNA #2447.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.2%; Score 54.4; DB 9; Length 514;
Best Local Similarity 62.3%; Pred. No. 0.00093;
RESULT 769
ID ABL32788 standard; DNA; 6171 BP.
DE Human immune system associated gene SEQ ID NO: 761.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.2%; Score 54.4; DB 6; Length 6171;
Best Local Similarity 61.1%; Pred. No. 0.0033;
RESULT 770
ID AAI86998 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 7058.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.2%; Score 53.2; DB 4; Length 390;
Best Local Similarity 58.0%; Pred. No. 0.0017;
RESULT 771
ID AAD05318 standard; cDNA; 671 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HWLFQ64, SEQ ID NO:29.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.2%; Score 53.2; DB 4; Length 671;
Best Local Similarity 60.3%; Pred. No. 0.0022;
RESULT 772
ID ABV58693 standard; cDNA; 607 BP.
DE Human prostate expression marker cDNA 58684.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.2%; Score 53; DB 5; Length 607;
Best Local Similarity 56.6%; Pred. No. 0.0024;
RESULT 773
ID ABV48356 standard; cDNA; 392 BP.
DE Human prostate expression marker cDNA 48347.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 52.8; DB 5; Length 392;
Best Local Similarity 57.1%; Pred. No. 0.0022;
RESULT 774
ID ADH23363 standard; cDNA; 3351 BP.
DE Fruit fly PAK4 serine/threonine kinase cDNA.
PN US2003186254-A1.
PD 02-OCT-2003.
PA (CELL-) CELL SIGNALING TECHNOLOGY INC.
Query Match 3.1%; Score 52.8; DB 12; Length 3351;
Best Local Similarity 58.1%; Pred. No. 0.0064;
RESULT 775
ID ABL33589 standard; DNA; 5567 BP.
DE Human immune system associated gene SEQ ID NO: 1562.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.8; DB 6; Length 5567;
Best Local Similarity 63.3%; Pred. No. 0.0082;
RESULT 776
ID ABL92273 standard; DNA; 5567 BP.
DE Chemically treated DNA repair gene fragment complementary to #41.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.8; DB 6; Length 5567;
Best Local Similarity 63.3%; Pred. No. 0.0082;
RESULT 777
ID ADA71938 standard; DNA; 2000 BP.
DE Rice gene, SEQ ID 5263.
PN WO2003000898-A1.
PD 03-JAN-2003.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 3.1%; Score 52.6; DB 8; Length 2000;
Best Local Similarity 8.4%; Pred. No. 0.0055;
RESULT 778
ID ABQ25430 standard; DNA; 579 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12021.
PN WO200218632-A2.
PD 07-MAR-2002.

PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.4; DB 6; Length 579;
Best Local Similarity 60.6%; Pred. No. 0.0033;
RESULT 779
ID AB025431 standard; DNA; 579 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 12022.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.4; DB 6; Length 579;
Best Local Similarity 60.6%; Pred. No. 0.0033;
RESULT 780
ID ACN81600 standard; DNA; 679 BP.
DE Breast cancer related marker, seq id 2750.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.1%; Score 52.4; DB 11; Length 679;
Best Local Similarity 55.2%; Pred. No. 0.0036;
RESULT 781
ID ABK40004 standard; DNA; 5586 BP.
DE Human chemically pretreated gene sequence #43 strand 2.
PN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.4; DB 6; Length 5586;
Best Local Similarity 59.3%; Pred. No. 0.011;
RESULT 782
ID ACN52334 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-N6-E11, SEQ:7115.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.1%; Score 52.2; DB 13; Length 571;
Best Local Similarity 57.8%; Pred. No. 0.0038;
RESULT 783
ID AAL11399 standard; cDNA; 666 BP.
DE Human breast cancer expressed polynucleotide 3856.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 52.2; DB 4; Length 666;
Best Local Similarity 56.8%; Pred. No. 0.0041;
RESULT 784
ID ABUL1515 standard; cDNA; 2010 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 3.1%; Score 52.2; DB 4; Length 2010;
Best Local Similarity 45.6%; Pred. No. 0.0071;
RESULT 785
ID AAF72803 standard; DNA; 2057 BP.
DE Secreted protein gene #5.
PN WO200107459-A1.
PD 01-FEB-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 52.2; DB 4; Length 2057;
Best Local Similarity 57.8%; Pred. No. 0.0072;
RESULT 786
ID ABS67818 standard; DNA; 3063 BP.
DE Human receptors and membrane associated protein REMAP-40 gene.
PN WO200263006-A2.
PD 15-AUG-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.1%; Score 52.2; DB 6; Length 3063;
Best Local Similarity 64.5%; Pred. No. 0.0088;
RESULT 787
ID ABL33948 standard; DNA; 18218 BP.
DE Human immune system associated gene SEQ ID NO: 1921.

PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52.2; DB 6; Length 18218;
RESULT 788
ID ADS73024 standard; cDNA; 183 BP.
DE Human kidney tumour specific cDNA, SEQ ID 1621.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 3.1%; Score 52; DB 7; Length 183;
Best Local Similarity 60.7%; Pred. No. 0.0024;
RESULT 789
ID ABV58708 standard; cDNA; 484 BP.
DE Human prostate expression marker cDNA 58699.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.1%; Score 52; DB 5; Length 484;
Best Local Similarity 58.3%; Pred. No. 0.0039;
RESULT 790
ID ABT08076 standard; cDNA; 791 BP.
DE Human breast specific coding sequence SEQ ID NO: 22.
PN WO200266607-A2.
PD 29-AUG-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 3.1%; Score 52; DB 6; Length 791;
Best Local Similarity 60.7%; Pred. No. 0.005;
RESULT 791
ID ABL32719 standard; DNA; 5739 BP.
DE Human immune system associated gene SEQ ID NO: 692.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 52; DB 6; Length 5739;
Best Local Similarity 59.5%; Pred. No. 0.014;
RESULT 792
ID ABQ54403 standard; cDNA; 2911 BP.
DE Human ovarian antigen HAPOB30 cDNA, SEQ ID NO:283.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.1%; Score 51.6; DB 6; Length 2911;
Best Local Similarity 59.6%; Pred. No. 0.012;
RESULT 793
ID AAL16619 standard; cDNA; 3508 BP.
DE Human secreted protein clone l0311_8 nucleotide sequence SEQ ID NO:3.
PN WO200009552-A1.
PD 24-FEB-2000.
PA (GEMY) GENETICS INST INC.
Query Match 3.1%; Score 51.6; DB 3; Length 3508;
Best Local Similarity 62.3%; Pred. No. 0.014;
RESULT 794
ID ADS89723 standard; DNA; 5759 BP.
DE Oligonucleotide of the invention SEQ ID NO:739.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 13; Length 5759;
Best Local Similarity 56.5%; Pred. No. 0.017;
RESULT 795
ID AB210109 standard; DNA; 8759 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #249.
PN WO200272722-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 8; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 796
ID AB210237 standard; DNA; 8759 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #377.
PN WO200272722-A2.

PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 8; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 797
ID ADS44213 standard; DNA; 8759 BP.
DE Pretreated genomic DNA region 137.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 10; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 798
ID ADE84147 standard; DNA; 8759 BP.
DE Human lymphoid cell proliferative disorder gene derived DNA #83.
PN WO2003044226-A2.
PD 30-MAY-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 10; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 799
ID ADS89513 standard; DNA; 8759 BP.
DE Oligonucleotide of the invention SEQ ID NO:529.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 13; Length 8759;
Best Local Similarity 56.5%; Pred. No. 0.022;
RESULT 800
ID ABL32784 standard; DNA; 8979 BP.
DE Human immune system associated gene SEQ ID NO: 757.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 801
ID ABK31270 standard; DNA; 8979 BP.
DE Signal transduction associated gene modified DNA #57.
PN WO200200926-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 802
ID ABL70231 standard; DNA; 8979 BP.
DE Chemically treated cell signalling DNA sequence#61.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 803
ID AAS61178 standard; DNA; 8979 BP.
DE Human gene regulation-associated gene oligonucleotide #133.
PN WO20017375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.1%; Score 51.6; DB 6; Length 8979;
Best Local Similarity 63.9%; Pred. No. 0.022;
RESULT 804
ID AAT87807 standard; CDNA; 419 BP.
DE Human polynucleotide SEQ ID NO 7867.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.1%; Score 51.4; DB 4; Length 419;
Best Local Similarity 60.3%; Pred. No. 0.0052;
RESULT 805
ID ACN52877 standard; CDNA; 421 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-018-Q1-N6-H7, SEQ:7658.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.1%; Score 51.4; DB 13; Length 421;
Best Local Similarity 58.0%; Pred. No. 0.0052;
RESULT 806
ID ACN50120 standard; CDNA; 585 BP.
DE Cotton non-primed seed EST Clone ID: LIB3826-001-Q1-K6-D8, SEQ:4901.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.1%; Score 51.4; DB 13; Length 585;
Best Local Similarity 58.0%; Pred. No. 0.0062;
RESULT 807
ID ABV58626 standard; CDNA; 504 BP.
DE Human prostate expression marker CDNA 58617.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 51.2; DB 5; Length 504;
Best Local Similarity 57.5%; Pred. No. 0.0065;
RESULT 808
ID ABK43454 standard; CDNA; 894 BP.
DE DNA encoding novel central nervous system protein #34.
PN WO200155318-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 51.2; DB 4; Length 894;
Best Local Similarity 66.1%; Pred. No. 0.0087;
RESULT 809
ID ADI53841 standard; CDNA; 894 BP.
DE CDNA encoding novel human protein seq id 44.
PN US2004018969-A1.
PD 29-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 3.0%; Score 51.2; DB 12; Length 894;
Best Local Similarity 66.1%; Pred. No. 0.0087;
RESULT 810
ID AAI83204 standard; CDNA; 386 BP.
DE Human polynucleotide SEQ ID NO 3264.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 3.0%; Score 51; DB 4; Length 386;
Best Local Similarity 59.2%; Pred. No. 0.0064;
RESULT 811
ID ACN56273 standard; CDNA; 517 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-033-Q6-N6-E7, SEQ:11054.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.0%; Score 51; DB 13; Length 517;
Best Local Similarity 59.2%; Pred. No. 0.0074;
RESULT 812
ID ADJ81646 standard; DNA; 10428 BP.
DE Human tyrosine phosphatase SHP1 bisulphited genomic DNA SeqID 6.
PN JP2004000128-A.
PD 08-JAN-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 3.0%; Score 51; DB 12; Length 10428;
Best Local Similarity 59.2%; Pred. No. 0.034;
RESULT 813
ID ACN87837 standard; DNA; 643 BP.
DE Breast cancer related marker, seq id 8987.

PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.0%; Score 50.8; DB 11; Length 643;
Best Local Similarity 57.8%; Pred. No. 0.0094;
RESULT 814
ID ADU41364 standard; DNA; 393 BP.
DE Human ovarian cancer DNA marker #15254.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.6; DB 5; Length 393;
Best Local Similarity 57.1%; Pred. No. 0.0082;
RESULT 815
ID ABN98845 standard; DNA; 856 BP.
DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 613.
PN US2002023281-A1.
PD 21-FEB-2002.
PA (GORL/) GORLACH J.
PA (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHEW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
Query Match 3.0%; Score 50.6; DB 6; Length 856;
Best Local Similarity 54.8%; Pred. No. 0.012;
RESULT 816
ID AAC63439 standard; cDNA; 876 BP.
DE Human secreted protein coding sequence SEQ ID NO: 40.
PN WO200061779-A1.
PD 19-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50.6; DB 3; Length 876;
Best Local Similarity 63.6%; Pred. No. 0.012;
RESULT 817
ID AB273647 standard; cDNA; 876 BP.
DE Secreted protein-encoding gene 367 cDNA clone HUSIR18, SEQ ID NO:377.
PN WO200277013-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50.6; DB 8; Length 876;
Best Local Similarity 63.6%; Pred. No. 0.012;
RESULT 818
ID ADA98139 standard; cDNA; 876 BP.
DE Human secreted protein cDNA sequence #233.
PN WO2003004623-A2.
PD 16-JAN-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50.6; DB 8; Length 876;
Best Local Similarity 63.6%; Pred. No. 0.012;
RESULT 819
ID AB267241 standard; cDNA; 876 BP.
DE Human secreted protein encoding cDNA SEQ ID NO 361.
PN WO200277186-A2.
PD 03-OCT-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50.6; DB 10; Length 876;
Best Local Similarity 63.6%; Pred. No. 0.012;
RESULT 820
ID ADD71195 standard; cDNA; 2200 BP.

DE Human intracellular signalling molecule INTSIG-32 cDNA SEQ ID NO:84.
PN WO2003039348-A2.
PD 15-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 3.0%; Score 50.6; DB 10; Length 2200;
Best Local Similarity 70.1%; Pred. No. 0.02;
RESULT 821
ID ADE79863 standard; DNA; 2924 BP.
DE Rat myosin heavy chain coding sequence, SEQ ID 103.
PN EPI279744-A2.
PD 29-JAN-2003.
PA (WARN-) WARNER LAMBERT CO.
Query Match 3.0%; Score 50.6; DB 10; Length 2924;
Best Local Similarity 63.6%; Pred. No. 0.023;
RESULT 822
ID ABV25005 standard; cDNA; 4990 BP.
DE Human prostate expression marker cDNA 24996.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.6; DB 5; Length 4990;
Best Local Similarity 58.2%; Pred. No. 0.03;
RESULT 823
ID ABV25400 standard; cDNA; 4990 BP.
DE Human prostate expression marker cDNA 25391.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.6; DB 5; Length 4990;
Best Local Similarity 58.2%; Pred. No. 0.03;
RESULT 824
ID ACN89861 standard; DNA; 5001 BP.
DE Breast cancer related marker, seq id 11011.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 3.0%; Score 50.6; DB 11; Length 5001;
Best Local Similarity 58.2%; Pred. No. 0.03;
RESULT 825
ID ABU92257 standard; DNA; 6029 BP.
DE Chemically treated DNA repair gene fragment complementary to#33.
PN WO200181622-A2.
PD 01-NOV-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.6; DB 6; Length 6029;
Best Local Similarity 57.1%; Pred. No. 0.033;
RESULT 826
ID AAD23226 standard; DNA; 6029 BP.
DE Chemically treated human genomic DNA #16 associated with DNA adducts.
PN WO200177378-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.6; DB 6; Length 6029;
Best Local Similarity 57.1%; Pred. No. 0.033;
RESULT 827
ID ABX41821 standard; cDNA; 272 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #6986.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 3.0%; Score 50.4; DB 8; Length 272;
Best Local Similarity 60.0%; Pred. No. 0.0077;
RESULT 828
ID AAH71505 standard; cDNA; 310 BP.
DE Human cervical cancer marker nucleic acid 2779.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.4; DB 4; Length 310;
Best Local Similarity 56.7%; Pred. No. 0.0082;

RESULT 829
ID ABL33696 standard; DNA; 6668 BP.
DE Human immune system associated gene SEQ ID NO: 1669.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.4; DB 6; Length 6668;
Best Local Similarity 58.8%; Pred. No. 0.039;
RESULT 830
ID ABV19038 standard; cDNA; 201 BP.
DE Human prostate expression marker cDNA 19029.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 201;
Best Local Similarity 59.8%; Pred. No. 0.0075;
RESULT 831
ID AAT76782 standard; DNA; 240 BP.
DE Staphylococcus aureus exfoliative toxin A gene capture probe.
PN US5627054-A.
PD 06-MAY-1997.
PA (USSA-) US SEC OF ARMY.
Query Match 3.0%; Score 50.2; DB 2; Length 240;
Best Local Similarity 58.3%; Pred. No. 0.0082;
RESULT 832
ID ABV42927 standard; cDNA; 382 BP.
DE Human prostate expression marker cDNA 42918.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 382;
Best Local Similarity 55.4%; Pred. No. 0.01;
RESULT 833
ID ABV34060 standard; cDNA; 383 BP.
DE Human prostate expression marker cDNA 34051.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 383;
Best Local Similarity 55.4%; Pred. No. 0.01;
RESULT 834
ID ABV18980 standard; cDNA; 384 BP.
DE Human prostate expression marker cDNA 18971.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 48.1%; Pred. No. 0.01;
RESULT 835
ID ADI69792 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #2534.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 52.6%; Pred. No. 0.01;
RESULT 836
ID ADI76128 standard; DNA; 384 BP.
DE Human ovarian cancer DNA marker #8870.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 384;
Best Local Similarity 52.6%; Pred. No. 0.01;
RESULT 837
ID ABV48817 standard; cDNA; 448 BP.
DE Human prostate expression marker cDNA 48808.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50.2; DB 5; Length 448;
Best Local Similarity 59.8%; Pred. No. 0.011;
RESULT 838

ID ABL32540 standard; DNA; 6476 BP.
DE Human immune system associated gene SEQ ID NO: 513.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50.2; DB 6; Length 6476;
Best Local Similarity 62.2%; Pred. No. 0.043;
RESULT 839
ID ABV59017 standard; cDNA; 325 BP.
DE Human prostate expression marker cDNA 59008.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 325;
Best Local Similarity 61.5%; Pred. No. 0.011;
RESULT 840
ID ABV50931 standard; cDNA; 464 BP.
DE Human prostate expression marker cDNA 50922.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 464;
Best Local Similarity 63.1%; Pred. No. 0.013;
RESULT 841
ID ABV54323 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 54314.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 50; DB 5; Length 471;
Best Local Similarity 52.4%; Pred. No. 0.013;
RESULT 842
ID ACH45627 standard; cDNA; 520 BP.
DE Human foetal brain cDNA #6352.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 50; DB 9; Length 520;
Best Local Similarity 53.8%; Pred. No. 0.014;
RESULT 843
ID AAC79893 standard; cDNA; 680 BP.
DE Human secreted protein encoding cDNA for gene 45.
PN WO200055176-A2.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 3; Length 680;
Best Local Similarity 58.9%; Pred. No. 0.016;
RESULT 844
ID AAA61261 standard; DNA; 870 BP.
DE Human secreted protein gene 2 clone HHFBY53.
PN WO200029422-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 3; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 845
ID ADA39860 standard; cDNA; 870 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 50; DB 8; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 846
ID ACC50464 standard; cDNA; 870 BP.
DE Human secreted protein coding sequence, SEQ ID 131.
PN WO200295010-A2.
PD 28-NOV-2002.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 3.0%; Score 50; DB 8; Length 870;
Best Local Similarity 59.7%; Pred. No. 0.018;
RESULT 847
ID AD062706 standard; DNA; 1971 BP.
DE Transcription factor G2550 orthologous sequence, SEQ ID 1173.
PN WO2004031349-A2.
PD 15-APR-2004.
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
Query Match 3.0%; Score 50; DB 12; Length 1971;
Best Local Similarity 67.0%; Pred. No. 0.027;
RESULT 848
ID ADQ24914 standard; DNA; 3469 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7734.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 3.0%; Score 50; DB 12; Length 3469;
Best Local Similarity 56.8%; Pred. No. 0.036;
RESULT 849
ID ABR80041 standard; DNA; 5387 BP.
DE Human chemically modified disease associated gene SEQ ID NO 58.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50; DB 6; Length 5387;
Best Local Similarity 57.8%; Pred. No. 0.045;
RESULT 850
ID ABX56303 standard; DNA; 8243 BP.
DE Human NOV25b CG93858-02 DNA SEQ ID 85.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 3.0%; Score 50; DB 8; Length 8243;
Best Local Similarity 49.7%; Pred. No. 0.055;
RESULT 851
ID ABJ33999 standard; DNA; 21537 BP.
DE Human immune system associated gene SEQ ID NO: 1972.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 3.0%; Score 50; DB 6; Length 21537;
Best Local Similarity 60.1%; Pred. No. 0.09;
RESULT 852
ID ABV49239 standard; cDNA; 311 BP.
DE Human prostate expression marker cDNA 49230.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 311;
Best Local Similarity 58.4%; Pred. No. 0.012;
RESULT 853
ID ABV57904 standard; cDNA; 376 BP.
DE Human prostate expression marker cDNA 57895.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 376;
Best Local Similarity 58.4%; Pred. No. 0.013;
RESULT 854
ID ABV54466 standard; cDNA; 381 BP.
DE Human prostate expression marker cDNA 54457.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 381;
Best Local Similarity 62.4%; Pred. No. 0.013;
RESULT 855
ID ACH39052 standard; cDNA; 465 BP.
DE Human foetal brain cDNA #419.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 49.8; DB 9; Length 465;
Best Local Similarity 55.9%; Pred. No. 0.015;
RESULT 856
ID ACH22893 standard; cDNA; 506 BP.
DE Human adult ovary cDNA #1273.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 3.0%; Score 49.8; DB 9; Length 506;
Best Local Similarity 60.4%; Pred. No. 0.015;
RESULT 857
ID ABV56485 standard; cDNA; 543 BP.
DE Human prostate expression marker cDNA 56476.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 5; Length 543;
Best Local Similarity 57.3%; Pred. No. 0.016;
RESULT 858
ID AAH70126 standard; cDNA; 545 BP.
DE Human cervical cancer marker nucleic acid 1400.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 3.0%; Score 49.8; DB 4; Length 545;
Best Local Similarity 53.9%; Pred. No. 0.016;
RESULT 859
ID ACN53724 standard; cDNA; 571 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-010-Q1-K6-H4, SEQ:8505.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 3.0%; Score 49.8; DB 13; Length 571;
Best Local Similarity 64.1%; Pred. No. 0.016;
RESULT 860
ID AAA26373 standard; cDNA; 1048 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200006698-A1.
PD 10-FEB-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 3.0%; Score 49.8; DB 3; Length 1048;
Best Local Similarity 59.6%; Pred. No. 0.022;
RESULT 861
ID ADL71434 standard; cDNA; 1048 BP.
DE Novel human secreted protein cDNA seqid 38.
PN US2004034196-A1.
PD 19-FEB-2004.
PA (KOMA/) KOMATSOUJIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAPL/) LAPLEUR D W.
PA (WEIY/) WEI Y.
Query Match 3.0%; Score 49.8; DB 12; Length 1048;
Best Local Similarity 59.6%; Pred. No. 0.022;
RESULT 862
ID ADH02701 standard; DNA; 1317 BP.
DE Human elongation factor ESF1A1 cDNA fragment, SEQ ID NO:7.
PN WO2003104488-A1.
PD 18-DEC-2003.
PA (CANC-) CANCER CARE ONTARIO.

Query Match
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1317;
RESULT 863
ID ACP34510 standard; DNA; 1833 BP.
DE Gene encoding angiogenesis protein BNO144.
PN WO2003027285-A1.
PD 03-APR-2003.
PA (BION-) BIONOMICS LTD.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 8; Length 1833;
RESULT 864
ID ADJ35468 standard; DNA; 1833 BP.
DE Human eukaryotic translation elongation factor 1 alpha 1 (EEF1A1) DNA.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RICE-) RIGEL PHARM INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1833;
RESULT 865
ID ADJ88611 standard; cDNA; 1833 BP.
DE Human housekeeping gene cDNA sequence SEQ ID NO:154.
PN WO2004035785-A1.
PD 29-APR-2004.
PA (NITGA-) NGK INSULATORS LTD.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 13; Length 1833;
RESULT 866
ID ADJ62805 standard; cDNA; 1837 BP.
DE Human cDNA differentially expressed in response to docetaxel #75.
PN US2004018527-A1.
PD 29-JAN-2004.
PA (CHAN/) CHANG J C.
PA (OCON/) O'CONNELL P.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1837;
RESULT 867
ID ADP10528 standard; DNA; 1837 BP.
DE Reference mRNA sequences for marker probe #205.
PN WO2004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 1837;
RESULT 868
ID AAF18296 standard; DNA; 2044 BP.
DE Lung cancer associated polynucleotide sequence SEQ ID 315.
PN WO200055180-A2.
PD 21-SEP-2000.
PA (ROSE/) ROSEN C A.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 3; Length 2044;
RESULT 869
ID AAA95790 standard; cDNA; 2045 BP.
DE Apoptosis related gene 1 clone HLDOK36.
PN WO200056752-A2.
PD 28-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 3; Length 2045;
RESULT 870
ID AAH33283 standard; cDNA; 2045 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:339.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 2045;
RESULT 871
ID AAV63189 standard; cDNA; 2496 BP.
DE cDNA from clone crll62_25 which encodes a secreted protein.
PN WO9844113-A1.
PD 08-OCT-1998.

PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 2; Length 2496;
RESULT 872
ID ABQ92039 standard; cDNA; 2496 BP.
DE Human polynucleotide SEQ ID NO 36.
PN US2002065394-A1.
PD 30-MAY-2002.
PA (JACO/) JACOBS K.
PA (MCCO/) MCCOY J M.
PA (LAVA/) LAVALLIE E R.
PA (COLL/) COLLINS-RACIE L A.
PA (EVAN/) EVANS C.
PA (MERB/) MERBERG D.
PA (TREA/) TREACY M.
PA (SPAU/) SPAULDING V.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 2496;
RESULT 873
ID ADI03925 standard; DNA; 2496 BP.
DE Human B7-1L1 polypeptide encoding DNA.
PN WO2003105887-A1.
PD 24-DEC-2003.
PA (AMHP) WYETH.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 12; Length 2496;
RESULT 874
ID AAF91859 standard; cDNA; 3436 BP.
DE Human secreted protein-encoding gene 2 cDNA clone HDPFB02, SEQ ID NO:12.
PN WO200118022-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 3436;
RESULT 875
ID AAS00767 standard; cDNA; 3436 BP.
DE Human B7-H3 cDNA clone.
PN WO200118021-A1.
PD 15-MAR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (MAYO-) MAYO CLINIC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 4; Length 3436;
RESULT 876
ID ADA39737 standard; cDNA; 3436 BP.
DE Human secreted protein encoding cDNA.
PN WO2002102993-A2.
PD 27-DEC-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 8; Length 3436;
RESULT 877
ID ADC73453 standard; DNA; 3436 BP.
DE Human secreted protein-related DNA - SEQ ID 86.
PN WO2003038063-A2.
PD 08-MAY-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 10; Length 3436;
RESULT 878
ID ABL32345 standard; DNA; 7346 BP.
DE Human immune system associated gene SEQ ID NO: 318.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 7346;
RESULT 879
ID ABN80102 standard; DNA; 8712 BP.
DE Human chemically modified disease associated gene SEQ ID NO 119.
PN WO200200927-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.

Query Match
Best Local Similarity 3.0%; Score 49.8; DB 6; Length 8712;
RESULT 880
ID AAI92106 standard; cDNA; 425 BP.
DE Human polynucleotide SEQ ID NO 12166.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 4; Length 425;
RESULT 881
ID ACG60136 standard; cDNA; 481 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-018-Q6-K6-C5, SEQ:14917.
FN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 13; Length 481;
RESULT 882
ID ADQ22716 standard; DNA; 1486 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5536.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 12; Length 1486;
RESULT 883
ID ACC59907 standard; cDNA; 1678 BP.
DE Human REMAP-20 encoding cDNA SEQ ID NO:56.
FN WO2003025130-A2.
PD 27-MAR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 9; Length 1678;
RESULT 884
ID ADL63386 standard; DNA; 2161 BP.
DE Human ovarian cancer DNA marker #21598.
FN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 5; Length 2161;
RESULT 885
ID ADG32748 standard; DNA; 2870 BP.
DE Human DNA differentially expressed in patients with SLE SeqID72.
FN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 10; Length 2870;
RESULT 886
ID ADD18806 standard; DNA; 3232 BP.
DE Human disease related protein DNA sequence SeqID238.
FN WO2003018621-A2.
PD 06-MAR-2003.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 10; Length 3232;
RESULT 887
ID ADH61306 standard; DNA; 3420 BP.
DE INTSIG encoding DNA 7512383CB1, SEQ ID 23.
FN WO2004001005-A2.
PD 31-DEC-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 12; Length 3420;
RESULT 888
ID ABL33518 standard; DNA; 5520 BP.
DE Human immune system associated gene SEQ ID NO: 1491.
FN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 6; Length 5520;
RESULT 889
ID ABL32677 standard; DNA; 6015 BP.
DE Human immune system associated gene SEQ ID NO: 650.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match
Best Local Similarity 3.0%; Score 49.6; DB 6; Length 6015;
RESULT 890
ID AAI87537 standard; cDNA; 366 BP.
DE Human polynucleotide SEQ ID NO 7597.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 366;
RESULT 891
ID ABV56666 standard; cDNA; 408 BP.
DE Human prostate expression marker cDNA 56657.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 408;
RESULT 892
ID AAI82260 standard; cDNA; 412 BP.
DE Human polynucleotide SEQ ID NO 2320.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 412;
RESULT 893
ID ABV45890 standard; cDNA; 438 BP.
DE Human prostate expression marker cDNA 45881.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 438;
RESULT 894
ID AAI82206 standard; cDNA; 480 BP.
DE Human polynucleotide SEQ ID NO 2266.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 4; Length 480;
RESULT 895
ID ACH25146 standard; cDNA; 561 BP.
DE Human adult ovary cDNA #3526.
FN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 9; Length 561;
RESULT 896
ID ABV58690 standard; cDNA; 579 BP.
DE Human prostate expression marker cDNA 58681.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match
Best Local Similarity 2.9%; Score 49.4; DB 5; Length 579;
RESULT 897

ID AAL20340 standard; cDNA; 622 BP.
DE Human breast cancer expressed polynucleotide 12797.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 4; Length 622;
Best Local Similarity 57.4%; Pred. No. 0.022;
RESULT 898
ID AAC80551 standard; cDNA; 658 BP.
DE Human secreted protein gene 21 SEQ ID NO:31.
PN WO200058467-A1.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 3; Length 658;
Best Local Similarity 57.4%; Pred. No. 0.022;
RESULT 899
ID AAH35003 standard; cDNA; 788 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:2085.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 788;
Best Local Similarity 58.5%; Pred. No. 0.024;
RESULT 900
ID AAS02414 standard; cDNA; 797 BP.
DE Human secreted protein, cDNA #20.
PN WO200123546-A1.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 797;
Best Local Similarity 58.5%; Pred. No. 0.024;
RESULT 901
ID ABV28953 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 28944.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 902
ID ABV22100 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 22091.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 903
ID ABV23114 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 23105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 904
ID ABV27940 standard; cDNA; 1603 BP.
DE Human prostate expression marker cDNA 27931.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.4; DB 5; Length 1603;
Best Local Similarity 64.3%; Pred. No. 0.035;
RESULT 905
ID AAS31262 standard; cDNA; 2645 BP.
DE Human cDNA encoding a novel extracellular matrix protein, Seq ID No 76.
PN WO200155368-A1.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 4; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 906
ID ABQ66586 standard; cDNA; 2645 BP.

DE Human polynucleotide SEQ ID NO 76.
PN US2002042386-A1.
PD 11-APR-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Query Match 2.9%; Score 49.4; DB 6; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 907
ID ADC10608 standard; cDNA; 2645 BP.
DE Human cDNA from extracellular matrix gene 66.
PN US2003059875-A1.
PD 27-MAR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.4; DB 10; Length 2645;
Best Local Similarity 58.5%; Pred. No. 0.045;
RESULT 908
ID ADQ23227 standard; DNA; 3480 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6047.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.4; DB 12; Length 3480;
Best Local Similarity 57.4%; Pred. No. 0.052;
RESULT 909
ID ADQ24537 standard; DNA; 3480 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7357.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.4; DB 12; Length 3480;
Best Local Similarity 57.4%; Pred. No. 0.052;
RESULT 910
ID AAI88514 standard; cDNA; 389 BP.
DE Human polynucleotide SEQ ID NO 8574.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 389;
Best Local Similarity 57.0%; Pred. No. 0.019;
RESULT 911
ID AAI88643 standard; cDNA; 396 BP.
DE Human polynucleotide SEQ ID NO 8703.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 396;
Best Local Similarity 57.0%; Pred. No. 0.019;
RESULT 912
ID AAI87424 standard; cDNA; 429 BP.
DE Human polynucleotide SEQ ID NO 7484.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 429;
Best Local Similarity 60.0%; Pred. No. 0.02;
RESULT 913
ID ABV58527 standard; cDNA; 442 BP.
DE Human prostate expression marker cDNA 58518.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 442;
Best Local Similarity 57.0%; Pred. No. 0.021;
RESULT 914
ID ACH25161 standard; cDNA; 448 BP.
DE Human adult ovary cDNA #3541.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.
Query Match 2.9%; Score 49.2; DB 9; Length 448;
Best Local Similarity 59.1%; Pred. No. 0.021;
RESULT 915
ID AAI84689 standard; cDNA; 453 BP.
DE Human polynucleotide SEQ ID NO 4749.
FN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 49.2; DB 4; Length 453;
Best Local Similarity 60.4%; Pred. No. 0.021;
RESULT 916
ID ABV58840 standard; cDNA; 539 BP.
DE Human prostate expression marker cDNA 58831.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 539;
Best Local Similarity 59.2%; Pred. No. 0.023;
RESULT 917
ID ABV56624 standard; cDNA; 544 BP.
DE Human prostate expression marker cDNA 56615.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 544;
Best Local Similarity 60.4%; Pred. No. 0.023;
RESULT 918
ID ABV58620 standard; cDNA; 554 BP.
DE Human prostate expression marker cDNA 58611.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 554;
Best Local Similarity 61.9%; Pred. No. 0.023;
RESULT 919
ID ABV58414 standard; cDNA; 575 BP.
DE Human prostate expression marker cDNA 58405.
FN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 5; Length 575;
Best Local Similarity 57.0%; Pred. No. 0.023;
RESULT 920
ID AAH71551 standard; cDNA; 621 BP.
DE Human cervical cancer marker nucleic acid 2825.
FN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49.2; DB 4; Length 621;
Best Local Similarity 57.0%; Pred. No. 0.024;
RESULT 921
ID AAH34312 standard; cDNA; 712 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1394.
FN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49.2; DB 4; Length 712;
Best Local Similarity 59.2%; Pred. No. 0.026;
RESULT 922
ID ADJ80203 standard; cDNA; 877 BP.
DE Novel human nucleic acid-associated protein coding sequence #21.
FN WO2003038052-A2.
PD 08-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 2.9%; Score 49.2; DB 10; Length 877;
Best Local Similarity 59.2%; Pred. No. 0.029;
RESULT 923
ID AAK58876 standard; cDNA; 1503 BP.
DE Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:3936.
FN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.

Query Match 2.9%; Score 49.2; DB 4; Length 1503;
Best Local Similarity 59.6%; Pred. No. 0.038;
RESULT 924
ID ABA93758 standard; cDNA; 1537 BP.
DE Human testis derived cDNA clone tes3_22124.
FN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 2.9%; Score 49.2; DB 6; Length 1537;
Best Local Similarity 63.6%; Pred. No. 0.039;
RESULT 925
ID AQO22988 standard; DNA; 1576 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5808.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.2; DB 12; Length 1576;
Best Local Similarity 57.0%; Pred. No. 0.039;
RESULT 926
ID AQO23425 standard; DNA; 2408 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6245.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49.2; DB 12; Length 2408;
Best Local Similarity 61.9%; Pred. No. 0.048;
RESULT 927
ID AB210224 standard; DNA; 2501 BP.
DE Haematopoietic cell proliferation disorder related DNA sequence #364.
FN WO200277272-A2.
PD 03-OCT-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 8; Length 2501;
Best Local Similarity 58.0%; Pred. No. 0.049;
RESULT 928
ID AQO08601 standard; DNA; 3030 BP.
DE Clona intestinalis nervous system associated gene SeqID3.
FN JP2004057127-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 2.9%; Score 49.2; DB 12; Length 3030;
Best Local Similarity 60.4%; Pred. No. 0.054;
RESULT 929
ID AAX33181 standard; DNA; 6644 BP.
DE Base sequence of the plasmid pRx-ires-bsr.
FN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 6644;
Best Local Similarity 60.4%; Pred. No. 0.081;
RESULT 930
ID ABK40051 standard; DNA; 7058 BP.
DE Human chemically pretreated gene sequence #67 strand 1.
FN WO200202806-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49.2; DB 6; Length 7058;
Best Local Similarity 63.6%; Pred. No. 0.083;
RESULT 931
ID AAX33182 standard; DNA; 7372 BP.
DE Base sequence of the plasmid pRx-Bcl-xl-bsr.
FN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 7372;
Best Local Similarity 60.4%; Pred. No. 0.085;
RESULT 932
ID AAX33180 standard; DNA; 7797 BP.
DE Cowpox virus bsr full length gene sequence.
FN WO9913073-A2.
PD 18-MAR-1999.
PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.
Query Match 2.9%; Score 49.2; DB 2; Length 7797;

Best Local Similarity 60.4%; Pred. No. 0.088;

RESULT 933

ID AAX33184 standard; DNA; 7996 BP.

DE Base sequence of the plasmid PRX-Bcl 2-i-hCD 25.

PN WO9913073-A2.

PD 18-MAR-1999.

PA (RPRG-) RPR GENCELL ASIA PACIFIC INC.

Query Match 2.9%; Score 49.2; DB 2; Length 7996;

Best Local Similarity 60.4%; Pred. No. 0.089;

RESULT 934

ID ABR28222 standard; DNA; 11394 BP.

DE DNA transcription associated complementary genomic DNA #48.

PN WO200192565-A2.

PD 06-DEC-2001.

PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 49.2; DB 6; Length 11394;

Best Local Similarity 57.0%; Pred. No. 0.11;

RESULT 935

ID AB210104 standard; DNA; 35962 BP.

DE Haematopoietic cell proliferation disorder related DNA sequence #244.

PN WO20027272-A2.

PD 03-OCT-2002.

PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 49.2; DB 8; Length 35962;

Best Local Similarity 58.0%; Pred. No. 0.19;

RESULT 936

ID AAS07790 standard; DNA; 256 BP.

DE Cervical cancer pre-malignant condition DNA marker #89.

PN WO200142792-A2.

PD 14-JUN-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 4; Length 256;

Best Local Similarity 59.0%; Pred. No. 0.018;

RESULT 937

ID ACN55002 standard; cDNA; 342 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-A9, SEQ:9783.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 342;

Best Local Similarity 57.5%; Pred. No. 0.02;

RESULT 938

ID ABV58528 standard; cDNA; 347 BP.

DE Human prostate expression marker cDNA 58519.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 347;

Best Local Similarity 57.5%; Pred. No. 0.02;

RESULT 939

ID AAI84446 standard; cDNA; 348 BP.

DE Human polynucleotide SEQ ID NO 4506.

PN WO200164835-A2.

PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 49; DB 4; Length 348;

Best Local Similarity 59.9%; Pred. No. 0.021;

RESULT 940

ID AAI85202 standard; cDNA; 390 BP.

DE Human polynucleotide SEQ ID NO 5262.

PN WO200164835-A2.

PD 07-SEP-2001.

PA (HYSE-) HYSEQ INC.

Query Match 2.9%; Score 49; DB 4; Length 390;

Best Local Similarity 58.6%; Pred. No. 0.022;

RESULT 941

ID ACN53426 standard; cDNA; 403 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-007-Q1-K6-F9, SEQ:8207.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.

Query Match

Best Local Similarity 57.5%; Pred. No. 0.022;

RESULT 942

ID ACH23125 standard; cDNA; 426 BP.

DE Human adult ovary cDNA #1505.

PN US2003073623-A1.

PD 17-APR-2003.

PA (DRMA/) DRMANAC R T.

PA (LABA/) LABAT I.

PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.

PA (JONE/) JONES L W.

Query Match 2.9%; Score 49; DB 9; Length 426;

Best Local Similarity 58.6%; Pred. No. 0.023;

RESULT 943

ID ABV57380 standard; cDNA; 429 BP.

DE Human prostate expression marker cDNA 57371.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 429;

Best Local Similarity 59.9%; Pred. No. 0.023;

RESULT 944

ID ABV56638 standard; cDNA; 469 BP.

DE Human prostate expression marker cDNA 56629.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 469;

Best Local Similarity 58.6%; Pred. No. 0.024;

RESULT 945

ID ACN51887 standard; cDNA; 469 BP.

DE Cotton androecium tissue EST Clone ID: LIB3828-009-Q1-N6-C10, SEQ:6668.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 469;

Best Local Similarity 57.5%; Pred. No. 0.024;

RESULT 946

ID ACN58415 standard; cDNA; 469 BP.

DE Cotton gynoeceum tissue EST Clone ID: LIB3829-009-Q6-K6-H8, SEQ:13196.

PN US2004123340-A1.

PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.

PA (FENG/) FENG P C C.

PA (FINC/) FINCHER K L.

PA (ZIEG/) ZIEGLER T E.

Query Match 2.9%; Score 49; DB 13; Length 469;

Best Local Similarity 57.5%; Pred. No. 0.024;

RESULT 947

ID ABV57020 standard; cDNA; 472 BP.

DE Human prostate expression marker cDNA 57011.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 472;

Best Local Similarity 55.6%; Pred. No. 0.024;

RESULT 948

ID ABV54546 standard; cDNA; 541 BP.

DE Human prostate expression marker cDNA 54537.

PN WO200160860-A2.

PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

Query Match 2.9%; Score 49; DB 5; Length 541;

Best Local Similarity 58.6%; Pred. No. 0.026;

RESULT 949

ID ACN53890 standard; cDNA; 547 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-014-Q1-K6-F10, SEQ:8671.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 49; DB 13; Length 547;
Best Local Similarity 56.2%; Pred. No. 0.026;
RESULT 950
ID ABQ52063 standard; DNA; 553 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38654.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 553;
Best Local Similarity 62.3%; Pred. No. 0.026;
RESULT 951
ID ABQ52062 standard; DNA; 553 BP.
DE Oligonucleotide for detecting cytosine methylation SEQ ID NO 38653.
PN WO200218632-A2.
PD 07-MAR-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 553;
Best Local Similarity 62.3%; Pred. No. 0.026;
RESULT 952
ID ADR63596 standard; cDNA; 1041 BP.
DE Cotton cDNA sequence, SEQ ID 4377.
PN US2004181830-A1.
PD 16-SEP-2004.
PA (KOVA/) KOVALIC D K.
PA (ZHOU/) ZHOU Y.
PA (CAOY/) CAO Y.
Query Match 2.9%; Score 49; DB 13; Length 1041;
Best Local Similarity 58.6%; Pred. No. 0.036;
RESULT 953
ID ADQ24168 standard; DNA; 1698 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6988.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 1698;
Best Local Similarity 61.2%; Pred. No. 0.046;
RESULT 954
ID ADM47920 standard; DNA; 1882 BP.
DE Polynucleotide sequence #338 useful in producing transgenic plants.
PN US2003233870-A1.
PD 18-DEC-2003.
PA (EDGE/) EDGERTON M D.
PA (CHOM/) CHOMET P S.
PA (LACC/) LACCETTI L B.
Query Match 2.9%; Score 49; DB 12; Length 1882;
Best Local Similarity 59.9%; Pred. No. 0.048;
RESULT 955
ID AAA23441 standard; cDNA; 1954 BP.
DE cDNA encoding human secreted protein vc51_1, SEQ ID NO:37.
PN WO20011015-A1.
PD 02-MAR-2000.
PA (ALPH-) ALPHAGENE INC.
Query Match 2.9%; Score 49; DB 3; Length 1954;
Best Local Similarity 59.9%; Pred. No. 0.049;
RESULT 956
ID ACN88781 standard; DNA; 2024 BP.
DE Breast cancer related marker, seq id 9931.
PN US2003099974-A1.
PD 29-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 49; DB 11; Length 2024;
Best Local Similarity 58.6%; Pred. No. 0.05;
RESULT 957
ID AAZ43781 standard; cDNA; 2685 BP.
DE Human fetal brain cDNA clone vb6_1.

PN WO9955721-A1.
PD 04-NOV-1999.
PA (ALPH-) ALPHAGENE INC.
Query Match 2.9%; Score 49; DB 3; Length 2685;
Best Local Similarity 59.9%; Pred. No. 0.058;
RESULT 958
ID ADQ24699 standard; DNA; 2936 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7519.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 2936;
Best Local Similarity 57.5%; Pred. No. 0.06;
RESULT 959
ID ADQ24532 standard; DNA; 2936 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7352.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 49; DB 12; Length 2936;
Best Local Similarity 57.5%; Pred. No. 0.06;
RESULT 960
ID ABQ54675 standard; cDNA; 1044 BP.
DE Human ovarian antigen HVCAR76 cDNA, SEQ ID NO:555.
PN WO200200677-A1.
PD 03-JAN-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 49; DB 6; Length 3044;
Best Local Similarity 59.0%; Pred. No. 0.062;
RESULT 961
ID ABLJ3662 standard; DNA; 5845 BP.
DE Human immune system associated gene SEQ ID NO: 1635.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 5845;
Best Local Similarity 59.9%; Pred. No. 0.086;
RESULT 962
ID ADI45710 standard; DNA; 5930 BP.
DE Human ovarian cancer DNA marker #19600.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 49; DB 5; Length 5930;
Best Local Similarity 58.6%; Pred. No. 0.086;
RESULT 963
ID ABLJ34058 standard; DNA; 6012 BP.
DE Human immune system associated gene SEQ ID NO: 2031.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6012;
Best Local Similarity 59.9%; Pred. No. 0.087;
RESULT 964
ID ABLJ2411 standard; DNA; 6161 BP.
DE Human immune system associated gene SEQ ID NO: 384.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6161;
Best Local Similarity 64.6%; Pred. No. 0.088;
RESULT 965
ID ABLJ2806 standard; DNA; 6211 BP.
DE Human immune system associated gene SEQ ID NO: 779.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 49; DB 6; Length 6211;
Best Local Similarity 59.9%; Pred. No. 0.088;
RESULT 966
ID ABLJ3050 standard; DNA; 6522 BP.
DE Human immune system associated gene SEQ ID NO: 1023.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG. 2.9%; Score 49; DB 6; Length 6522;
Best Local Similarity 59.9%; Pred. No. 0.09;
RESULT 967
ID ABLJ32118 standard; DNA; 11416 BP.
DE Human immune system associated gene SEQ ID NO: 91.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG. 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 968
ID ABL70135 standard; DNA; 11416 BP.
DE Chemically treated cell signalling DNA sequence#13.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG. 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 969
ID AAS61063 standard; DNA; 11416 BP.
DE Human gene regulation-associated gene oligonucleotide #10.
PN WO200177375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG. 2.9%; Score 49; DB 6; Length 11416;
Best Local Similarity 59.9%; Pred. No. 0.12;
RESULT 970
ID ABLJ34072 standard; DNA; 40862 BP.
DE Human immune system associated gene SEQ ID NO: 2045.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG. 2.9%; Score 49; DB 6; Length 40862;
Best Local Similarity 59.9%; Pred. No. 0.23;
RESULT 971
ID ADI72102 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #4844.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 299;
Best Local Similarity 56.0%; Pred. No. 0.021;
RESULT 972
ID ADL37251 standard; DNA; 299 BP.
DE Human ovarian cancer DNA marker #11141.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 299;
Best Local Similarity 56.0%; Pred. No. 0.021;
RESULT 973
ID ABV49426 standard; cDNA; 308 BP.
DE Human prostate expression marker cDNA 49417.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 308;
Best Local Similarity 57.1%; Pred. No. 0.022;
RESULT 974
ID ABV55289 standard; cDNA; 313 BP.
DE Human prostate expression marker cDNA 55280.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 313;
Best Local Similarity 63.8%; Pred. No. 0.022;
RESULT 975
ID ABV04395 standard; cDNA; 326 BP.
DE Human prostate expression marker cDNA 4386.
PN WO200160860-A2.
PD 23-AUG-2001.

PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 326;
Best Local Similarity 61.2%; Pred. No. 0.022;
RESULT 976
ID AAI89034 standard; cDNA; 413 BP.
DE Human polynucleotide SEQ ID NO 9094.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC. 2.9%; Score 48.8; DB 4; Length 413;
Best Local Similarity 57.1%; Pred. No. 0.025;
RESULT 977
ID AAI91775 standard; cDNA; 421 BP.
DE Human polynucleotide SEQ ID NO 11835.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC. 2.9%; Score 48.8; DB 4; Length 421;
Best Local Similarity 60.6%; Pred. No. 0.026;
RESULT 978
ID ACN56150 standard; cDNA; 436 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-032-Q6-N6-D9, SEQ:10931.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J. 2.9%; Score 48.8; DB 13; Length 436;
PA (FENG/) FENG P C C. 2.9%; Score 48.8; DB 13; Length 436;
PA (FINC/) FINCHER K L. 2.9%; Score 48.8; DB 13; Length 436;
PA (ZIEG/) ZIEGLER T E. 2.9%; Score 48.8; DB 13; Length 436;
Best Local Similarity 53.7%; Pred. No. 0.026;
RESULT 979
ID ABV19606 standard; cDNA; 446 BP.
DE Human prostate expression marker cDNA 19597.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 446;
Best Local Similarity 59.2%; Pred. No. 0.026;
RESULT 980
ID AAI80552 standard; cDNA; 448 BP.
DE Human polynucleotide SEQ ID NO 612.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC. 2.9%; Score 48.8; DB 4; Length 448;
Best Local Similarity 59.3%; Pred. No. 0.026;
RESULT 981
ID ACN45690 standard; cDNA; 486 BP.
DE Cotton primed seed EST Clone ID: LIB3825-007-Q1-K6-F5, SEQ:471.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J. 2.9%; Score 48.8; DB 13; Length 486;
PA (FENG/) FENG P C C. 2.9%; Score 48.8; DB 13; Length 486;
PA (FINC/) FINCHER K L. 2.9%; Score 48.8; DB 13; Length 486;
PA (ZIEG/) ZIEGLER T E. 2.9%; Score 48.8; DB 13; Length 486;
Best Local Similarity 62.1%; Pred. No. 0.027;
RESULT 982
ID ABV23693 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 23684.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 489;
Best Local Similarity 59.3%; Pred. No. 0.028;
RESULT 983
ID ABV29562 standard; cDNA; 489 BP.
DE Human prostate expression marker cDNA 29553.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC. 2.9%; Score 48.8; DB 5; Length 489;
Best Local Similarity 59.3%; Pred. No. 0.028;

RESULT 984
ID ABV58114 standard; cDNA; 510 BP.
DE Human prostate expression marker cDNA 58105.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.8; DB 5; Length 510;
Best Local Similarity 59.3%; Pred. No. 0.028;
RESULT 985
ID AAC74364 standard; cDNA; 639 BP.
DE Human secreted protein gene 28 SEQ ID NO:38.
PN WO200058340-A2.
PD 05-OCT-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 3; Length 639;
Best Local Similarity 63.8%; Pred. No. 0.032;
RESULT 986
ID AAD05366 standard; cDNA; 655 BP.
DE Human secreted protein-encoding gene 19 cDNA clone HMLFQ64, SEQ ID NO:77.
PN WO200134626-A1.
PD 17-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 4; Length 655;
Best Local Similarity 62.1%; Pred. No. 0.032;
RESULT 987
ID AAH34055 standard; cDNA; 673 BP.
DE Human colon cancer antigen encoding cDNA SEQ ID NO:1137.
PN WO200122920-A2.
PD 05-APR-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.8; DB 4; Length 673;
Best Local Similarity 59.3%; Pred. No. 0.032;
RESULT 988
ID ABG76269 standard; cDNA; 836 BP.
DE Human GENSET cDNA clone name NBART.
PN WO2003014151-A2.
PD 20-FEB-2003.
PA (GEST) GENSET SA.
Query Match 2.9%; Score 48.8; DB 8; Length 836;
Best Local Similarity 59.3%; Pred. No. 0.036;
RESULT 989
ID ADQ22074 standard; DNA; 980 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 4894.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.8; DB 12; Length 980;
Best Local Similarity 57.1%; Pred. No. 0.039;
RESULT 990
ID AAU70895 standard; cDNA; 1813 BP.
DE cDNA encoding an allelic variant of human Zcytor5.
PN WO9849307-A1.
PD 05-NOV-1998.
PA (ZYMO) ZYMOGENETICS INC.
Query Match 2.9%; Score 48.8; DB 2; Length 1813;
Best Local Similarity 56.1%; Pred. No. 0.053;
RESULT 991
ID ABL33879 standard; DNA; 5378 BP.
DE Human immune system associated gene SEQ ID NO: 1852.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.8; DB 6; Length 5378;
Best Local Similarity 57.1%; Pred. No. 0.093;
RESULT 992
ID ABQ67094 standard; DNA; 83391 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 124.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.8; DB 6; Length 83391;
Best Local Similarity 58.1%; Pred. No. 0.37;
RESULT 993

ID ADI72391 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #5133.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 291;
Best Local Similarity 52.2%; Pred. No. 0.024;
RESULT 994
ID ADL37534 standard; DNA; 291 BP.
DE Human ovarian cancer DNA marker #11424.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 291;
Best Local Similarity 52.2%; Pred. No. 0.024;
RESULT 995
ID ABV49069 standard; cDNA; 320 BP.
DE Human prostate expression marker cDNA 49060.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 320;
Best Local Similarity 56.5%; Pred. No. 0.025;
RESULT 996
ID AA186367 standard; cDNA; 379 BP.
DE Human polynucleotide SEQ ID NO 6427.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.6; DB 4; Length 379;
Best Local Similarity 54.9%; Pred. No. 0.027;
RESULT 997
ID ACH19935 standard; cDNA; 423 BP.
DE Human adult lung cDNA #938.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Query Match 2.9%; Score 48.6; DB 9; Length 423;
Best Local Similarity 52.5%; Pred. No. 0.029;
RESULT 998
ID ABV38062 standard; cDNA; 425 BP.
DE Human prostate expression marker cDNA 38053.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 425;
Best Local Similarity 57.6%; Pred. No. 0.029;
RESULT 999
ID ABV47755 standard; cDNA; 471 BP.
DE Human prostate expression marker cDNA 47746.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 471;
Best Local Similarity 58.7%; Pred. No. 0.031;
RESULT 1000
ID ACN54837 standard; cDNA; 489 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-025-Q6-K6-D11, SEQ:9618.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.6; DB 13; Length 489;
Best Local Similarity 57.6%; Pred. No. 0.031;
RESULT 1001
ID ABV17965 standard; cDNA; 816 BP.
DE Human prostate expression marker cDNA 17956.

PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.6; DB 5; Length 816;
Best Local Similarity 58.7%; Pred. No. 0.04;
RESULT 1002
ID ABA93702 standard; cDNA; 835 BP.
DE Human signal transduction cDNA clone amy2_10h17.
PN WO200198454-A2.
PD 27-DEC-2001.
PA (GEHU-) GERMAN HUMAN GENOME PROJECT.
Query Match 2.9%; Score 48.6; DB 6; Length 835;
Best Local Similarity 61.4%; Pred. No. 0.041;
RESULT 1003
ID AAC98083 standard; cDNA; 1377 BP.
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:93.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.6; DB 3; Length 1377;
Best Local Similarity 58.3%; Pred. No. 0.053;
RESULT 1004
ID ABX92004 standard; cDNA; 1808 BP.
DE Lung specific nucleic acid (LSNA) #46.
PN WO200268633-A2.
PD 06-SEP-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 2.9%; Score 48.6; DB 6; Length 1808;
Best Local Similarity 58.7%; Pred. No. 0.06;
RESULT 1005
ID AB857347 standard; cDNA; 1851 BP.
DE cDNA encoding human cancer cell growth suppressing protein PP6068.
PN CN1351080-A.
PD 29-MAY-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.9%; Score 48.6; DB 6; Length 1851;
Best Local Similarity 58.7%; Pred. No. 0.061;
RESULT 1006
ID AAD06011 standard; DNA; 2034 BP.
DE Human neuronal apoptosis regulated candidate (NARC) 10C DNA.
PN WO200131007-A2.
PD 03-MAY-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 4; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1007
ID ABS6722 standard; cDNA; 2034 BP.
DE Human NARC10 cDNA.
PN WO200281516-A2.
PD 17-OCT-2002.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 8; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1008
ID ADJ57918 standard; cDNA; 2034 BP.
DE Human NARC 10C cDNA.
PN US2004009553-A1.
PD 15-JAN-2004.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 2.9%; Score 48.6; DB 12; Length 2034;
Best Local Similarity 56.6%; Pred. No. 0.064;
RESULT 1009
ID ADQ23617 standard; DNA; 2050 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6437.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.6; DB 12; Length 2050;
Best Local Similarity 60.0%; Pred. No. 0.064;
RESULT 1010
ID ABU32778 standard; DNA; 5532 BP.
DE Human immune system associated gene SEQ ID NO: 751.
PN WO200200928-A2.

PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 6; Length 5532;
Best Local Similarity 63.0%; Pred. No. 0.11;
RESULT 1011
ID ABL32911 standard; DNA; 8946 BP.
DE Human immune system associated gene SEQ ID NO: 884.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 6; Length 8946;
Best Local Similarity 57.6%; Pred. No. 0.14;
RESULT 1012
ID AAS46704 standard; DNA; 14615 BP.
DE Tumour suppressor gene derived chemically modified sequence #427.
PN WO200168912-A2.
PD 20-SEP-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.6; DB 4; Length 14615;
Best Local Similarity 57.6%; Pred. No. 0.17;
RESULT 1013
ID ABX47137 standard; cDNA; 341 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #12302.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48.4; DB 8; Length 341;
Best Local Similarity 62.3%; Pred. No. 0.029;
RESULT 1014
ID AAI67525 standard; cDNA; 367 BP.
DE Human polynucleotide SEQ ID NO 7585.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 367;
Best Local Similarity 64.0%; Pred. No. 0.03;
RESULT 1015
ID AAI84785 standard; cDNA; 388 BP.
DE Human polynucleotide SEQ ID NO 4845.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 388;
Best Local Similarity 60.8%; Pred. No. 0.031;
RESULT 1016
ID ADL43635 standard; DNA; 388 BP.
DE Human ovarian cancer DNA marker #17525.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.4; DB 5; Length 388;
Best Local Similarity 57.1%; Pred. No. 0.031;
RESULT 1017
ID AAI89093 standard; cDNA; 415 BP.
DE Human polynucleotide SEQ ID NO 9153.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.4; DB 4; Length 415;
Best Local Similarity 65.4%; Pred. No. 0.032;
RESULT 1018
ID ABV56837 standard; cDNA; 432 BP.
DE Human prostate expression marker cDNA 56828.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.4; DB 5; Length 432;
Best Local Similarity 64.0%; Pred. No. 0.033;
RESULT 1019
ID ABX47746 standard; cDNA; 442 BP.

DE Bovine EST associated with lactation/muscle/fat deposition #12911.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48.4; DB 8; Length 442;
Best Local Similarity 66.0%; Pred. No. 0.033;
RESULT 1020
ID ABV56778 standard; cDNA; 451 BP.
DE Human prostate expression marker cDNA 56769.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.4; DB 5; Length 451;
Best Local Similarity 60.8%; Pred. No. 0.034;
RESULT 1021
ID ACN45855 standard; cDNA; 608 BP.
DE Cotton primed seed EST Clone ID: L1B3825-009-Q1-K6-G7, SEQ:636.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.4; DB 13; Length 608;
Best Local Similarity 57.1%; Pred. No. 0.039;
RESULT 1022
ID ACN35365 standard; cDNA; 619 BP.
DE Cotton androecium tissue EST Clone ID: L1B3828-009-Q1-K6-C10, SEQ:8346.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.4; DB 13; Length 619;
Best Local Similarity 57.1%; Pred. No. 0.04;
RESULT 1023
ID AAA59475 standard; DNA; 1117 BP.
DE Nucleotide sequence of a soybean type III glutathione-S-transferase.
PN WO200047728-A2.
PD 17-AUG-2000.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 2.9%; Score 48.4; DB 3; Length 1117;
Best Local Similarity 58.6%; Pred. No. 0.053;
RESULT 1024
ID ADQ22714 standard; DNA; 1661 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5534.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 1661;
Best Local Similarity 68.4%; Pred. No. 0.065;
RESULT 1025
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 12; Length 2136;
Best Local Similarity 49.4%; Pred. No. 0.074;
RESULT 1026
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 8; Length 2153;
Best Local Similarity 49.4%; Pred. No. 0.074;
RESULT 1027
ID ADH72101 standard; DNA; 2153 BP.

Best Local Similarity 49.4%; Pred. No. 0.1;
RESULT 1033
ID ADQ23023 standard; DNA; 4046 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5843.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 4046;
Best Local Similarity 58.2%; Pred. No. 0.1;
RESULT 1034
ID AAI72024 standard; cDNA; 4073 BP.
DE Human thrombospondin protein, BTL012, coding sequence.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Query Match 2.9%; Score 48.4; DB 6; Length 4073;
Best Local Similarity 49.4%; Pred. No. 0.1;
RESULT 1035
ID ADB54096 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 20.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1036
ID ADB54224 standard; DNA; 4316 BP.
DE Pretreated genomic DNA region 148.
PN WO2003072821-A2.
PD 04-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1037
ID ADS89522 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:538.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 13; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1038
ID ADS89248 standard; DNA; 4316 BP.
DE Oligonucleotide of the invention SEQ ID NO:264.
PN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 13; Length 4316;
Best Local Similarity 62.3%; Pred. No. 0.11;
RESULT 1039
ID ABL32921 standard; DNA; 5195 BP.
DE Human immune system associated gene SEQ ID NO: 894.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 5195;
Best Local Similarity 62.3%; Pred. No. 0.12;
RESULT 1040
ID ADL9396 standard; cDNA; 5877 BP.
DE Human G-coupled protein receptor-related gene #44.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL) LI L.
PA (GERL) GERLACH V.
PA (LIUX) LIU X.
PA (MILL) MILLER C E.
PA (SPYT) SPYTEK K A.
PA (ZERSH) ZERHUSEN B D.
PA (PENA) PENA C E A.
PA (SHEN) SHENOY S G.
PA (ZHON) ZHONG H.
PA (SMIT) SMITHSON G.
PA (CASM) CASMAN S J.

PA (BOLD) BOLDOG F L.
PA (VOSS) VOSS E Z.
PA (VERN) VERNET C A.
PA (MACD) MACDOUGALL J R.
PA (RAST) RASTELLI L.
PA (ANDE) ANDERSON D W.
PA (ZHON) ZHONG M.
PA (MEZE) MEZES P S.
PA (FURT) FURTAK K.
PA (PATI) PATURAJAN M.
PA (BURG) BURGESS C E.
PA (MALY) MALYANKAR U M.
PA (SHIM) SHIMKETS R A.
PA (TAUP) TAUPIER R J.
PA (EDIN) EDINGER S.
PA (MAZU) MAZUR A.
Query Match 2.9%; Score 48.4; DB 12; Length 5877;
Best Local Similarity 49.4%; Pred. No. 0.12;
RESULT 1041
ID ADE16057 standard; DNA; 5935 BP.
DE G-coupled protein receptor related polypeptide DNA, SEQ ID NO 87.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 10; Length 5935;
Best Local Similarity 49.4%; Pred. No. 0.12;
RESULT 1042
ID ABU33679 standard; DNA; 6070 BP.
DE Human immune system associated gene SEQ ID NO: 1652.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1043
ID ABL34579 standard; DNA; 6070 BP.
DE Human metastasis associated gene SEQ ID NO: 132.
PN WO200177376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1044
ID ABL70372 standard; DNA; 6070 BP.
DE Chemically treated cell signalling DNA sequence complementary to#131.
PN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1045
ID ABQ67130 standard; DNA; 6070 BP.
DE Human angiogenesis associated polynucleotide SEQ ID NO 160.
PN WO200246454-A2.
PD 13-JUN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1046
ID ADS99840 standard; DNA; 6070 BP.
DE Complement of bisulphite treated metastasis-associated human gene #66.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK) OLEK A.
PA (PIEP) PIEPENBROCK C.
PA (BERL) BERLIN K.
Query Match 2.9%; Score 48.4; DB 7; Length 6070;
Best Local Similarity 54.5%; Pred. No. 0.13;
RESULT 1047
ID ABX56304 standard; DNA; 6343 BP.
DE Human NOV25c CG56914-03 DNA SEQ ID 87.
PN WO200281625-A2.
PD 17-OCT-2002.

PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 8; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.13;
RESULT 1048
ID ADH72107 standard; DNA; 6343 BP.
DE Human gene of the invention NOV43d SEQ ID NO:1003.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 12; Length 6343;
Best Local Similarity 49.4%; Pred. No. 0.13;
RESULT 1049
ID ABL33356 standard; DNA; 6577 BP.
DE Human immune system associated gene SEQ ID NO: 1329.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1050
ID ABL70561 standard; DNA; 6577 BP.
DE Chemically treated cell signalling DNA sequence#226.
FN WO200202807-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1051
ID AA61221 standard; DNA; 6577 BP.
DE Human gene regulation-associated gene oligonucleotide #176.
FN WO20017375-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6577;
Best Local Similarity 58.2%; Pred. No. 0.13;
RESULT 1052
ID ABK34027 standard; DNA; 6944 BP.
DE Human DNA for staging of Astrocytomas, complement, #57.
FN WO200202808-A2.
PD 10-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1053
ID ADA20447 standard; DNA; 6944 BP.
DE Prostate tumour related genomic DNA complement sample #56.
FN WO2002103042-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 8; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1054
ID ADA84254 standard; DNA; 6944 BP.
DE Human renal/prostate carcinoma associated DNA SEQ ID NO:112.
FN WO2002103041-A2.
PD 27-DEC-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 8; Length 6944;
Best Local Similarity 62.3%; Pred. No. 0.13;
RESULT 1055
ID ADQ22776 standard; DNA; 7281 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5596.
FN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 7281;
Best Local Similarity 57.1%; Pred. No. 0.14;
RESULT 1056
ID ADS89706 standard; DNA; 7467 BP.
DE Oligonucleotide of the invention SEQ ID NO:722.
FN WO2004035803-A2.
PD 29-APR-2004.
PA (EPIG-) EPIGENOMICS AG.

Query Match 2.9%; Score 48.4; DB 13; Length 7467;
Best Local Similarity 60.8%; Pred. No. 0.14;
RESULT 1057
ID ADK60477 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
FN FR283687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1058
ID ADK60778 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
FN FR283686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1059
ID ADP73100 standard; DNA; 8546 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N52.
FN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 2.9%; Score 48.4; DB 12; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1060
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
FN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 2.9%; Score 48.4; DB 13; Length 8546;
Best Local Similarity 49.4%; Pred. No. 0.15;
RESULT 1061
ID ABL33068 standard; DNA; 9117 BP.
DE Human immune system associated gene SEQ ID NO: 1041.
FN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 6; Length 9117;
Best Local Similarity 62.3%; Pred. No. 0.15;
RESULT 1062
ID ADF50896 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 4).
FN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 11097;
Best Local Similarity 62.3%; Pred. No. 0.17;
RESULT 1063
ID ADF50894 standard; DNA; 11097 BP.
DE Chemically modified promoter region of human melastatin gene (SeqID 2).
FN EPI344832-A1.
PD 17-SEP-2003.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.4; DB 10; Length 11097;
Best Local Similarity 62.3%; Pred. No. 0.17;
RESULT 1064
ID ADO08272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
FN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.

PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOV S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZSRH/) ZERHUSEN B D.
Query Match 2.9%; Score 48.4; DB 12; Length 15659;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1065
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 8; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1066
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 2.9%; Score 48.4; DB 12; Length 15660;
Best Local Similarity 49.4%; Pred. No. 0.2;
RESULT 1067
ID ABQ86156 standard; DNA; 16908 BP.
DE Novel human gene. SEQ ID 27.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Query Match 2.9%; Score 48.4; DB 6; Length 16908;
Best Local Similarity 49.4%; Pred. No. 0.21;
RESULT 1068
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1069
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1070
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
PN FR2843753-A1.
PD 27-FEB-2004.

PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 2.9%; Score 48.4; DB 12; Length 18207;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1071
ID ADQ22570 standard; DNA; 18248 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.4; DB 12; Length 18248;
Best Local Similarity 49.4%; Pred. No. 0.22;
RESULT 1072
ID ABL37453 standard; cDNA; 153 BP.
DE Human colon tumour antigen polynucleotide SEQ ID NO:1042.
PN WO200196388-A2.
PD 20-DEC-2001.
PA (CORI-) CORIXA CORP.
Query Match 2.9%; Score 48.2; DB 6; Length 153;
Best Local Similarity 59.3%; Pred. No. 0.022;
RESULT 1073
ID AAH70080 standard; cDNA; 268 BP.
DE Human cervical cancer marker nucleic acid 1354.
PN WO200142467-A2.
PD 14-JUN-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 4; Length 268;
Best Local Similarity 51.9%; Pred. No. 0.029;
RESULT 1074
ID ACN45531 standard; cDNA; 272 BP.
DE Cotton primed seed EST Clone ID: LIB3825-003-Q1-K6-E5, SEQ:312.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 272;
Best Local Similarity 63.2%; Pred. No. 0.03;
RESULT 1075
ID ABV58763 standard; cDNA; 317 BP.
DE Human prostate expression marker cDNA 58754.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 317;
Best Local Similarity 57.7%; Pred. No. 0.032;
RESULT 1076
ID ACN50558 standard; cDNA; 325 BP.
DE Cotton mature seed EST Clone ID: LIB3827-002-Q1-K6-E8, SEQ:5339.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 325;
Best Local Similarity 62.2%; Pred. No. 0.032;
RESULT 1077
ID AAL23694 standard; cDNA; 359 BP.
DE Human breast cancer expressed polynucleotide 16151.
PN WO200151628-A2.
PD 19-JUL-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 4; Length 359;
Best Local Similarity 61.6%; Pred. No. 0.034;
RESULT 1078
ID ADL37765 standard; DNA; 385 BP.
DE Human ovarian cancer DNA marker #11655.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 385;

Best Local Similarity 53.5%; Pred. No. 0.035;
RESULT 1079
ID ADF172626 standard; DNA; 385 BP.
DE Human ovarian cancer DNA marker #5368.
PN WO200170979-A2.
PD 27-SEP-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 385;
Best Local Similarity 53.5%; Pred. No. 0.035;
RESULT 1080
ID AAI84791 standard; cDNA; 390 BP.
DE Human polynucleotide SEQ ID NO 4851.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 390;
Best Local Similarity 57.7%; Pred. No. 0.035;
RESULT 1081
ID AAI83999 standard; cDNA; 411 BP.
DE Human polynucleotide SEQ ID NO 4059.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 411;
Best Local Similarity 60.2%; Pred. No. 0.036;
RESULT 1082
ID AAI88617 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 8677.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 416;
Best Local Similarity 58.9%; Pred. No. 0.037;
RESULT 1083
ID AAI89032 standard; cDNA; 416 BP.
DE Human polynucleotide SEQ ID NO 9092.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48.2; DB 4; Length 416;
Best Local Similarity 61.6%; Pred. No. 0.037;
RESULT 1084
ID ABV49374 standard; cDNA; 453 BP.
DE Human prostate expression marker cDNA 49365.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 453;
Best Local Similarity 63.2%; Pred. No. 0.038;
RESULT 1085
ID ACN57722 standard; cDNA; 492 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-005-Q6-N6-B12, SEQ:12503.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 492;
Best Local Similarity 60.2%; Pred. No. 0.04;
RESULT 1086
ID ABV57520 standard; cDNA; 504 BP.
DE Human prostate expression marker cDNA 57511.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48.2; DB 5; Length 504;
Best Local Similarity 58.9%; Pred. No. 0.04;
RESULT 1087
ID ACN55029 standard; cDNA; 518 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-028-Q6-K6-D8, SEQ:9810.
PN US2004123340-A1.
PD 24-JUN-2004.

PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 518;
Best Local Similarity 55.3%; Pred. No. 0.041;
RESULT 1088
ID ACN60563 standard; cDNA; 585 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-025-Q6-K6-B11, SEQ:15344.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 585;
Best Local Similarity 56.7%; Pred. No. 0.043;
RESULT 1089
ID ACN62771 standard; cDNA; 594 BP.
DE Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-K6-C5, SEQ:17552.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48.2; DB 13; Length 594;
Best Local Similarity 61.6%; Pred. No. 0.044;
RESULT 1090
ID AAD34114 standard; cDNA; 921 BP.
DE Human secreted protein-encoding gene 9 cDNA clone H89NQ42, SEQ ID NO:19.
PN WO200222654-A1.
PD 21-MAR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48.2; DB 6; Length 921;
Best Local Similarity 63.2%; Pred. No. 0.055;
RESULT 1091
ID AAD54409 standard; cDNA; 990 BP.
DE Lolium perenne defensin a (LpDEFa) cDNA.
PN WO200288359-A1.
PD 07-NOV-2002.
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA (AGRE-) AGRESEARCH LTD.
Query Match 2.9%; Score 48.2; DB 8; Length 990;
Best Local Similarity 54.1%; Pred. No. 0.057;
RESULT 1092
ID AAL57070 standard; DNA; 1040 BP.
DE Human G-protein coupled receptor GAVE18 DNA sequence.
PN WO2003042399-A2.
PD 22-MAY-2003.
PA (AVET) AVENTIS PHARM INC.
Query Match 2.9%; Score 48.2; DB 9; Length 1040;
Best Local Similarity 63.2%; Pred. No. 0.058;
RESULT 1093
ID ADG73631 standard; cDNA; 1259 BP.
DE Human cDNA of the invention SEQ ID NO:16.
PN CN1369506-A.
PD 18-SEP-2002.
PA (SHAN-) SHANGHAI INST ONCOLOGY.
Query Match 2.9%; Score 48.2; DB 10; Length 1259;
Best Local Similarity 65.1%; Pred. No. 0.064;
RESULT 1094
ID ADF94940 standard; cDNA; 1311 BP.
DE Human gene 8-derived ACRP30-like cDNA, SEQ ID NO:36.
PN WO2003031586-A2.
PD 17-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
PA (BLON-) BLONDEL O.
PA (RUBE-) RUBEN S M.
Query Match 2.9%; Score 48.2; DB 10; Length 1311;
Best Local Similarity 62.2%; Pred. No. 0.065;
RESULT 1095
ID ABS53034 standard; DNA; 2038 BP.

DE Arabidopsis thaliana squalene epoxidase polynucleotide #4.
PN WO200261072-A2.
PA (MONS) MONSANTO TECHNOLOGY LLC.
Query Match 2.9%; Score 48.2; DB 6; Length 2038;
Best Local Similarity 58.9%; Pred. No. 0.082;
RESULT 1096
ID AD023275 standard; DNA; 3056 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6095.
PN WO200404838-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 2.9%; Score 48.2; DB 12; Length 3056;
Best Local Similarity 63.2%; Pred. No. 0.1;
RESULT 1097
ID ABL33751 standard; DNA; 7037 BP.
DE Human immune system associated gene SEQ ID NO: 1724.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 7037;
Best Local Similarity 60.2%; Pred. No. 0.15;
RESULT 1098
ID ABL32448 standard; DNA; 7238 BP.
DE Human immune system associated gene SEQ ID NO: 421.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 7238;
Best Local Similarity 60.2%; Pred. No. 0.16;
RESULT 1099
ID ABL32332 standard; DNA; 8895 BP.
DE Human immune system associated gene SEQ ID NO: 305.
PN WO200200928-A2.
PD 03-JAN-2002.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 8895;
Best Local Similarity 58.9%; Pred. No. 0.17;
RESULT 1100
ID ABL34492 standard; DNA; 11996 BP.
DE Human metastasis associated gene SEQ ID NO: 45.
PN WO20017376-A2.
PD 18-OCT-2001.
PA (EPIG-) EPIGENOMICS AG.
Query Match 2.9%; Score 48.2; DB 6; Length 11996;
Best Local Similarity 65.1%; Pred. No. 0.2;
RESULT 1101
ID ADS99753 standard; DNA; 11996 BP.
DE Bisulphite treated human gene associated with metastasis #23.
PN US2003148327-A1.
PD 07-AUG-2003.
PA (OLEK/) OLEK A.
PA (PIEP/) PIEPENBROCK C.
PA (BERL/) BERLIN K.
Query Match 2.9%; Score 48.2; DB 7; Length 11996;
Best Local Similarity 65.1%; Pred. No. 0.2;
RESULT 1102
ID ACH50958 standard; cDNA; 139 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-002-Q1-N6-E3, SEQ:5739.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 139;
Best Local Similarity 64.3%; Pred. No. 0.024;
RESULT 1103
ID ABX46273 standard; cDNA; 239 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #11438.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.

PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48; DB 8; Length 239;
Best Local Similarity 59.6%; Pred. No. 0.031;
RESULT 1104
ID ABX42739 standard; cDNA; 241 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #7904.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48; DB 8; Length 241;
Best Local Similarity 59.6%; Pred. No. 0.031;
RESULT 1105
ID ADS72366 standard; cDNA; 269 BP.
DE Human kidney tumour specific cDNA, SEQ ID 963.
PN US2003109434-A1.
PD 12-JUN-2003.
PA (CORI-) CORIXA CORP.
Query Match 2.9%; Score 48; DB 7; Length 269;
Best Local Similarity 56.2%; Pred. No. 0.033;
RESULT 1106
ID ABX43930 standard; cDNA; 283 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #9095.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48; DB 8; Length 283;
Best Local Similarity 64.3%; Pred. No. 0.034;
RESULT 1107
ID ABV56758 standard; cDNA; 323 BP.
DE Human prostate expression marker cDNA 56749.
PN WO200160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 323;
Best Local Similarity 56.2%; Pred. No. 0.036;
RESULT 1108
ID ABX38490 standard; cDNA; 373 BP.
DE Bovine EST associated with lactation/muscle/fat deposition #3655.
PN US2002137139-A1.
PD 26-SEP-2002.
PA (BYAT/) BYATT J C.
PA (MATH/) MATHIALAGAN N.
PA (TAON/) TAO N.
PA (WARR/) WARREN W C.
Query Match 2.9%; Score 48; DB 8; Length 373;
Best Local Similarity 58.3%; Pred. No. 0.039;
RESULT 1109
ID AAI89019 standard; cDNA; 386 BP.
DE Human polynucleotide SEQ ID NO 9079.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 386;
Best Local Similarity 64.3%; Pred. No. 0.04;
RESULT 1110
ID AAI85430 standard; cDNA; 401 BP.
DE Human polynucleotide SEQ ID NO 5490.
PN WO200164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 401;
Best Local Similarity 55.6%; Pred. No. 0.041;
RESULT 1111
ID AAI85304 standard; cDNA; 404 BP.
DE Human polynucleotide SEQ ID NO 5364.

PN WO2000164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 404;
Best Local Similarity 64.3%; Pred. No. 0.041;
RESULT 1112
ID AA183194 standard; cDNA; 407 BP.
DE Human polynucleotide SEQ ID NO 3254.
PN WO2000164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 407;
Best Local Similarity 64.3%; Pred. No. 0.041;
RESULT 1113
ID AA183744 standard; cDNA; 408 BP.
DE Human polynucleotide SEQ ID NO 3804.
PN WO2000164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 408;
Best Local Similarity 57.9%; Pred. No. 0.041;
RESULT 1114
ID ABV59282 standard; cDNA; 452 BP.
DE Human prostate expression marker cDNA 59273.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 452;
Best Local Similarity 64.3%; Pred. No. 0.043;
RESULT 1115
ID AA182085 standard; cDNA; 466 BP.
DE Human polynucleotide SEQ ID NO 2145.
PN WO2000164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 466;
Best Local Similarity 64.3%; Pred. No. 0.044;
RESULT 1116
ID AA188612 standard; cDNA; 478 BP.
DE Human polynucleotide SEQ ID NO 8672.
PN WO2000164835-A2.
PD 07-SEP-2001.
PA (HYSE-) HYSEQ INC.
Query Match 2.9%; Score 48; DB 4; Length 478;
Best Local Similarity 64.3%; Pred. No. 0.044;
RESULT 1117
ID ACN61416 standard; cDNA; 490 BP.
DE Cotton gynoecium tissue EST Clone ID: LIB3829-015-Q1-N6-H1, SEQ:16197.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 490;
Best Local Similarity 49.6%; Pred. No. 0.045;
RESULT 1118
ID ABV58419 standard; cDNA; 515 BP.
DE Human prostate expression marker cDNA 58410.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 515;
Best Local Similarity 56.2%; Pred. No. 0.046;
RESULT 1119
ID ABV57482 standard; cDNA; 533 BP.
DE Human prostate expression marker cDNA 57473.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 533;
Best Local Similarity 56.2%; Pred. No. 0.047;
RESULT 1120

ID ABV58372 standard; cDNA; 540 BP.
DE Human prostate expression marker cDNA 58363.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 540;
Best Local Similarity 56.2%; Pred. No. 0.047;
RESULT 1121
ID ABV58085 standard; cDNA; 585 BP.
DE Human prostate expression marker cDNA 58076.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 585;
Best Local Similarity 56.2%; Pred. No. 0.049;
RESULT 1122
ID ADF76609 standard; cDNA; 602 BP.
DE Novel human secreted and transmembrane protein cDNA SeqID 283.
PN WO2003072035-A2.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 10; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1123
ID ADU83210 standard; cDNA; 602 BP.
DE Human PRO52174 cDNA, SEQ ID 412.
PN WO2004024097-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1124
ID ADU91506 standard; cDNA; 602 BP.
DE Human immune-related polypeptide PRO52174-encoding cDNA, SEQ ID NO:21.
PN WO2004024072-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1125
ID ADM41666 standard; cDNA; 602 BP.
DE PRO52174 cDNA, associated with B-cell activation.
PN WO2004024069-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 12; Length 602;
Best Local Similarity 60.9%; Pred. No. 0.05;
RESULT 1126
ID ABV43916 standard; cDNA; 606 BP.
DE Human prostate expression marker cDNA 43907.
PN WO2000160860-A2.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
Query Match 2.9%; Score 48; DB 5; Length 606;
Best Local Similarity 58.3%; Pred. No. 0.05;
RESULT 1127
ID ACN54555 standard; cDNA; 627 BP.
DE Cotton androecium tissue EST Clone ID: LIB3828-024-Q6-K6-C2, SEQ:9336.
PN US2004123340-A1.
PD 24-JUN-2004.
PA (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FENG/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
Query Match 2.9%; Score 48; DB 13; Length 627;
Best Local Similarity 64.3%; Pred. No. 0.051;
RESULT 1128
ID ADF04748 standard; cDNA; 1352 BP.
DE Sea squirt cDNA with tissue specific expression in development Seq 343.
PN JP2004057129-A.
PD 26-FEB-2004.
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
Query Match 2.9%; Score 48; DB 12; Length 1352;

Best Local Similarity 59.6%; Pred. No. 0.075;
RESULT 1129
ID ADG32734 standard; DNA; 1483 BP.
DE Human DNA differentially expressed in patients with SLE SeqID58.
FN WO2003090694-A2.
PD 06-NOV-2003.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 2.9%; Score 48; DB 10; Length 1483;
Best Local Similarity 59.6%; Pred. No. 0.079;
RESULT 1130
ID AAI72316 standard; cDNA; 1637 BP.
DE Human transporter protein cDNA.
FN WO2002026335-A2.
PD 10-JAN-2002.
PA (APPL-) APPLERA CORP.
Query Match 2.9%; Score 48; DB 6; Length 1637;
Best Local Similarity 58.3%; Pred. No. 0.083;
RESULT 1131
ID AAZ90632 standard; DNA; 1690 BP.
DE Human adipose tissue protein #2 encoding DNA.
FN JP2000037190-A.
PD 08-FEB-2000.
PA (NLSB-) JAPAN TOBACCO INC.
Query Match 2.9%; Score 48; DB 3; Length 1690;
Best Local Similarity 64.3%; Pred. No. 0.084;
RESULT 1132
ID AAD32523 standard; DNA; 1726 BP.
DE Human B7-H10 Gene.
FN WO200202587-A1.
PD 10-JAN-2002.
PA (HUNA-) HUMAN GENOME SCI INC.
Query Match 2.9%; Score 48; DB 6; Length 1726;
Best Local Similarity 59.6%; Pred. No. 0.085;
RESULT 1133
ID AAX52252 standard; DNA; 1984 BP.
DE Protein PRO271 cDNA clone DNA39423-1182.
FN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 2; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1134
ID ADC78532 standard; cDNA; 1984 BP.
DE Human PRO271 cDNA.
FN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 3; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1135
ID ADR18008 standard; cDNA; 1984 BP.
DE Human secreted/transmembrane protein cDNA, #42.
FN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.

PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Query Match 2.9%; Score 48; DB 13; Length 1984;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1136
ID AAF72410 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
FN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 4; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1137
ID AAS45938 standard; cDNA; 1985 BP.
DE Human DNA encoding PRO polypeptide sequence #14.
FN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1138
ID ACA60174 standard; cDNA; 1985 BP.
DE Human cDNA for secreted/transmembrane protein PRO271.
FN US200303530-A1.
PD 02-JAN-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1139
ID ACA89388 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003036141-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1140
ID ACA73398 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1141
ID ACA05713 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1142
ID ACA66547 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
FN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1143
ID ACD07574 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
FN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH-) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1144
ID ACF20122 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003040063-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1155
ID AC88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003040064-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1146
ID AC211796 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027267-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1147
ID ACF12961 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1148
ID ACD25064 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1149
ID ACF00113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1150
ID ACA72170 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1151
ID ACD04694 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1152
ID ACD18155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1153
ID ACD08162 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1154
ID ABX71622 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
PN US2002132240-A1.
PD 19-SEP-2002.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1155
ID AC88596 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1156
ID ACA70038 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1157
ID ACD12260 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1158
ID ACC74175 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1159
ID ACD15803 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1160
ID ACD25371 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1161
ID ACD17848 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1162
ID ACC88135 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1163
ID ACD21489 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;
RESULT 1164
ID ACD18556 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1165
ID ACH06954 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane polypeptide PRO271 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1166
ID ABX98166 standard; cDNA; 1985 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 27.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1167
ID ACU13917 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1168
ID ACU09697 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1169
ID ACC88442 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1170
ID ACD21182 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1171
ID ABX75554 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO271.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1172
ID ABX97757 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1173
ID ACA97233 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1174
ID ACA57696 standard; cDNA; 1985 BP.
DE Human PRO271 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1175
ID ACD14224 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1176
ID ACC91007 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1177
ID ACC88749 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1178
ID ACD06946 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US200308353-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1179
ID ACA67397 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1180
ID ACC81452 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1181
ID ACC89056 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1182
ID ACC86412 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027268-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1183
ID ACC89670 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1184
ID ACC92849 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1185
ID ACA72477 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1186
ID ACA88995 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1187
ID ACA69731 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1188
ID ACA96874 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1189
ID ACA90870 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1190
ID ACA70652 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1191
ID ACA95162 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1192
ID ACC86105 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1193
ID ACC89977 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1194
ID ACD12585 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1195
ID ACF19815 standard; cDNA; 1985 BP.

DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1196
ID ABX76759 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1197
ID ABX96191 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #40.
PN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1198
ID ACA73091 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1199
ID ACA05512 standard; cDNA; 1985 BP.
DE cDNA encoding human secreted protein PRO271.
PN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1200
ID ACA68634 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1201
ID ACA74478 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1202
ID ACA70345 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1203
ID ACD14531 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1204
ID ACD20179 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1205
ID ACA68203 standard; cDNA; 1985 BP.

DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1206
ID ABX98668 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032103-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1207
ID ACC81145 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1208
ID ACA95469 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032155-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1209
ID ACD04387 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032296-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1210
ID ACC87828 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032781-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1211
ID ACF12490 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1212
ID ACA96205 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1213
ID ACA64979 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1214
ID ACA73705 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1215
ID ACA74117 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032131-A1.

PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1216
ID ACA96512 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1217
ID ACD10618 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1218
ID ACC91314 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1219
ID ACD02649 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1220
ID ACC87214 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1221
ID ACC85798 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1222
ID ACA65286 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1223
ID ACA94103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032142-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1224
ID ACA97847 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032145-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1225
ID ACA91349 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032154-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1226
ID ACA90563 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1227
ID ACD16110 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1228
ID ACD17271 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1229
ID ACC91928 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1230
ID ACA74785 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1231
ID ACA91656 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1232
ID ACA71300 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1233
ID ACC90700 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1234
ID ACA65710 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO protein #14.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1235
ID ACA54982 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1236

ID ACA94855 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1237
ID ACD16417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1238
ID ACD15496 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1239
ID ABX16599 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein #14.
PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 8; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1240
ID ACA97540 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003032115-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1241
ID ACA98989 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003032140-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1242
ID ACC91621 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1243
ID ACD11032 standard; cDNA; 1985 BP.
DE Novel human secreted and transmembrane protein PRO271 cDNA.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1244
ID ACD14882 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044922-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1245
ID ACD19817 standard; cDNA; 1985 BP.
DE Human secreted / transmembrane polypeptide PRO271 cDNA.
PN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1246
ID ACD11646 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032118-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1247
ID ACC95775 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036135-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1248
ID ACF16338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054455-A1.
PD 20-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1249
ID ACF02456 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049741-A1.
PD 13-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1250
ID ACF02763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049743-A1.
PD 13-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1251
ID ACF21350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049769-A1.
PD 13-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1252
ID ACF10034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068743-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1253
ID ACF77927 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054479-A1.
PD 20-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1254
ID ACD46632 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068685-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ACD49395 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

PN US2003068725-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1256
ID ACF28162 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068752-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068682-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1257
ID ACD88852 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068701-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ACD84247 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068701-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1259
ID ACD99021 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068755-A1.
PD 10-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1260
ID ADA77779 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073180-A1.
PD 17-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1261
ID ACF48763 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1262
ID ADB29417 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003092002-A1.
PD 15-MAY-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1263
ID ACD09083 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1264
ID ACF11876 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1265
ID ACF41110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1266
ID ACF15724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044930-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1267
ID ACF16031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1268
ID ACD31858 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1269
ID ACF18666 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1270
ID ACF09113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1271
ID ACF78234 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1272
ID ACF51833 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064440-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1273
ID ACF26320 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1274
ID ACF24113 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1275
ID ACF63424 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1276
ID ACF50298 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1277
ID ACH07769 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049749-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1278
ID ACF13575 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064462-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1279
ID ACD41501 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003065159-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1280
ID ACF31914 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064447-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1281
ID ACF23192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003073184-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1282
ID ACF39882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064463-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1283
ID ACD45404 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.

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PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1293
ID ACF49684 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104542-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1294
ID ACF49991 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104543-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1295
ID ACD09390 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036127-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1296
ID ACD08469 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040061-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1297
ID ACF12183 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003036130-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1298
ID ACC94691 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1299
ID ACD22410 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1300
ID ACF15110 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044917-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1301
ID ACC97205 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003044929-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1302
ID ADA18273 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039571-A1.
PD 27-FEB-2003.

PN US2003064451-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1284
ID ACF53061 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068721-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1285
ID ACF27241 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068699-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1286
ID ACF45079 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068707-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1287
ID ACF29697 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073175-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1288
ID ACD89773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068695-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1289
ID ACD84554 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068703-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1290
ID ACD98714 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003068732-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1291
ID ACF77006 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082717-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1292
ID ACF76699 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104548-A1.
PD 05-JUN-2003.
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PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1303
ID ACP6964 standard; cDNA; 1985 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO271.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1304
ID ACC92235 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1305
ID ACF13882 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1306
ID ACF14189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1307
ID ACF09420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1308
ID ACD45711 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1309
ID ACD47860 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1310
ID ACD67591 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1311
ID ACP25399 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.

Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1312
ID ACP29083 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1313
ID ACD84861 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1314
ID ACD83940 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
FN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1315
ID ACD87931 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068776-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1316
ID ACF30618 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1317
ID ACF32221 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1318
ID ACH11881 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1319
ID ACH12188 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1320
ID ACD40580 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032134-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1321
ID ACF18052 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1322
ID ACF08499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1323
ID ACF31300 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1324
ID ACF52140 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1325
ID ACD50009 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1326
ID ACF38712 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1327
ID ACF26627 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1328
ID ACF24727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1329
ID ACF46307 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1330

ID ACF27855 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1331
ID ACD89159 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1332
ID ACF63731 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1333
ID ACF60371 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1334
ID ACH12495 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1335
ID ACH09918 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049777-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1336
ID ACD03773 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1337
ID ACD10311 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1338
ID ACD11953 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1339
ID ACD83125 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1340
ID ACF42338 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1341
ID ADAL6248 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1342
ID ACF18359 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1343
ID ACF02149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1344
ID ACF21657 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1345
ID ACF10341 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1346
ID ACF33793 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1347
ID ACF44755 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1348
ID ACF90387 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;

RESULT 1349
ID ACD91000 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049751-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1350
ID ACF30311 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1351
ID ACD87010 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1352
ID ACF60064 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1353
ID ACF46614 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003087373-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1354
ID ACF75471 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096353-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1355
ID ADA79571 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003073173-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1356
ID ACF17131 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054458-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1357
ID ACF2885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003059886-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1358
ID ACF07885 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049758-A1.
PD 13-MAR-2003.

PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1359
ID ACF08192 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049772-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1360
ID ACF40496 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064448-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1361
ID ACF53675 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064456-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1362
ID ACD46939 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1363
ID ACF47842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068735-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1364
ID ACF47228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068753-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1365
ID ACF46000 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068742-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1366
ID ACD86089 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068756-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1367
ID ACF52447 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;

Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1368
ID ACF52754 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1369
ID ACF64747 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068737-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1370
ID ACF76392 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104547-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1371
ID ACF61292 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003096359-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1372
ID ACF61599 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003100061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1373
ID ACD30630 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032125-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1374
ID ACD31551 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054454-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1375
ID ACD32472 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1376
ID ACF17438 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1377
ID ACF07271 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

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PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1387
ID ADA42393 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1388
ID ADA81298 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1389
ID ACD22103 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003027276-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1390
ID ACD24450 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044920-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1391
ID ACD39653 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003027265-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1392
ID ACD39960 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1393
ID ACF13268 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1394
ID ACF03070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1395
ID ACD23303 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #38.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1396
ID ACF78541 standard; cDNA; 1985 BP.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1378
ID ACF20429 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1379
ID ACF21043 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1380
ID ACF20736 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1381
ID ACD47553 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1382
ID ACF47535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1383
ID ACF53368 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068679-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1384
ID ACD86703 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1385
ID ACH04951 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1386
ID ACF44448 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1397
ID ACF11262 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1398
ID ACF50605 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1399
ID ACF34100 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1400
ID ACD46325 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1401
ID ACD48167 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1402
ID ACF27548 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1403
ID ACF24420 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1404
ID ACD85475 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1405
ID ACD90080 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068729-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1406
ID ACD83633 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1407
ID ACF49070 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1408
ID ACH07155 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1409
ID ACH07462 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049747-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1410
ID ACH08076 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1411
ID ACH11267 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1412
ID ACH11574 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1413
ID ACH10225 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1414
ID ACF01228 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

RESULT 1415
ID ACF40803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1416
ID ACD24143 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1417
ID ACD31244 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1418
ID ACF17745 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1419
ID ACF32528 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1420
ID ACF40189 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1421
ID ACF48149 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1422
ID ACF38098 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1423
ID ACF25034 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1424
ID ACF26934 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068730-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1425
ID ACF29390 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1426
ID ACD87624 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1427
ID ACF76085 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1428
ID ACF49377 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104541-A1.
PD 05-JUN-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1429
ID ACF43834 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1430
ID ACH06179 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1431
ID ACH06486 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1432
ID ADA83096 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1433
ID ACC92542 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003032133-A1.
PD 13-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

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RESULT 1434
ID ACC93156 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003032136-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1435
ID ACF19201 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US200303036129-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1436
ID ACD12892 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003040053-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1437
ID ACF06350 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003040057-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1438
ID ACC94384 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054467-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1439
ID ACC97812 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003044932-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1440
ID ACC94077 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027270-A1.
PD 06-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1441
ID ACF42031 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003054469-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1442
ID ACD30937 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003032126-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1443
ID ACD42966 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054463-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1444
ID ACD43273 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003054466-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1445
ID ACF14803 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003059879-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1446
ID ACF01535 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003049738-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1447
ID ACF31607 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003064469-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1448
ID ACD67284 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003064453-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1449
ID ACD48474 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064466-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1450
ID ACD48781 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003064468-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1451
ID ACF51219 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068760-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1452
ID ACF53982 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068769-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
56.2%; Pred. No. 0.091;
RESULT 1453
ID ACF25706 standard; cDNA; 1985 BP.
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DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1454
ID ACF39019 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1455
ID ACF28776 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1456
ID ACD90693 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1457
ID ACD86396 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1458
ID ACH05258 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1459
ID ACF65054 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1460
ID ADB20139 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1461
ID ACF43527 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1462
ID ACH08997 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049774-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1463
ID ACH09304 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1464
ID ADA78391 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1465
ID ACF09727 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1466
ID ACF50912 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1467
ID ACF23806 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1468
ID ACD88238 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1469
ID ACH09611 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1470
ID ACH10532 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1471
ID ACD11339 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003036126-A1.
PD 20-FEB-2003.

Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1472
ID ACF96389 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US200304924-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1473
ID ACC98419 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US200304927-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1474
ID ADA16672 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1475
ID ACF41724 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040072-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1476
ID ACF16645 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003040073-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1477
ID ADA13101 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
PN US2003054475-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1478
ID ACD32165 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1479
ID ACD30323 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003032124-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1480
ID ACD41194 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1481
ID ACF07578 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003049759-A1.

PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1482
ID ACF30993 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1483
ID ACF77313 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1484
ID ACF10955 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073170-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1485
ID ACF32835 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1486
ID ACF26013 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068717-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1487
ID ACD83326 standard; cDNA; 1985 BP.
DE Human PRO polynucleotide #14.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1488
ID ACF23499 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1489
ID ACF42913 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 2.9%; Score 48; DB 9; Length 1985;
RESULT 1490
ID ACF43220 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.

Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1491
ID ACH05872 standard; cDNA; 1985 BP.
DE cDNA encoding human PRO polypeptide #14.
FN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1492
ID ACH08690 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1493
ID ADA41969 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
FN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1494
ID ACC90284 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003027273-A1.
PD 06-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1495
ID ACF10648 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036119-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1496
ID ACC93463 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036120-A1.
PD 20-FEB-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1497
ID ACC96082 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.
FN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1498
ID ACD24757 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #14.
FN US2003044921-A1.
PD 06-MAR-2003.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1499
ID ADA17316 standard; cDNA; 1985 BP.
DE Human secreted/transmembrane protein cDNA, #42.
FN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;
RESULT 1500
ID ACF01842 standard; cDNA; 1985 BP.
DE Human secreted polypeptide PRO271-encoding cDNA, SEQ ID NO:27.

PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 2.9%; Score 48; DB 9; Length 1985;
Best Local Similarity 56.2%; Pred. No. 0.091;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:48:31 ; Search time 5809 Seconds
(without alignments)
11001.878 Million cell updates/sec

Title: US-10-017-084a-522

Perfect score: 1679

Sequence: 1 gttgtgccttcgcaaac.....ataaaagagcaaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1119.4	66.7	1808	3	AK046377 Mus muscu
3	1014.6	60.4	2512	3	CR602526 full-leng
4	852	50.7	874	9	AY406347 Homo sapi
5	743.2	44.3	773	9	AY406348 Pan trogl
6	733.4	43.7	1033	4	BM807426 AGENCOURT
7	720.2	42.9	1083	4	BM809227 AGENCOURT
8	709.6	42.3	874	9	AY406349 Mus muscu
9	674	40.1	865	4	BI666583 603291469
10	669.8	39.9	673	7	CR736885 CR736885
11	664.8	39.6	856	5	BU155617 AGENCOURT
12	645	38.4	1027	1	AL533026 AL533026
13	643	38.3	732	4	BI551784 603197479
14	640	38.1	748	7	CR362539 170004705
15	635.2	37.8	1039	2	BE798585 601581610
16	628.4	37.4	784	4	BI549318 603194765
17	621.2	37.0	870	4	BI913885 603183295
18	619.6	36.9	765	6	CD354474 UI-M-GMO-
19	611	36.4	737	4	BM679797 UI-E-EJ0-
20	602.4	35.9	604	2	AW025115 wu1h04.x
21	598.8	35.7	602	5	BU741589 UI-E-EJ0-
22	594.8	35.4	770	2	AW117456 xd92a06.x
23	590.6	35.2	680	7	CR751151 DKF2p459F
24	567.8	33.8	1450	7	C0635648 Contig266

25	556.2	33.1	633	4	BG706987
26	549	32.7	661	4	BM009450
27	548.2	32.7	580	4	BI548566
28	544.4	32.4	754	4	BI598759
29	544	32.4	600	7	CR548212
30	542.4	32.3	759	7	CF737474
31	541.8	32.3	737	7	CN533076
32	532.4	31.7	768	1	AU080629
33	531.4	31.6	545	2	BE263639
34	522.2	31.1	613	7	CR540607
35	522	31.1	534	4	BM686717
36	516	30.7	664	7	CN362538
37	507.8	30.2	563	6	CB296974
38	507	29.1	636	7	CR540711
39	488.8	29.1	660	6	BY723873
40	488	29.1	488	5	BX477962
41	486.8	29.0	905	5	BX432064
42	485.6	28.9	953	4	BM423716
43	479.8	28.6	671	2	BB644996
44	479.2	28.5	601	6	CB582386
45	475.4	28.3	486	1	AI753140
46	469	27.9	522	4	BI553032
47	465.6	27.7	479	1	AA843782
48	457.4	27.2	524	2	BE014142
49	456.4	27.2	728	6	CD353574
50	455	27.1	740	5	BU368328
51	455	27.1	979	4	BG261691
52	454.6	27.1	890	6	CD327172
53	450	26.8	849	4	BI755360
54	448.8	26.7	840	5	BU320256
55	447.6	26.7	553	2	BE864555
56	445	26.5	456	1	AI369684
57	444.4	26.5	548	2	BE015245
58	443.8	26.4	655	4	BI548049
59	439	26.1	440	1	AI318423
60	437	26.0	582	5	BP194945
61	432.6	25.8	1138	4	BM556708
62	427.8	25.5	683	2	BB640070
63	427.8	25.5	3166	3	AK042854
64	426	25.4	426	1	AI332824
65	417.2	24.8	795	7	CO395735
66	413	24.6	806	1	AU051132
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74	384.2	22.9	437	6	CB724811
75	384	22.9	663	4	BM724307
76	381.2	22.7	608	5	BQ188988
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79	378.8	22.6	390	4	BM719375
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83	377.2	22.5	394	4	BM684852
84	377.2	22.5	394	5	BQ184395
85	377.2	22.5	394	5	BQ184512
86	377.2	22.5	394	7	CK300895
87	377.2	22.5	403	4	BM684212
88	376	22.4	376	1	AI246488
89	372.2	22.2	705	4	BG704152
90	368.8	22.0	590	5	BQ807621
91	368.4	21.9	389	1	AA450107
92	366.8	21.8	804	7	CN232247
93	360.4	21.5	739	5	BU277649
94	351.4	20.9	819	5	BU750937
95	351.4	20.9	823	5	BU750936
96	347.2	20.7	724	7	CK312152
97	344.4	20.5	346	1	AI951451

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BI598759	603245538
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CF737474	UI-M-HD0-
CN533076	UI-M-HD0-
AU080629	AU080629
BE263639	601192064
CR540607	DKF2p459A
BM686717	UI-E-C00-
CN362538	170006001
CB296974	12822045
CR540711	DKF2p459F
BY723873	BY723873
BX477962	DKF2p686N
BX432064	BX432064
BM423716	AGENCOURT
BB644996	BB644996
CB582386	AMGNNUC:N
AI753140	cr05g10.x
BI553032	603193672
AA843782	aj18d10.8
BE014142	125737.MA
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BU368328	603789424
BG261691	602373361
CD327172	AGENCOURT
BI755360	603024964
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BI369684	qy71903.x
BE015245	127482.MA
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BB640070	BB640070
AK042854	Mus muscu
AI332824	qp96e10.x
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AA450107	zx42d09.8
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101	340.4	20.3	1017	9	AY406973	AY406973 Mus muscu	C 174	233.2	13.9	599	7	CN229507	CN229507 RJB072D02
102	339.4	20.2	2768	3	AK030681	AK030681 Mus muscu	C 175	232	13.8	277	7	R88615	R88615 Ym93f06.r1
103	338	20.1	1015	9	AY406972	AY406972 Pan trogl	C 176	231.8	13.8	245	4	BI011319	BI011319 QV2-EN009
104	337.2	20.1	596	4	BM726313	BM726313 UI-E-EJ0-	C 177	225.8	13.4	564	7	CO602836	CO602836 DGB-24911
105	336.6	20.0	579	2	B8644523	B8644523	C 178	225.8	13.4	639	7	CV030684	CV030684 9878 Full1
106	336	20.0	336	1	AI262562	AI262562 QK42f01.x	C 179	225	13.4	660	7	CR543517	CR543517 DKF2p459N
107	333	19.8	2467	3	AK044845	AK044845 Mus muscu	C 180	221.8	13.2	415	5	BY263876	BY263876
108	330.2	19.7	478	7	H05429	H05429 Y180R09.r1	C 181	220	13.1	444	1	AA682970	AA682970 ae89a04.s
109	325	19.4	329	7	F06205	F06205 HSC10F041.n	C 182	218	13.0	229	1	AA450172	AA450172 zx43d09.r
110	323.4	19.3	478	5	BY245406	BY245406	C 183	216	12.9	563	5	BQ637244	BQ637244 he07e09.y
111	323.2	19.2	859	6	CD325278	CD325278	C 184	215.4	12.8	697	5	BQ021243	BQ021243 UI-H-DH1-
112	322	19.2	772	7	CK776016	CK776016 967158 MA	C 185	213.8	12.7	640	7	CR545244	CR545244 DKF2p459F
113	320	19.1	896	5	BQ890272	BQ890272 AGENCOURT	C 186	213	12.7	672	6	CA444805	CA444805 UI-H-DH1-
114	310.2	18.5	602	2	B8611718	B8611718	C 187	212.4	12.7	867	6	CD300857	CD300857 AGENCOURT
115	310	18.5	2798	3	AK028345	AK028345 Mus muscu	C 188	211.2	12.6	456	5	BY249027	BY249027
116	306	18.2	780	7	CK313831	CK313831 SB0203882	C 189	210.6	12.5	656	7	CK619540	CK619540 mk25d06.y
117	305.8	18.2	445	5	BY269882	BY269882	C 190	209	12.4	257	2	AW327110	AW327110 20640 MAR
118	302.4	18.0	513	5	BX279850	BX279850	C 191	208.4	12.4	678	5	BU624639	BU624639 UI-H-FGI-
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120	302.2	18.0	759	7	CN094277	CN094277 EC2BBA9CA	C 193	207.6	12.4	226	2	AW374585	AW374585 MRI-CT005
121	301.4	18.0	643	5	BU3090882	BU3090882 603807132	C 194	204.2	12.2	726	5	CK843444	CK843444 UI-R-BJ2-
122	299.2	17.8	704	7	CN228803	CN228803 RJB061B04	C 195	204.2	12.2	636	5	EX912600	EX912600 BX912600
123	297.4	17.7	764	4	BI752729	BI752729 603028343	C 196	204	12.2	357	5	BY303236	BY303236
124	292.4	17.4	764	5	BM945665	BM945665 UI-M-EM0-	C 197	203.6	12.1	656	6	CA307492	CA307492 UI-H-FTL-
125	291.6	17.4	415	7	R18841	R18841 Y922906.r1	C 198	203.4	12.1	625	2	BB643056	BB643056
126	290.4	17.3	778	7	CN078143	CN078143 EC2BBA14C	C 199	203.4	12.1	771	7	CN528825	CN528825 UI-M-HQ0-
127	290.2	17.3	457	5	BY249728	BY249728	C 200	202.6	12.1	1084	6	CD255729	CD255729 AGENCOURT
128	290	17.2	567	7	F05894	F05894 HSC0PH101.n	C 201	202.2	12.0	538	7	CK842319	CK842319 UI-R-AD0-
129	288.8	17.2	590	2	BF078551	BF078551 228917 MA	C 202	200.2	11.9	719	7	CK465166	CK465166 936244 MA
130	287.6	17.1	481	5	BY256150	BY256150	C 203	200	11.9	786	7	CO811192	CO811192 AGENCOURT
131	286.2	17.0	497	2	B8854833	B8854833	C 204	200	11.9	858	7	CO914076	CO914076 AGENCOURT
132	284.8	17.0	684	5	B0625289	B0625289 UI-H-FGI-	C 205	199.8	11.9	468	2	BF110673	BF110673
133	284.2	16.9	578	2	B8856778	B8856778	C 206	198.6	11.8	663	2	BB633037	BB633037
134	280	16.7	627	5	BQ444788	BQ444788 UI-M-ER0-	C 207	198	11.8	519	7	CV038761	CV038761 4136000 B
135	279.8	16.7	590	7	CD217649	CD217649 p9r1n.pk0	C 208	198	11.8	525	4	BG373976	BG373976 UI-R-CV1-
136	277.6	16.5	577	6	CR545391	CR545391 DKF2p459M	C 209	197.6	11.8	537	2	BB770360	BB770360
137	276.2	16.5	297	1	AA037351	AA037351 zc03b06.s	C 210	195.6	11.6	347	7	CN094278	CN094278 EC2BBA9CA
138	272.6	16.3	815	5	BU230452	BU230452 603320607	C 211	194.4	11.6	670	7	CN083622	CN083622 EC2BBA22D
139	272.6	16.2	827	6	CA306798	CA306798 UI-H-FTL-	C 212	194.4	11.6	708	7	CN083621	CN083621
140	271.8	16.2	2096	3	AK035218	AK035218 Mus muscu	C 213	193	11.5	559	5	BY476545	BY476545
141	270.2	16.1	1953	3	AK030503	AK030503 Mus muscu	C 214	192.8	11.5	825	5	BP166655	BP166655
142	267.6	15.9	858	6	CD325821	CD325821 AGENCOURT	C 215	192	11.4	659	2	AW149545	AW149545 xf39c10.x
143	267.2	15.9	284	7	CR543721	CR543721 DKF2p459H	C 216	191.4	11.4	294	7	W15256	W15256 zc16h07.s1
144	264.8	15.8	695	7	CN28731	CN28731 RJB060E12	C 217	189.4	11.3	764	6	CA350929	CA350929 621861 NC
145	263.6	15.7	683	2	B8318882	B8318882	C 218	188	11.2	611	6	CA355517	CA355517 627428 NC
146	263.6	15.7	2534	3	AK039193	AK039193 Mus muscu	C 219	187.6	11.2	593	7	CK845949	CK845949 968393 MA
147	263	15.7	2330	3	BC080168	BC080168 Xenopus l	C 220	186.8	11.1	565	2	BB663866	BB663866 147903 MA
148	256.8	15.3	754	7	CO043662	CO043662 UI-M-ER0-	C 221	186.8	11.1	880	6	CD303536	CD303536 AGENCOURT
149	256	15.2	257	7	Z39203	Z39203 HSC13G042.n	C 222	186.6	11.1	509	2	BB771080	BB771080
150	255.2	15.2	587	7	CN088583	CN088583 EC2BBA30B	C 223	186.2	11.1	572	6	CB265380	CB265380 1004285 H
151	253	15.1	410	5	BY276506	BY276506	C 224	186	11.1	640	7	CO351229	CO351229 RAOV.FL
152	247	14.7	796	7	CO399311	CO399311 AGENCOURT	C 225	186	11.1	753	1	AI589824	AI589824 tm74909.x
153	246.8	14.7	442	5	BX112198	BX112198	C 226	185.2	11.0	906	5	BU186468	BU186468 AGENCOURT
154	246.8	14.7	523	2	BE550993	BE550993 7b67a03.x	C 227	184.4	11.0	392	2	BE651010	BE651010 UI-M-BH3-
155	246.4	14.7	849	6	CA472810	CA472810 AGENCOURT	C 228	183	10.9	835	5	EX881962	EX881962
156	243.8	14.5	652	7	CN078144	CN078144 EC2BBA14C	C 229	182.8	10.9	527	5	BY243052	BY243052
157	241.8	14.4	653	7	CF180026	CF180026 815076 MA	C 230	181	10.8	755	5	EX913106	EX913106
158	241.6	14.4	434	1	AI360870	AI360870 qy01b10.x	C 231	180.6	10.8	647	7	CV030870	CV030870 10123 Full1
159	240.6	14.3	621	5	BX312928	BX312928	C 232	179.8	10.7	220	7	H16176	H16176 Ym21909.r1
160	240.6	14.3	496	5	BP201259	BP201259	C 233	179.2	10.7	578	2	BE121132	BE121132 UI-R-CA0-
161	240.6	14.3	926	6	CD325412	CD325412 AGENCOURT	C 234	179.2	10.7	836	4	BI733097	BI733097 603554684
162	240.2	14.3	456	6	CD0803885	CD0803885 UI-M-GV0-	C 235	178	10.6	178	6	CB118055	CB118055 K-EST0164
163	239.8	14.3	502	1	AI796834	AI796834 we22h06.x	C 236	178	10.6	909	5	BU132565	BU132565 603120307
164	239	14.2	511	5	BX493152	BX493152 DKF2p781G	C 237	176.4	10.5	448	4	BG375509	BG375509 UI-R-CV1-
165	238.8	14.2	611	7	CN075612	CN075612 EC2BBA10C	C 238	176.4	10.5	496	2	BF232086	BF232086 UI-R-C2p-
166	238	14.2	282	7	R75391	R75391 M0B0556R.MO	C 239	176	10.5	666	5	BM951674	BM951674 UI-M-EG0-
167	235.6	14.0	788	4	BI767217	BI767217 603057906	C 240	175.6	10.5	2296	3	CR592222	CR592222 Full1-len9
168	235.4	14.0	492	2	AW967001	AW967001 EST379075	C 241	175.2	10.4	795	1	AU080106	AU080106
169	235	14.0	674	6	CD767791	CD767791 AGENCOURT	C 242	174.6	10.4	867	7	CO543917	CO543917 LyeST116
170	234.8	14.0	258	7	R42884	R42884 Y906h12.s1	C 243	174.4	10.4	572	2	BF407747	BF407747 UI-R-BJ2-

C 244	171.4	10.2	491	5	BQ174475	UI-M-DJ2-	BQ174475	UI-M-DJ2-	C 317	140.4	8.4	585	7	CO628980	DG9-3m14
245	171.4	10.2	862	7	CK397022	AGENCOURT	CK397022	AGENCOURT	318	140.4	8.4	969	6	BY718203	BY718203
246	170.8	10.2	526	2	BB692328	BB692328	BB692328	BB692328	319	140.4	8.4	1447	3	AK018085	Mus muscu
247	170.6	10.2	768	5	AX868437	AX868437	AX868437	AX868437	320	139.8	8.3	380	6	BY606458	BY606458
248	170.2	10.1	434	1	A1279142	qm18e02.x	A1279142	qm18e02.x	321	139.4	8.3	801	5	BU357013	603475462
249	169.8	10.1	584	5	BP257486	BP257486	BP257486	BP257486	322	139.4	8.3	809	2	BF304194	6018887043
C 250	169.6	10.1	637	6	CB528708	UI-H-F72-	CB528708	UI-H-F72-	323	138.4	8.2	402	5	BY289266	BY289266
251	169	10.1	378	2	BF601149	266043 MA	BF601149	266043 MA	324	138.2	8.2	914	5	AX843874	AX843874
252	169	10.1	470	5	AX954423	DKF2P781K	AX954423	DKF2P781K	325	138	8.2	775	4	BI119955	602761121
253	167.8	10.0	791	7	CK308721	SB02047A2	CK308721	SB02047A2	326	137.8	8.2	530	5	BY480409	BY480409
254	167.4	10.0	923	1	AL583491	AL583491	AL583491	AL583491	327	137.8	8.2	718	6	CB460692	720592 MA
C 255	167	9.9	617	6	BY730405	BY730405	BY730405	BY730405	328	136.4	8.1	661	6	CA452139	UI-M-F20-
C 256	166.6	9.9	458	7	CO667956	DG33-31f8	CO667956	DG33-31f8	329	136.2	8.1	304	7	CR472042	CR472042
C 257	166.6	9.9	541	5	BU735309	UI-B-DW0-	BU735309	UI-B-DW0-	330	136	8.1	496	7	CK693129	ZF101-F00
C 258	166.2	9.9	566	7	CF977262	2-84-B04-	CF977262	2-84-B04-	331	135.4	8.1	372	6	BY768835	BY768835
259	166	9.9	442	2	BB676735	BB676735	BB676735	BB676735	332	134.6	8.0	386	5	BY263646	BY263646
C 260	165.6	9.9	535	9	AY409767	Homo sapi	AY409767	Homo sapi	333	134.4	8.0	594	5	BU400899	BU400899
C 261	165.4	9.9	544	6	CA439326	UI-H-D71-	CA439326	UI-H-D71-	334	134.2	8.0	778	7	CK315507	CK315507
C 262	165.4	9.9	580	7	CN089827	EC2BBA32B	CN089827	EC2BBA32B	335	134	8.0	855	5	BP158085	BP158085
263	164.4	9.8	651	6	BY726997	BY726997	BY726997	BY726997	336	130.6	7.8	700	7	CK458398	CK458398
264	164.2	9.8	450	5	BY263302	BY263302	BY263302	BY263302	337	130.6	7.8	801	7	CK303983	CK303983
265	164	9.8	773	4	BQ208674	RST28306	BQ208674	RST28306	338	129.4	7.7	372	2	BE990143	BE990143
C 266	163.2	9.7	894	6	CB199088	AGENCOURT	CB199088	AGENCOURT	339	129	7.7	483	7	CR536826	CR536826
C 267	162.4	9.7	424	1	AI556916	UI-R-C2p-	AI556916	UI-R-C2p-	340	128.8	7.7	265	1	AI577248	AI577248
268	162.4	9.7	535	9	AY409769	Mus muscu	AY409769	Mus muscu	341	128.6	7.7	807	5	BP168056	BP168056
269	161.8	9.6	434	2	BB676742	BB676742	BB676742	BB676742	342	128.4	7.6	641	2	AM379374	AM379374
270	161.8	9.6	936	5	BQ227365	AGENCOURT	BQ227365	AGENCOURT	343	128.2	7.6	641	2	AM379374	CM2-HT024
C 271	161.6	9.6	402	1	AI072844	UI-R-Y0-1	AI072844	UI-R-Y0-1	344	127.6	7.6	421	2	BB674781	BB674781
C 272	160.8	9.6	892	5	BP462753	BP462753	BP462753	BP462753	345	126.6	7.5	825	5	BP464677	BP464677
273	160.6	9.6	268	1	AA296886	EST112550	AA296886	EST112550	346	125	7.4	645	6	CA334396	CA334396
C 274	160.4	9.6	529	2	BB680624	BB680624	BB680624	BB680624	347	124.4	7.4	377	7	CF977263	CF977263
C 275	159.6	9.5	494	1	AA548396	AA548396	AA548396	AA548396	348	124.2	7.4	868	5	BQ672092	BQ672092
276	158.8	9.5	481	5	BY247646	BY247646	BY247646	BY247646	349	123.8	7.4	617	4	BU381982	BU381982
277	157.4	9.4	169	7	T06151	EST04040 Fe	T06151	EST04040 Fe	350	123.4	7.3	562	5	BU381982	603582664
278	157.2	9.4	858	2	BP676478	602086277	BP676478	602086277	351	123	7.3	463	1	AI341423	AI341423
279	157	9.4	426	2	BB677725	BB677725	BB677725	BB677725	352	121.4	7.2	312	2	BI37307	BI37307
280	156.4	9.3	739	7	CK679857	ZF101-F00	CK679857	ZF101-F00	353	121.4	7.2	441	2	BE504685	BE504685
281	156.4	9.3	884	5	BU323269	603405983	BU323269	603405983	354	121.4	7.2	711	5	CO669353	DG33-50D1
282	156.2	9.3	464	2	BB311856	BB311856	BB311856	BB311856	355	120	7.1	504	5	EX281785	EX281785
283	155.8	9.3	815	1	AU079716	AU079716	AU079716	AU079716	356	120	7.1	729	2	BB585976	BB585976
284	155.6	9.3	533	2	BB767692	BB767692	BB767692	BB767692	357	119.4	7.1	613	7	CF892168	CF892168
C 285	155.2	9.2	431	5	BY276402	BY276402	BY276402	BY276402	358	119.4	7.1	863	6	CA475514	CA475514
C 286	154.6	9.2	733	7	CO619752	DG9-1D13	CO619752	DG9-1D13	359	119	7.1	801	5	EX852740	EX852740
C 287	153	9.1	520	7	CK618674	mk15a07.Y	CK618674	mk15a07.Y	360	118.8	7.1	508	2	BE703900	BE703900
C 288	152.8	9.1	436	2	BE991815	UI-M-B21-	BE991815	UI-M-B21-	361	118.4	7.1	278	2	BI393864	BI393864
C 289	151.6	9.0	364	1	AI940007	QVO-CT001	AI940007	QVO-CT001	362	117	7.0	552	4	BI337752	BI337752
290	151	9.0	411	5	BY288341	BY288341	BY288341	BY288341	363	116.6	6.9	422	1	AI288864	AI288864
C 291	150.8	9.0	254	7	CR774354	DKF2p459P	CR774354	DKF2p459P	364	116.6	6.9	461	2	BF463934	BF463934
C 292	149.2	8.9	465	1	AI934791	wp89e04.x	AI934791	wp89e04.x	365	115.6	6.9	308	2	BI187802	BI187802
293	149.2	8.9	497	7	CV036959	4134532 B	CV036959	4134532 B	366	115.6	6.9	790	5	BP141505	BP141505
294	149	8.9	547	6	BY727136	BY727136	BY727136	BY727136	367	115.4	6.9	336	5	BY134531	BY134531
295	149	8.9	854	3	AK020998	Mus muscu	AK020998	Mus muscu	368	115	6.8	368	2	BF350775	BF350775
296	148.8	8.9	412	2	BB668189	BB668189	BB668189	BB668189	369	113.8	6.8	281	2	BE985090	BE985090
297	147.4	8.8	429	5	BY272572	BY272572	BY272572	BY272572	370	113.8	6.8	579	7	CN089828	CN089828
298	146.4	8.7	600	6	CA562928	8023-83 M	CA562928	8023-83 M	371	113.6	6.8	514	1	AI285235	AI285235
299	146.2	8.7	862	5	BP462754	BP462754	BP462754	BP462754	372	112.8	6.7	665	9	EX243020	EX243020
300	146	8.7	411	5	BY276562	BY276562	BY276562	BY276562	373	112.4	6.7	528	2	AW490008	AW490008
301	145.8	8.7	409	6	BY607794	BY607794	BY607794	BY607794	374	112.4	6.7	582	7	CO626674	CO626674
302	145.4	8.7	386	6	CB806970	AMGNNUC-N	CB806970	AMGNNUC-N	375	112	6.7	316	1	AI188493	AI188493
303	145	8.6	703	5	BY278505	BY278505	BY278505	BY278505	376	111.2	6.6	446	7	CO352257	CO352257
304	144.8	8.6	418	7	CF530869	UI-N-GH0-	CF530869	UI-N-GH0-	377	110.8	6.6	994	6	CD325921	CD325921
C 305	144.6	8.6	519	1	AA826266	od3e04.s	AA826266	od3e04.s	378	110.6	6.6	293	2	BB187368	BB187368
306	144.6	8.6	703	5	BU117309	603138889	BU117309	603138889	379	110.6	6.6	422	4	BI390270	BI390270
C 307	144	8.6	511	1	AI415689	mc70a03.x	AI415689	mc70a03.x	380	110.4	6.6	382	9	AY400235	AY400235
308	144	8.6	953	5	BU116264	603139651	BU116264	603139651	381	110.4	6.6	417	6	CA884109	CA884109
309	143.4	8.5	878	5	BP165624	BP165624	BP165624	BP165624	382	110.4	6.6	782	8	AZ731274	AZ731274
C 310	142.2	8.4	535	9	AY409768	Pan trogl	AY409768	Pan trogl	383	110.2	6.6	267	7	R75390	R75390
C 311	141.8	8.4	470	1	AI580850	ta33e06.x	AI580850	ta33e06.x	384	110.2	6.6	451	1	AA933871	AA933871
C 312	141.4	8.4	397	2	AW046074	UI-M-BH1-	AW046074	UI-M-BH1-	385	109.4	6.5	525	1	AL919221	AL919221
C 313	141.4	8.4	875	4	BI734218	603351323	BI734218	603351323	386	109	6.5	283	2	BI194430	BI194430
314	141.2	8.4	437	1	AA219849	mv62c03.x	AA219849	mv62c03.x	387	109	6.5	711	5	BU363662	BU363662
315	141.2	8.4	853	5	BP164129	BP164129	BP164129	BP164129	388	108.2	6.4	272	1	AV165649	AV165649
316	140.4	8.4	478	6	CA885050	B0115E08-	CA885050	B0115E08-	389	107.2	6.4	514	4	BG814603	BG814603

330	106	6.3	276	2	BB304840	BB304840	BB304840	463	80.4	4.8	529	6	CD284927	CD284927	G39161.77
331	106	6.3	705	7	CN108877	EC2CAA32D	AI108877	464	79.8	4.8	272	2	BB255894	BB255894	BB255894
C 332	105.8	6.3	598	1	AI815935	ua43g02.x	AI815935	465	79.6	4.7	221	2	BB306421	BB306421	BB306421
333	105.6	6.3	394	9	AY400233	Homo sapi	AY400233	466	79.4	4.7	583	6	CA353359	CA353359	624860 NC
334	105.6	6.3	394	9	AY400233	Pan trogl	AY400234	467	79.2	4.7	562	5	EX5952176	DKF2p781K	DKF2p781K
335	105.4	6.3	525	6	C8720159	AMGNNUC:N	CB720159	C 468	78.8	4.7	560	4	BG065676	BY2252584	BY2252584
C 336	105.2	6.3	314	7	CN075611	EC2BBA10C	CN075611	469	78.6	4.7	375	5	BY292584	BY292584	BY292584
337	105	6.3	288	7	BB262900	BB262900	BB262900	470	78.6	4.7	442	7	CN081576	EC2BBA19C	EC2BBA19C
338	104.6	6.2	651	6	C9557691	AMGNNUC:N	C9557691	471	78.6	4.7	513	3	AK080669	Mus muscu	Mus muscu
339	104.2	6.2	284	2	BB054624	BB054624	BB054624	472	78.6	4.7	522	2	BB271167	BB271167	BB271167
400	104.2	6.2	473	5	BZ261511	BZ261511	BZ261511	473	78.6	4.7	916	5	BQ672140	AGENCOURT	AGENCOURT
401	103.8	6.2	761	6	CD755145	AGENCOURT	CD755145	474	78.4	4.7	206	2	BB589469	BB589469	BB589469
402	103.4	6.2	262	1	AV030145	AV030145	AV030145	475	78.2	4.7	336	4	RG199531	RST18822	RST18822
403	103.4	6.2	279	2	BB326555	BB326555	BB326555	476	78	4.6	457	7	W39242	2c16h07.r1	2c16h07.r1
404	103.4	6.2	327	2	BB320625	BB320625	BB320625	477	78	4.6	57	5	BW337636	BW337636	BW337636
405	102.2	6.1	291	2	BB248659	BB248659	BB248659	C 478	77.6	4.6	368	7	CN086072	EC2BBA26C	EC2BBA26C
406	101.2	6.0	412	5	BY274659	BY274659	BY274659	479	77	4.6	297	6	BY724443	BY724443	BY724443
C 407	101	6.0	298	1	AA906739	ok78h08.s	AA906739	C 480	77	4.6	538	6	C76456	C76456	C76456
408	100.8	6.0	283	2	BB265542	BB265542	BB265542	C 481	76.8	4.6	467	4	BI134406	BI134406	BI134406
409	100.8	6.0	483	8	A2457316	1M0260A07	A2457316	C 482	76.8	4.6	581	8	BH269028	CH230-66P	CH230-66P
410	100.6	6.0	260	2	BP455798	UI-M-CG0P	BP455798	C 483	76.8	4.6	779	8	BH292378	CH230-44D	CH230-44D
411	100.6	6.0	260	2	AA491830	UI-M-BH3-	AA491830	C 484	76.8	4.6	1127	9	GGA200118	GGA200118	GGA200118
C 412	100.2	6.0	359	2	BE156390	QV0-HT036	BE156390	485	76.6	4.6	281	1	AV227016	AV227016	AV227016
C 413	100	6.0	402	2	AW522667	UI-R-B00-	AW522667	486	76.6	4.6	492	4	BI359722	BI359722	BI359722
414	99.4	5.9	292	2	BB375591	BB375591	BB375591	C 487	76.2	4.5	960	5	BQ933325	AGENCOURT	AGENCOURT
415	99.2	5.9	489	6	CB726015	AMGNNUC:N	CB726015	C 488	75.6	4.5	433	1	AL921475	AL921475	AL921475
C 416	98.6	5.9	207	2	BP469799	UI-M-BH3-	BP469799	C 489	75.2	4.5	652	8	BH269030	CH230-66P	CH230-66P
417	98.6	5.9	694	7	CK699353	ZF101-P00	CK699353	C 490	74.4	4.4	202	2	BB380085	BB380085	BB380085
418	98.4	5.9	392	5	BY267956	BY267956	BY267956	C 491	74.2	4.4	526	7	CO634943	DG9-96h24	DG9-96h24
419	97.2	5.8	421	5	BY275639	BY275639	BY275639	492	73.2	4.4	284	3	AK020745	Mus muscu	Mus muscu
420	96.1	5.7	656	2	BB617916	BB617916	BB617916	493	73.2	4.4	293	2	BB284230	BB284230	BB284230
421	95.8	5.7	763	1	A1427225	mc70a03.y	A1427225	494	72.8	4.3	687	5	BP461989	BP461989	BP461989
422	95.6	5.7	385	5	BY275013	BY275013	BY275013	495	72.8	4.3	893	9	CNS02MVY	Tetraodon	Tetraodon
423	94.8	5.6	240	2	BB047231	BB047231	BB047231	496	72.6	4.3	339	2	BE826667	QV1-EN004	QV1-EN004
424	94.4	5.6	646	4	B1393264	p9pin.pk0	B1393264	497	72.6	4.3	816	5	BO385923	603858616	603858616
C 425	94.2	5.6	354	2	BE826697	QV1-EN004	BE826697	C 498	72.4	4.3	378	8	AZ089779	RPCI-23-2	RPCI-23-2
426	94.2	5.6	740	7	CO884202	CO884202	CO884202	C 499	72	4.3	334	1	AI422503	tfl1e04.x	tfl1e04.x
427	93.6	5.6	401	5	BY266910	BY266910	BY266910	500	71.8	4.3	264	1	AV325817	AV325817	AV325817
428	93	5.5	285	2	BB053997	BB053997	BB053997	501	71.8	4.3	274	1	AV338287	AV338287	AV338287
C 429	92.8	5.5	377	2	BP358688	QV1-ET000	BP358688	502	71.8	4.3	474	2	BB682022	BB682022	BB682022
430	92.6	5.5	229	1	AV350601	AV350601	AV350601	503	71.4	4.3	196	1	AV344490	AV344490	AV344490
431	92.4	5.5	302	2	BB389565	BB389565	BB389565	504	71.4	4.3	202	1	AV031929	AV031929	AV031929
432	92	5.5	304	2	BB282896	BB282896	BB282896	505	71.4	4.3	255	2	BB563869	BB563869	BB563869
433	92	5.5	640	9	CC573801	CH240.450	CC573801	506	70.8	4.2	198	1	AV030665	AV030665	AV030665
434	91.4	5.4	374	5	BY294857	BY294857	BY294857	507	70.8	4.2	216	1	AV341533	AV341533	AV341533
C 435	91.4	5.4	452	1	A1262821	QK35h10.x	A1262821	508	70.6	4.2	199	2	BB127593	BB127593	BB127593
436	91	5.4	318	2	BB321476	BB321476	BB321476	509	70.2	4.2	214	1	AV345671	AV345671	AV345671
437	91	5.4	656	2	BB645027	BB645027	BB645027	510	69.6	4.1	742	7	CO395507	AGENCOURT	AGENCOURT
C 438	90.4	5.4	233	2	AW047822	UI-M-BH1-	AW047822	511	69.4	4.1	261	2	BB278160	BB278160	BB278160
439	90.2	5.4	267	2	BB480567	BB480567	BB480567	512	69	4.1	191	2	BB301025	BB301025	BB301025
440	90	5.4	194	4	BI337742	361263.MA	BI337742	513	68.6	4.1	581	7	CO879831	BovGen.08	BovGen.08
C 441	90	5.4	317	2	BP056760	7K08C03.x	BP056760	514	68.4	4.1	221	2	BB048644	BB048644	BB048644
442	88.6	5.3	700	2	BB652926	BB652926	BB652926	515	68.4	4.1	292	2	BB198259	BB198259	BB198259
C 443	88.4	5.3	733	9	BB190380	Danio rer	BB190380	516	68.2	4.1	313	2	AW430704	AW430704	AW430704
444	88.2	5.3	374	2	BB826640	QV1-EN004	BB826640	517	68	4.0	223	2	BB380518	BB380518	BB380518
445	86	5.1	304	2	BB265140	BB265140	BB265140	C 518	67.6	4.0	514	7	CK769283	956841.MA	956841.MA
446	85.8	5.1	285	7	CN209637	4115576.B	CN209637	519	67.2	4.0	821	5	BU389844	603511165	603511165
C 447	85.6	5.1	332	2	BB826737	QV1-EN004	BB826737	520	67	4.0	417	1	AV588904	AV588904	AV588904
448	84.8	5.1	625	6	BY729404	BY729404	BY729404	521	66	3.9	226	2	BB048138	BB048138	BB048138
449	84.6	5.0	326	2	BB641806	BB641806	BB641806	522	66	3.9	433	4	BG515406	dae04h10.	dae04h10.
450	84.4	5.0	320	2	BB312195	BB312195	BB312195	523	65.8	3.9	296	2	BB193169	BB193169	BB193169
C 451	84.4	5.0	479	2	AW524531	UI-R-B00-	AW524531	524	65.8	3.9	726	5	BU395513	BU395513	BU395513
452	84	5.0	657	2	BB618284	BB618284	BB618284	525	65.6	3.9	502	4	BG078950	H3033H12-	H3033H12-
C 453	84	5.0	723	9	AG035406	Pan trogl	AG035406	526	65	3.9	259	2	BB607028	BB607028	BB607028
454	83.8	5.0	2594	3	AK047122	Mus muscu	AK047122	C 527	64.8	3.9	702	9	CNS02PTU	AL208443	Tetraodon
455	83.4	5.0	550	2	BE012499	121990.MA	BE012499	C 528	64.4	3.8	527	1	AA741334	OB30f08.s	OB30f08.s
456	83.2	5.0	233	1	AV335954	AV335954	AV335954	529	64.4	3.8	558	7	CK875240	CK875240	CK875240
457	82.8	4.9	262	2	BB078578	BB078578	BB078578	530	63.8	3.8	217	2	BB197705	BB197705	BB197705
458	82.4	4.9	728	7	CN530285	UI-M-H00-	CN530285	531	62.6	3.7	226	1	AA776056	ae79a07.s	ae79a07.s
459	82	4.9	272	2	BB596160	BB596160	BB596160	C 532	62.6	3.7	539	1	AL918370	AL918370	AL918370
460	81.8	4.9	392	2	AW291014	UI-H-B12-	AW291014	533	61.8	3.7	201	1	AV227064	AV227064	AV227064
461	81.6	4.9	586	4	BM696801	UI-E-DW0-	BM696801	C 534	61.8	3.7	247	7	CR474371	CR474371	CR474371
C 462	80.6	4.8	1463	8	CC288776	CH261-170	CC288776	535	61.8	3.7	550	7	CR544460	DKF2p459F	DKF2p459F

536	61	3.6	200	1	AV028623	AV028623	AV028623	609	54.2	3.2	806	4	BI762516	BI762516	603048638
537	60.8	3.6	189	1	AV029446	AV029446	AV029446	610	54.2	3.2	859	6	CB319037	CB319037	AGENCOURT
538	60.8	3.6	255	1	BB577810	BB577810	BB577810	C 611	54	3.2	212	4	BG981747	BG981747	MR3-CN014
539	60.4	3.6	222	2	BB053503	BB053503	BB053503	C 612	54	3.2	241	4	BG980534	BG980534	MR3-CN014
540	60.4	3.6	484	5	BX093260	BX093260	BX093260	613	54	3.2	365	6	CB573833	CB573833	AGENCOURT
541	60.2	3.6	1008	9	CL093894	CL093894	ISB1-24C2	614	54	3.2	774	1	AJ786997	AJ786997	AJ786997
542	60	3.6	702	4	BG695650	NISC-1V20		615	54	3.2	1176	5	BM927266	BM927266	AGENCOURT
543	59.6	3.5	420	6	CB798880	AMGNOC:N		C 616	53.8	3.2	244	2	BF362751	BF362751	RC1-NN007
544	59.6	3.5	845	4	BN042630	603615963		617	53.8	3.2	276	7	CO181006	CO181006	EC13331.5
C 545	59	3.5	303	1	A1422504	tf11e05.x		618	53.8	3.2	276	7	CO195427	CO195427	EC40320.5
546	58.6	3.5	276	2	BZ268580	BZ268580		619	53.8	3.2	286	7	CO182679	CO182679	EC23645.5
C 547	58.6	3.5	426	7	CK767772	968132 MA		620	53.8	3.2	303	7	CO181557	CO181557	EC14539.5
C 548	58.6	3.5	736	8	AE298621	2M0273104		621	53.8	3.2	350	7	CO181915	CO181915	EC32401.5
C 549	58.4	3.5	242	4	BG980478	MR3-CN014		622	53.8	3.2	361	5	BUS89906	BUS89906	AGENCOURT
C 550	58.4	3.5	565	7	CO590783	DG3-41K22		623	53.8	3.2	382	7	CO181851	CO181851	EC15101.5
551	58.2	3.5	369	7	CO182357	EC22490.5		624	53.8	3.2	385	7	CO180258	CO180258	EC01313.5
552	58.2	3.5	376	7	CO181363	EC14144.5		625	53.8	3.2	395	7	CO182619	CO182619	EC23422.5
553	58.2	3.5	421	7	CO181992	EC18396.5		626	53.8	3.2	398	7	CO193679	CO193679	EC36616.5
554	58.2	3.5	504	7	CO193442	EC35796.5		627	53.8	3.2	450	7	CO194401	CO194401	EC38508.5
555	58.2	3.5	531	7	CO193920	EC36996.5		628	53.8	3.2	452	7	CO193143	CO193143	EC3202.5
556	57.8	3.4	831	9	CNS011FZ	AL100217 Drosophil		629	53.8	3.2	464	7	CO183541	CO183541	EC25934.5
557	57.4	3.4	559	7	CF123525	UI-HF-CHO		630	53.8	3.2	487	7	CO195262	CO195262	EC39947.5
C 558	57	3.4	643	8	AQ327238	nbxb0040J		631	53.8	3.2	490	7	CO180558	CO180558	EC02047.5
559	57	3.4	841	5	BUS30009	AGENCOURT		632	53.8	3.2	523	7	CO183076	CO183076	EC24521.5
560	56.8	3.4	569	5	BP377634	BP377634		633	53.8	3.2	524	7	CO182642	CO182642	EC23489.5
561	56.8	3.4	574	5	BP321522	BP321522		634	53.8	3.2	547	7	CO185170	CO185170	EC29789.5
562	56.8	3.4	582	5	BP208357	BP208357		635	53.8	3.2	552	7	CO194609	CO194609	EC38890.5
563	56.6	3.4	324	7	CO192533	EC33980.5		C 636	53.8	3.2	569	8	AQ394216	AQ394216	CITBI-EI-
C 564	56.6	3.4	502	7	CO691139	DG11-10F1		637	53.8	3.2	582	4	BG219746	BG219746	RST39511
565	56.6	3.4	574	7	CO184164	EC27256.5		638	53.8	3.2	759	9	CNS06QXV	AL411257 T7 end of	
C 566	56.6	3.4	964	9	CNS05CLJ	ALJ31264 Tetraodon		639	53.8	3.2	880	6	CD522648	CD522648	AGENCOURT
567	56.4	3.4	1389	4	BF1911314	603062429		640	53.8	3.2	913	7	CK157193	CK157193	FGA503828
568	56.2	3.3	481	7	CO180995	EC13317.5		641	53.8	3.2	1511	3	BB432888	BB432888	Mus muscu
569	56.2	3.3	1019	5	BO723771	AGENCOURT		642	53.6	3.2	271	2	BB432888	BB432888	Mus muscu
570	56.2	3.3	1119	6	CD050433	AGENCOURT		643	53.6	3.2	532	6	CA354283	CA354283	625969 NC
571	56	3.3	497	7	CO180052	EC00836.5		644	53.6	3.2	551	1	AL036240	AL036240	DKF2P564J
572	56	3.3	710	7	CO961229	pe19c10.Y		645	53.6	3.2	692	7	CK654124	CK654124	AGENCOURT
573	56	3.3	771	5	BUS56340	AGENCOURT		C 646	53.6	3.2	754	9	AG483752	AG483752	Mus muscu
C 574	56	3.3	1472	9	CL490510	SAIL 539		647	53.6	3.2	772	5	BUS37238	BUS37238	AGENCOURT
C 575	55.8	3.3	929	9	CNS050XX	AG320971 Mus muscu		648	53.6	3.2	778	4	BI859188	BI859188	603385268
C 576	55.8	3.3	1376	9	AG320971	AG320971 Tetraodon		C 649	53.6	3.2	893	7	CK196964	CK196964	FGA500543
577	55.4	3.3	861	7	CK017071	CK017071 AGENCOURT		650	53.6	3.2	949	6	CD387866	CD387866	AGENCOURT
578	55.4	3.3	311	4	BG193769	BG193769 RST12905		651	53.4	3.2	226	6	CD765502	CD765502	EST000188
579	55.4	3.3	555	7	CO878692	BovGen .07		652	53.4	3.2	230	4	BF968205	BF968205	602268946
C 580	55.4	3.3	626	8	AZ385580	1M0144G07		653	53.4	3.2	363	2	BF076420	BF076420	225985 MA
581	55.4	3.3	835	5	BUS54638	AGENCOURT		654	53.4	3.2	422	7	CV525233	CV525233	Md1V4010h
582	55.2	3.3	285	6	CB986322	AGENCOURT		655	53.4	3.2	582	5	BP283085	BP283085	BP283085
583	55.2	3.3	518	7	CN974991	24676.125		656	53.4	3.2	584	5	BP327099	BP327099	BP327099
584	55.2	3.3	991	4	BG433647	602506930		657	53.4	3.2	584	5	BP327111	BP327111	BP327111
585	55.2	3.3	1175	6	CD504945	CD504945 CDA70-H09		658	53.4	3.2	661	7	CF358754	CF358754	CF358754
586	55	3.3	230	7	CO885649	BovGen.13		659	53.4	3.2	698	1	AV682763	AV682763	AV682763
587	55	3.3	647	9	AG044222	Pan trogl		660	53.4	3.2	816	5	BUS43005	BUS43005	AGENCOURT
588	55	3.3	1043	6	CD385012	CD385012 AGENCOURT		661	53.4	3.2	880	7	CN835143	CN835143	AGENCOURT
589	55	3.3	1123	5	BUS02918	BUS02918 AGENCOURT		662	53.4	3.2	884	5	BUS63135	BUS63135	AGENCOURT
590	54.8	3.3	262	6	CF3337385	laa33a05.		C 663	53.4	3.2	885	9	AG566030	AG566030	Mus muscu
591	54.8	3.3	400	7	CF578533	CF578533 AGENCOURT		664	53.4	3.2	935	5	BUS60555	BUS60555	AGENCOURT
592	54.8	3.3	684	7	CV274449	WS0173.B2		665	53.4	3.2	1101	9	CNS00HAY	AL073252 Drosophil	
C 593	54.6	3.3	204	4	BG980696	MR3-CN014		666	53.2	3.2	195	7	CF546382	CF546382	lae7e03.
594	54.6	3.3	246	1	AL040243	DKF2P434I		667	53.2	3.2	422	2	AW778899	AW778899	ho16e08.x
595	54.6	3.3	348	6	CB829769	r104h12.Y		C 668	53.2	3.2	560	6	CB333987	CB333987	CA23E103I
596	54.6	3.3	390	1	AA490022	ab02b04.B		669	53.2	3.2	609	6	CA367906	CA367906	934211 MA
597	54.6	3.3	434	6	CB1399771	EL01N0325		670	53.2	3.2	693	7	CK463316	CK463316	Tetraodon
598	54.6	3.3	478	6	CB179629	EST0729.Z		671	53.2	3.2	712	9	CNS04AL2	CF150373 AGENCOURT	
599	54.6	3.3	842	7	CK128791	CK128791 AGENCOURT		672	53.2	3.2	808	7	CF150373	CF150373	AGENCOURT
600	54.6	3.3	844	9	CNS0052P	AL056652 Drosophil		673	53.2	3.2	818	5	BUS64240	BUS64240	AGENCOURT
601	54.6	3.3	847	7	CK400611	CK400611 AGENCOURT		674	53.2	3.2	864	5	CKJ95877	CKJ95877	AGENCOURT
602	54.6	3.3	1049	4	BG623609	602648818		675	53.2	3.2	869	5	BUS938204	BUS938204	AGENCOURT
603	54.6	3.3	1056	4	BG032994	602300394		676	53.2	3.2	871	5	BUS40167	BUS40167	AGENCOURT
604	54.4	3.2	625	7	CF921039	gmr-hrw3-		677	53.2	3.2	895	5	BUS588665	BUS588665	AGENCOURT
605	54.4	3.2	637	7	CO541834	gm.K005.2		678	53.2	3.2	906	5	BUS31084	BUS31084	AGENCOURT
606	54.2	3.2	573	7	CF977921	PAR17GI.R		C 679	53.2	3.2	1101	9	CNS00KFT	AL077924 Drosophil	
607	54.2	3.2	736	9	CNS03WTW	AL264172 Tetraodon		680	53.2	3.2	1379	6	BM548276	BM548276	AGENCOURT
608	54.2	3.2	749	5	BUS34260	BUS34260 AGENCOURT		681	53	3.2	286	6	CD773252	CD773252	AGENCOURT

682	53	3.2	296	6	CB076532	CB076532 hf44g04.g	755	52.4	3.1	1298	5	BQ277164	BQ277164 AGENCOURT
683	53	3.2	335	7	CF381770	CF381770 lab84b07.	c 756	52.4	3.1	1357	9	CL080800	CL080800 CH216-159
c 684	53	3.2	432	1	AV665533	AV665533 AV665533	c 757	52.4	3.1	1381	9	AG350187	AG350187 Mus muscu
685	53	3.2	659	9	AG083939	AG083939 Pan trogl	758	52.4	3.1	1699	3	HSR01509	HSR01509 Homo sapi
686	53	3.2	837	9	CNS011F1	AL100200 Drocephil	759	52.4	3.1	1775	9	CL513862	CL513862 SAIL 880
687	53	3.2	864	7	CN177352	CN177352 AGENCOURT	c 760	52.4	3.1	1924	4	CL524436	CL524436 603051712
688	53	3.2	938	5	BU960786	BU960786 AGENCOURT	c 761	52.2	3.1	207	7	CF890463	CF890463 TcTR-1266
689	53	3.2	941	7	CK420653	CK420653 AUF Iptrk	c 762	52.2	3.1	211	211	AG891484	AG891484 MR3-CN014
c 690	53	3.2	999	5	BU423248	BU423248	763	52.2	3.1	214	6	CA689180	CA689180 wlm96.pko
c 691	53	3.2	1015	9	CL135318	CL135318 ISB1-106P	764	52.2	3.1	231	4	BM529684	BM529684 fyl14h03.y
c 692	53	3.2	1293	9	AG346949	AG346949 Mus muscu	765	52.2	3.1	234	7	CO193387	CO193387 EC35693.5
693	52.8	3.1	196	5	BQ786696	BQ786696 saq72a12.	766	52.2	3.1	276	7	CK379421	CK379421 lailid07.
694	52.8	3.1	234	1	AV349585	AV349585 AV349585	767	52.2	3.1	289	5	BU764209	BU764209 saes4a02.
695	52.8	3.1	250	7	CO191457	CO191457 CK30893.5	768	52.2	3.1	290	5	BQ640732	BQ640732 he32e05.y
696	52.8	3.1	279	7	CR559257	CR559257 DKZPd468M	769	52.2	3.1	301	7	CF622338	CF622338 laf02f12.
697	52.8	3.1	295	7	CF630157	CF630157 DKZPd469M	770	52.2	3.1	308	7	CK375298	CK375298 lai48a03.
c 698	52.8	3.1	302	2	BF362739	BF362739 RC1-NN007	771	52.2	3.1	352	7	CO181785	CO181785 EC14973.5
699	52.8	3.1	315	7	CF804740	CF804740 lad78h10.	c 772	52.2	3.1	381	9	CNS03001	AL252370 Tetraodon
c 700	52.8	3.1	317	7	CNS37157	CNS37157 UI-M-HS0-	773	52.2	3.1	387	8	AZ878524	AZ878524 RPC1-23-1
701	52.8	3.1	323	7	CK379820	CK379820 lai59a11.	774	52.2	3.1	400	7	CK384950	CK384950 lah56e09.
702	52.8	3.1	399	4	BG113662	BG113662 602284164	775	52.2	3.1	405	7	CF968846	CF968846 lag73f11.
703	52.8	3.1	650	6	CD773004	CD773004 AGENCOURT	776	52.2	3.1	428	1	AV681953	AV681953 AV681953
704	52.8	3.1	720	7	CV066275	CV066275 WNELJ32B4	777	52.2	3.1	431	6	CB524077	CB524077 UI-N-GK0-
705	52.8	3.1	813	5	BU850671	BU850671 AGENCOURT	778	52.2	3.1	445	7	CK632450	CK632450 AML-AP000
706	52.8	3.1	840	5	BM985947	BM985947 7_C05_T3	779	52.2	3.1	466	7	CK421958	CK421958 AUF_IpSpn
707	52.8	3.1	849	9	AG044091	AG044091 Pan trogl	780	52.2	3.1	473	4	BG622466	BG622466 602647179
708	52.8	3.1	862	6	CA463085	CA463085 AGENCOURT	781	52.2	3.1	548	7	CK983417	CK983417 re24g03.y
709	52.8	3.1	866	5	BU587173	BU587173 AGENCOURT	782	52.2	3.1	573	7	CV223060	CV223060 ta156f08.y
710	52.8	3.1	914	5	BU563375	BU563375 AGENCOURT	783	52.2	3.1	584	4	BU519721	BU519721 BJ519721
711	52.8	3.1	945	5	BU851541	BU851541 AGENCOURT	784	52.2	3.1	614	6	CD251677	CD251677 AGENCOURT
712	52.8	3.1	947	6	CB205316	CB205316 AGENCOURT	785	52.2	3.1	635	4	BG107420	BG107420 602377525
713	52.8	3.1	1131	4	BM542918	BM542918 AGENCOURT	786	52.2	3.1	688	7	CV522032	CV522032 0089P0069
714	52.8	3.1	2186	3	CR749590	CR749590 Homo sapi	787	52.2	3.1	710	7	CK590804	CK590804 TTBE000144
715	52.6	3.1	274	7	CV072032	CV072032 ESF4193.Z	c 788	52.2	3.1	712	4	BJ532300	BJ532300 BJ532300
716	52.6	3.1	304	7	CN927725	CN927725 000530ABP	789	52.2	3.1	723	7	CK451264	CK451264 904423.MA
c 717	52.6	3.1	350	5	BX553079	BX553079 BX553079	790	52.2	3.1	743	1	AV757929	AV757929 F975929
718	52.6	3.1	427	6	CA778567	CA778567 MPL384_9	791	52.2	3.1	819	5	BU534439	BU534439 AGENCOURT
719	52.6	3.1	493	7	CB377070	CB377070 lah97h03_	792	52.2	3.1	846	5	BU564052	BU564052 AGENCOURT
720	52.6	3.1	504	6	CB678747	CB678747 OSJNEF01F	793	52.2	3.1	906	7	CK159239	CK159239 FGAS04064
721	52.6	3.1	560	4	BG924474	BG924474 HNC27-1-D	794	52.2	3.1	1000	4	BG572421	BG572421 602593463
722	52.6	3.1	659	6	CD771540	CD771540 AGENCOURT	795	52	3.1	169	4	BJ0703874	BJ0703874
723	52.6	3.1	731	7	CF924696	CF924696 DD005C04.	796	52	3.1	172	5	BU504780	BU504780 DKF2p686F
724	52.6	3.1	778	5	BU534338	BU534338 AGENCOURT	797	52	3.1	192	1	AA276487	AA276487 Bvc3e10.r
725	52.6	3.1	811	6	CB951950	CB951950 AGENCOURT	798	52	3.1	202	7	CO883666	CO883666 Bvg3e10.1
726	52.6	3.1	812	9	AG031898	AG031898 Pan trogl	799	52	3.1	228	7	CK381405	CK381405 lag38a01.
727	52.6	3.1	825	5	BU850748	BU850748 AGENCOURT	800	52	3.1	243	4	BM187410	BM187410 fw17d12.y
728	52.6	3.1	829	7	CK794790	CK794790 AGENCOURT	801	52	3.1	266	1	AA616347	AA616347 vnt6b12.r
729	52.6	3.1	856	5	BU934849	BU934849 AGENCOURT	802	52	3.1	403	6	CA366868	CA366868 642552.NC
730	52.6	3.1	1002	6	CB206065	CB206065 AGENCOURT	803	52	3.1	425	7	CF424254	CF424254 lad27b04.
c 731	52.6	3.1	1380	9	AG311242	AG311242 Mus muscu	c 804	52	3.1	461	6	CB348689	CB348689 CAB2SG000
732	52.6	3.1	1920	3	BC047319	BC047319 Homo sapi	805	52	3.1	478	7	CF779197	CF779197 tad24e10.
733	52.4	3.1	160	2	AW318295	AW318295 eg63d05.y	806	52	3.1	500	7	CK406831	CK406831 AUF_Iflvr
734	52.4	3.1	172	7	CF983728	CF983728 IG02 grap	c 807	52	3.1	590	9	BX240864	BX240864 DanTo_Fer
735	52.4	3.1	199	4	BJ699239	BJ699239 BJ699239	808	52	3.1	615	4	BG435835	BG435835 602508457
736	52.4	3.1	244	7	CK430436	CK430436 oj49d02.y	809	52	3.1	743	5	BU108854	BU108854 603112530
737	52.4	3.1	293	4	BM155090	BM155090 fv93d10.y	810	52	3.1	852	5	BU946451	BU946451 AGENCOURT
738	52.4	3.1	374	4	BM154585	BM154585 fv86h02.y	c 811	52	3.1	882	7	CK160127	CK160127 FGAS04167
739	52.4	3.1	432	2	AW773386	AW773386 ip06c01.y	812	52	3.1	935	6	CD384935	CD384935 AGENCOURT
740	52.4	3.1	490	7	CO874828	CO874828 Boven_03	813	52	3.1	939	7	CN310359	CN310359 170005999
741	52.4	3.1	562	2	AW636413	AW636413 b146d05.w	814	52	3.1	1016	9	CNS01609	AL107211 Drocephil
742	52.4	3.1	579	7	CF752690	CF752690 om_A001.0	815	52	3.1	1331	5	BM904910	BM904910 AGENCOURT
743	52.4	3.1	603	7	CN004672	CN004672 ip21e12.g	816	51.8	3.1	194	5	BU530627	BU530627 AGENCOURT
744	52.4	3.1	619	7	CO535894	CO535894 tah10e04.g	817	51.8	3.1	218	7	CO727269	CO727269 UMC-bend
c 745	52.4	3.1	648	8	AZ379719	AZ379719 IM0135K02	818	51.8	3.1	225	4	BG736457	BG736457 rk57d03.y
746	52.4	3.1	803	6	CB318690	CB318690 AGENCOURT	819	51.8	3.1	236	2	AW657557	AW657557 110971.MA
747	52.4	3.1	826	4	BM041903	BM041903 603615963	820	51.8	3.1	252	4	BM531343	BM531343 fx86a07.y
748	52.4	3.1	870	5	BU843763	BU843763 AGENCOURT	c 821	51.8	3.1	269	4	BG980699	BG980699 MR3-CN014
749	52.4	3.1	873	6	CB844849	CB844849 M2PN-0411	c 822	51.8	3.1	278	4	BG983803	BG983803 MR4-CN014
c 750	52.4	3.1	880	7	CK159114	CK159114 FGAS04050	823	51.8	3.1	310	4	BM154701	BM154701 fv88c10.y
751	52.4	3.1	887	5	BU850963	BU850963 AGENCOURT	824	51.8	3.1	311	4	BM154695	BM154695 fv88c02.y
752	52.4	3.1	949	9	CNS002P1	AL097968 Drocephil	825	51.8	3.1	320	4	BM574233	BM574233 fx60q11.y
753	52.4	3.1	1010	6	CD171719	CD171719 AGENCOURT	826	51.8	3.1	320	4	BU709836	BU709836 f644d03.y
754	52.4	3.1	1148	6	CD500545	CD500545 CDA45-F05	827	51.8	3.1	321	4	BM154709	BM154709 fv88d07.y

828	51.8	3.1	323	4	BM155040	BM155040 fv32905.Y	901	51.6	3.1	963	7	CF780924	CF780924 AGENCOURT
829	51.8	3.1	336	5	BM785339	BM785339 fab30h11.	c 902	51.6	3.1	968	5	BM381631	BM381631
830	51.8	3.1	340	4	BM155408	BM155408 fw04e06.Y	c 903	51.6	3.1	969	7	CK426147	CK426147 AUF IpFes
831	51.8	3.1	345	4	BM534831	BM534831 fx71h06.Y	904	51.6	3.1	1002	5	BU590111	AGENCOURT
832	51.8	3.1	351	1	AL724883	AL724883 AL724883	905	51.6	3.1	1006	5	BU530175	AGENCOURT
833	51.8	3.1	354	4	BM154696	BM154696 fv88c03.Y	906	51.6	3.1	1035	6	CD246704	AGENCOURT
834	51.8	3.1	356	4	BM155084	BM155084 fv93c11.Y	907	51.6	3.1	1093	9	CNS04C0C	Tetraodon
835	51.8	3.1	358	6	CB721263	CB721263 jnn603C06	908	51.6	3.1	1122	4	BI259611	AGENCOURT
836	51.8	3.1	439	1	AV682218	AV682218 AV682218	c 909	51.6	3.1	1333	9	AG390651	Mus muscu
837	51.8	3.1	463	1	AV682001	AV682001 AV682001	910	51.6	3.1	1426	4	BG388238	602413232
838	51.8	3.1	503	8	BM08074	BM08074 TTG24-Sp6.1	911	51.4	3.1	201	2	AW102260	sd85d10.Y
839	51.8	3.1	540	6	CA320990	CA320990 UI-M-FV0-	912	51.4	3.1	232	4	BM280863	ki6eb01.Y
840	51.8	3.1	557	9	CB135710	CB135710 t1gr-gss-	913	51.4	3.1	252	4	BM574901	fx37e09.Y
841	51.8	3.1	563	7	CF805126	CF805126 lad62f08.	914	51.4	3.1	277	6	CD722233	oj07b05.Y
842	51.8	3.1	599	8	BI6188	BI6188 347E7.TV CI	915	51.4	3.1	334	7	CO194571	EC38826.5
843	51.8	3.1	606	6	CD239409	CD239409 FNPUB12	c 916	51.4	3.1	361	1	AI819970	wj8h03.x
844	51.8	3.1	610	8	BI7639	BI7639 347E7.TVB C	917	51.4	3.1	366	7	CO722305	Mdfr30190
845	51.8	3.1	632	7	CV193140	CV193140 km36h05.Y	918	51.4	3.1	371	1	AV689111	AV689111
846	51.8	3.1	674	6	CD638408	CD638408 AGENCOURT	919	51.4	3.1	372	7	CF331850	NACL--08-
847	51.8	3.1	700	6	CD640967	CD640967 AGENCOURT	920	51.4	3.1	401	4	BG108147	602280213
848	51.8	3.1	747	9	CNS011RQ	AL100640 Drosophil	c 921	51.4	3.1	440	4	BG944106	ax46e08.x
849	51.8	3.1	748	9	AG031854	AG031854 Pan trogl	922	51.4	3.1	441	4	BM285111	kh94h02.Y
850	51.8	3.1	780	7	CN323584	CN323584 AGENCOURT	923	51.4	3.1	464	5	BQ639526	he16g12.Y
851	51.8	3.1	797	5	BU555131	BU555131 AGENCOURT	924	51.4	3.1	475	5	BQ093142	fy94c12.Y
852	51.8	3.1	804	5	BU530964	BU530964 AGENCOURT	925	51.4	3.1	476	6	CB721269	jnn603D03
853	51.8	3.1	814	5	BU566469	BU566469 AGENCOURT	926	51.4	3.1	487	5	BQ196890	NXLV106.F
854	51.8	3.1	820	6	CA464889	CA464889 AGENCOURT	927	51.4	3.1	557	6	CA779552	MPL384.12
855	51.8	3.1	872	7	CK157539	CK157539 FGAS03867	928	51.4	3.1	557	7	CF123296	UI-HF-CH0
856	51.8	3.1	877	3	BC040855	BC040855 Homo sapi	929	51.4	3.1	578	5	BP265719	BP265719
857	51.8	3.1	920	5	BU563586	BU563586 AGENCOURT	930	51.4	3.1	583	6	CB073419	taa32f07.
858	51.8	3.1	973	5	BQ721625	BQ721625 AGENCOURT	931	51.4	3.1	591	4	BI378442	BFLG1_000
859	51.8	3.1	982	4	BG288697	BG288697 602385510	932	51.4	3.1	620	6	CA321372	UI-M-FV0-
860	51.8	3.1	1084	5	BU189453	BU189453 AGENCOURT	933	51.4	3.1	624	4	BG622353	602647035
861	51.8	3.1	1126	6	CD523341	CD523341 AGENCOURT	934	51.4	3.1	702	8	AQ256508	nbbx0016M
862	51.8	3.1	1452	9	CL125503	CL125503 ISB1-87B2	c 935	51.4	3.1	720	6	CD641235	AGENCOURT
863	51.6	3.1	191	7	CK895966	CK895966 SGP158500	936	51.4	3.1	762	7	CK655134	AGENCOURT
864	51.6	3.1	216	4	BU699031	BU699031 BU699031	937	51.4	3.1	783	7	CN385817	LE2TR04J2
865	51.6	3.1	220	2	BE014996	BE014996 126931.MA	938	51.4	3.1	789	6	BU571699	AGENCOURT
866	51.6	3.1	254	4	BG981471	BG981471 MR3-CN014	939	51.4	3.1	800	5	BU843107	AGENCOURT
867	51.6	3.1	300	7	CK428349	CK428349 laj14g03.Y	940	51.4	3.1	859	7	CN839423	AGENCOURT
868	51.6	3.1	309	4	BM186118	BM186118 fv98b09.Y	941	51.4	3.1	867	5	BU843011	AGENCOURT
869	51.6	3.1	335	7	CF211902	CF211902 CGF100066	942	51.4	3.1	871	6	CB204789	AGENCOURT
870	51.6	3.1	347	4	BM130321	BM130321 pb29e10.Y	943	51.4	3.1	883	7	CK865669	AGENCOURT
871	51.6	3.1	348	7	CK379136	CK379136 la131b08.	944	51.4	3.1	935	5	BQ958308	AGENCOURT
872	51.6	3.1	375	1	AL713177	AL713177 Df2p868L	945	51.4	3.1	939	7	CN014330	AGENCOURT
873	51.6	3.1	432	7	CF373277	CF373277 JMT--07-K	946	51.4	3.1	941	6	CB195504	AGENCOURT
874	51.6	3.1	438	4	BJ679676	BJ679676 BJ679676	947	51.4	3.1	973	5	BU945046	AGENCOURT
875	51.6	3.1	484	4	BM342763	BM342763 fw47902.Y	948	51.4	3.1	975	5	BU963322	AGENCOURT
876	51.6	3.1	495	5	BM903137	BM903137 NXLV_080	949	51.4	3.1	1011	6	CD388840	AGENCOURT
877	51.6	3.1	577	4	BG927541	BG927541 HNC10-1-B	c 950	51.4	3.1	1014	5	BU565689	AGENCOURT
878	51.6	3.1	602	5	BU589676	BU589676 AGENCOURT	c 951	51.4	3.1	1074	8	BZ696936	SP_Ba009
879	51.6	3.1	604	4	BG927528	BG927528 HNC10-1-C	c 952	51.4	3.1	1101	9	CNS00ED1	AGENCOURT
880	51.6	3.1	607	1	AA522011	AA522011 vht8c09.r	953	51.4	3.1	1112	5	BM920193	AGENCOURT
881	51.6	3.1	617	4	BI829090	BI829090 603079182	954	51.4	3.1	151	7	BC032411	Homo sapi
882	51.6	3.1	627	6	CA330151	CA330151 haa92b01.	c 955	51.2	3.0	185	4	CF203260	RR890915N
883	51.6	3.1	643	3	BI870743	BI870743 603392853	c 956	51.2	3.0	185	4	BG980530	MR3-CN014
884	51.6	3.1	673	6	CD707049	CD707049 AGENCOURT	c 957	51.2	3.0	193	7	CK615915	ou07c12.Y
885	51.6	3.1	697	6	CB319237	CB319237 AGENCOURT	c 958	51.2	3.0	213	4	BM981500	MR3-CN014
886	51.6	3.1	761	5	BU555158	BU555158 AGENCOURT	c 959	51.2	3.0	201	4	BM265810	fw36b10.Y
887	51.6	3.1	771	7	CN831817	CN831817 AGENCOURT	c 960	51.2	3.0	202	4	BM983780	MR4-CN014
888	51.6	3.1	780	9	CNS04142	AL291788 Tetraodon	961	51.2	3.0	210	4	BM573150	fx98h10.Y
889	51.6	3.1	787	5	AG364646	AG364646 Mus muscu	c 962	51.2	3.0	213	4	BM155328	fw02b03.Y
890	51.6	3.1	818	9	BU850480	BU850480 AGENCOURT	c 963	51.2	3.0	217	4	BM981736	MR3-CN014
891	51.6	3.1	833	5	BU850474	BU850474 AGENCOURT	964	51.2	3.0	218	4	BM154944	fv91e06.Y
892	51.6	3.1	853	1	AV758844	AV758844 AGENCOURT	c 965	51.2	3.0	219	1	AL714277	AL714277
893	51.6	3.1	855	7	CN330709	CN330709 AGENCOURT	966	51.2	3.0	219	4	BI709326	f963b09.Y
894	51.6	3.1	866	2	BS909150	BS909150 601501758	967	51.2	3.0	219	4	BM154546	fv86d07.Y
895	51.6	3.1	856	7	CF765154	CF765154 CES002716	968	51.2	3.0	220	4	BM573836	fy04f07.Y
896	51.6	3.1	868	5	BU530888	BU530888 AGENCOURT	969	51.2	3.0	225	4	BM154392	fv84e06.Y
897	51.6	3.1	869	5	BU566247	BU566247 AGENCOURT	970	51.2	3.0	225	4	BM186096	fv97h07.Y
898	51.6	3.1	902	2	BF575271	BF575271 602133679	971	51.2	3.0	230	4	BM186042	fv96h12.Y
899	51.6	3.1	926	5	BU554921	BU554921 AGENCOURT	972	51.2	3.0	231	7	COL81733	EC14891.5
900	51.6	3.1	932	3	CR648408	CR648408 Tetraodon	973	51.2	3.0	233	5	BQ786705	saq72b12.

974	51.2	3.0	234	4	BM154438	BM154438	fv85b03.y	1047	51	3.0	231	5	5	EX646093	BX646093	DKF2p781E
975	51.2	3.0	235	7	CF317850	CF317850	HD--07-L0	1048	51	3.0	239	6	6	CD000864	CD000864	AGENCOURT
976	51.2	3.0	237	4	BF679532	BF679532		1049	51	3.0	248	7	7	CR772335	CR772335	AGENCOURT
977	51.2	3.0	247	4	BM187242	BM187242	fw13g02.y	1050	51	3.0	261	4	4	BJ469921	BJ469921	BM521967
978	51.2	3.0	248	4	BM1704970	BM1704970	fr60g09.y	1051	51	3.0	281	4	4	BM521967	BM521967	ESSU0504
979	51.2	3.0	249	4	BJ682710	BJ682710		1052	51	3.0	315	7	7	CR753138	CR753138	DKF2p468E
980	51.2	3.0	254	4	BM105355	BM105355	fr57g11.y	1053	51	3.0	334	7	7	CO195973	CO195973	EC34776.5
981	51.2	3.0	274	4	BM181089	BM181089	fv94a06.y	1054	51	3.0	349	7	7	CO194580	CO194580	EC38842.5
982	51.2	3.0	278	7	CF123167	CF123167	UI-HF-CH0	1055	51	3.0	350	3	3	BH283073	BH283073	CH230-180
983	51.2	3.0	283	6	CF933364	CF933364	xi29a06.y	1056	51	3.0	359	7	7	CN949627	CN949627	000719AVF
984	51.2	3.0	302	7	CF511461	CF511461	CAbdu0006	1057	51	3.0	368	5	5	BQ635986	BQ635986	hd02h07.y
985	51.2	3.0	304	7	CF613058	CF613058	laf32b10.	1058	51	3.0	368	6	6	CB049672	CB049672	NISC_gj12
986	51.2	3.0	312	7	CF382308	CF382308	lac61h10.	1059	51	3.0	368	6	6	CD639770	CD639770	AGENCOURT
987	51.2	3.0	328	5	BUT63409	BUT63409	ea942c02.	1060	51	3.0	383	1	1	AA401292	AA401292	fv63g05.r
988	51.2	3.0	336	7	CK372384	CK372384	lai84a11.	1061	51	3.0	387	6	6	CB955957	CB955957	AGENCOURT
989	51.2	3.0	336	7	CO508976	CO508976	ta991f07.	1062	51	3.0	395	5	5	BM889038	BM889038	kb04e08.y
990	51.2	3.0	340	6	CB084036	CB084036	hq08d08.b	1063	51	3.0	406	7	7	CO184293	CO184293	EC27824.5
991	51.2	3.0	343	7	CK375218	CK375218	lai46h07.	1064	51	3.0	455	1	1	AA269939	AA269939	va64e10.r
992	51.2	3.0	347	5	BUS32791	BUS32791	AGENCOURT	1065	51	3.0	457	5	5	BQ527792	BQ527792	NISC_n024
993	51.2	3.0	397	6	CB257961	CB257961	85-E01113	1066	51	3.0	473	1	1	AL037117	AL037117	DKF2p564M
c 994	51.2	3.0	412	7	CV354891	CV354891	MR4-EN007	1067	51	3.0	546	7	7	CF123295	CF123295	UI-HF-CH0
c 995	51.2	3.0	428	6	CA803003	CA803003	SAU45G07.	1068	51	3.0	572	7	7	CO873859	CO873859	BovGen_02
996	51.2	3.0	453	4	BG959797	BG959797	CM2-CT077	1069	51	3.0	642	1	1	AV764206	AV764206	AV764206
997	51.2	3.0	467	7	CF980284	CF980284	re03a12.y	1070	51	3.0	642	7	7	CK656065	CK656065	AGENCOURT
998	51.2	3.0	470	4	BM187391	BM187391	fw17a01.y	1071	51	3.0	647	7	7	CF731589	CF731589	UI-N-HA0-
999	51.2	3.0	470	5	BQ093110	BQ093110	fy94a03.y	1072	51	3.0	785	4	4	B1523919	B1523919	603051662
c1000	51.2	3.0	488	6	CA811197	CA811197	CA22LI06I	1073	51	3.0	834	5	5	BUS54800	BUS54800	AGENCOURT
1001	51.2	3.0	489	1	AV682229	AV682229		1074	51	3.0	840	5	5	BUS30592	BUS30592	AGENCOURT
1002	51.2	3.0	527	5	BM943015	BM943015	UI-N-B21-	1075	51	3.0	860	5	5	BUS65723	BUS65723	AGENCOURT
1003	51.2	3.0	530	4	BM573742	BM573742	fy03b10.y	1076	51	3.0	860	7	7	CF289324	CF289324	AGENCOURT
1004	51.2	3.0	538	1	AL925790	AL925790	AL925790	c1077	51	3.0	861	7	7	CR288979	CR288979	CR288979
1005	51.2	3.0	541	7	CN840817	CN840817	AGENCOURT	1078	51	3.0	862	5	5	BUS61053	BUS61053	AGENCOURT
1006	51.2	3.0	566	4	BM155067	BM155067	fv93a12.y	1079	51	3.0	895	6	6	CB309933	CB309933	AGENCOURT
1007	51.2	3.0	622	4	BG106619	BG106619	602290443	1080	51	3.0	904	5	5	BUS940115	BUS940115	AGENCOURT
1008	51.2	3.0	649	2	BF788814	BF788814	602110522	1081	51	3.0	930	5	5	BUS89620	BUS89620	AGENCOURT
1009	51.2	3.0	650	6	CD767936	CD767936	AGENCOURT	1082	51	3.0	932	4	4	BM416498	BM416498	OP21593.M
1010	51.2	3.0	657	5	BQ078813	BQ078813	fy81c06.y	1083	51	3.0	944	6	6	CD051079	CD051079	AGENCOURT
1011	51.2	3.0	769	7	CV065944	CV065944	WNEL28f8	1084	51	3.0	951	5	5	BUS95950	BUS95950	AGENCOURT
1012	51.2	3.0	775	7	CK787487	CK787487	AGENCOURT	1085	51	3.0	973	5	5	BUS89938	BUS89938	AGENCOURT
1013	51.2	3.0	776	9	CNS009BD	AL053563	Drosophil	1086	51	3.0	1010	6	6	CA976113	CA976113	AGENCOURT
1014	51.2	3.0	779	4	BG539542	BG539542	602568176	1087	51	3.0	1102	4	4	BG564613	BG564613	602584102
1015	51.2	3.0	786	7	CF455765	CF455765	AGENCOURT	c1088	51	3.0	1168	9	9	AG347267	AG347267	Mus muscu
1016	51.2	3.0	794	4	B1695737	B1695737	603345085	1089	51	3.0	1189	5	5	BUS08070	BUS08070	AGENCOURT
c1017	51.2	3.0	798	9	CNS010HK	AL098978	Drosophil	c1090	51	3.0	1189	9	9	CG752264	CG752264	P046-4-G0
1018	51.2	3.0	822	7	CN168497	CN168497	AGENCOURT	1091	51	3.0	1448	9	9	CL073846	CL073846	CH216-130
1019	51.2	3.0	823	5	BUS30830	BUS30830	AGENCOURT	1092	51	3.0	1531	3	3	CL058486	CL058486	CH216-88C
1020	51.2	3.0	841	2	BF342119	BF342119	602012877	1093	51	3.0	1782	2	2	CR749618	CR749618	Homo sapi
1021	51.2	3.0	847	5	BUS54569	BUS54569	AGENCOURT	1094	51	3.0	2172	9	9	CL078016	CL078016	CH216-147
1022	51.2	3.0	872	7	CK022958	CK022958	AGENCOURT	1095	50.8	3.0	162	5	5	BQ094671	BQ094671	san50d03.
1023	51.2	3.0	891	5	BUS21330	BUS21330	AGENCOURT	1096	50.8	3.0	176	4	4	B1497039	B1497039	df131b05.
1024	51.2	3.0	921	5	BUS64012	BUS64012	AGENCOURT	1097	50.8	3.0	179	5	5	BX250051	BX250051	EX250051
1025	51.2	3.0	930	5	BUS63671	BUS63671	AGENCOURT	1098	50.8	3.0	192	4	4	BM569696	BM569696	ih96b12.y
c1026	51.2	3.0	941	8	A2539217	A2539217	ENTEBJ48TF	c1099	50.8	3.0	198	4	4	BG980744	BG980744	MR3-CN014
1027	51.2	3.0	961	4	BM416004	BM416004	OP21087.M	1100	50.8	3.0	209	7	7	CF546313	CF546313	lae1a04.
1028	51.2	3.0	1004	4	BG252914	BG252914	602365514	1101	50.8	3.0	213	2	2	AW423994	AW423994	sh59b11.y
1029	51.2	3.0	1005	9	AG417297	AG417297	Mus muscu	1102	50.8	3.0	223	5	5	BQ235609	BQ235609	hd83d07.g
c1030	51.2	3.0	1017	8	BH155389	BH155389	ENTOX73TF	1103	50.8	3.0	240	4	4	BM341802	BM341802	fw53a03.y
1031	51.2	3.0	1027	6	CB205525	CB205525	AGENCOURT	1104	50.8	3.0	251	4	4	BM533329	BM533329	fy16e09.y
1032	51.2	3.0	1085	4	BG027405	BG027405	602296130	1105	50.8	3.0	258	2	2	BE752483	BE752483	204884.MA
1033	51.2	3.0	1087	7	CK231437	CK231437	ILLUMIGEN	1106	50.8	3.0	264	1	1	AL598482	AL598482	DKF2p313J
c1034	51.2	3.0	1100	9	CL145579	CL145579	ISB1-146A	1107	50.8	3.0	271	5	5	EX497273	EX497273	DKF2p779JL
c1035	51.2	3.0	1101	9	CNS00186	AL058835	Drosophil	1108	50.8	3.0	293	4	4	BM186087	BM186087	fv97g08.y
1036	51.2	3.0	1101	9	CNS008U8	AL069859	Drosophil	1109	50.8	3.0	317	7	7	CO754046	CO754046	mdf73020p
1037	51.2	3.0	1609	9	CL080652	CL080652	CH216-159	1110	50.8	3.0	341	7	7	CR766009	CR766009	DKF2p468F
1038	51.2	3.0	1727	9	CL118815	CL118815	ISB1-7205	1111	50.8	3.0	354	1	1	AJ790178	AJ790178	AGENCOURT
1039	51	3.0	196	6	CA819430	CA819430	sauf78C12.	1112	50.8	3.0	396	4	4	B1538310	B1538310	428810.MA
c1040	51	3.0	197	2	BF936477	BF936477	EST459532	1113	50.8	3.0	419	6	6	BES14524	BES14524	601315968
1041	51	3.0	197	7	CF314022	CF314022	HD--02-G0	1114	50.8	3.0	419	6	6	CD102064	CD102064	AGENCOURT
c1042	51	3.0	200	6	CA814321	CA814321	CA48LN09I	c1115	50.8	3.0	431	7	7	CK304852	CK304852	SB02025B1
1043	51	3.0	202	6	CA819572	CA819572	sauf80G01	1116	50.8	3.0	442	6	6	CD679816	CD679816	lab08f08.
1044	51	3.0	221	7	CN834008	CN834008	AGENCOURT	1117	50.8	3.0	474	7	7	CK551618	CK551618	rbw1a0.00
1045	51	3.0	227	4	BI074139	BI074139	kt40e05.y	1118	50.8	3.0	495	6	6	CA379708	CA379708	65849.NC
1046	51	3.0	228	7	CO182911	CO182911	EC24271.5	1119	50.8	3.0	496	7	7	CN004590	CN004590	lp20e11.g

1120	50.8	3.0	499	7	C0726605	C0726605 ILLUMIGEN	1193	50.6	3.0	397	7	CF546355	CF546355 lae71h04.
1121	50.8	3.0	516	7	CN833696	CN833696 AGENCOURT	c1194	50.6	3.0	402	2	AW190286	AW190286 x113d04.x
1122	50.8	3.0	544	7	CF123716	CF123716 UI-HF-CHO	1195	50.6	3.0	408	7	CN048707	CN048707 v2.p1.O13
1123	50.8	3.0	556	7	CV199827	CV199827 km20h10.y	1196	50.6	3.0	409	4	BI899036	BI899036 480889.MA
1124	50.8	3.0	571	5	B0747579	B0747579 UI-M-FAO-	1197	50.6	3.0	409	7	CK384344	CK384344 lah222c05.
1125	50.8	3.0	577	6	CB524184	CB524184 UI-M-GKO-	1198	50.6	3.0	412	6	CB075778	CB075778 h251b09.b
1126	50.8	3.0	642	4	B1870677	B1870677 603394773	1199	50.6	3.0	414	5	BX504814	BX504814 DKE2p686J
1127	50.8	3.0	651	8	AQ510797	AQ510797 nbxb0048J	1200	50.6	3.0	431	7	CF123177	CF123177 UI-HF-CHO
1128	50.8	3.0	659	6	CD642013	CD642013 AGENCOURT	1201	50.6	3.0	432	1	AJ725854	AJ725854 AJ725854
1129	50.8	3.0	660	1	AV704928	AV704928 AV704928	1202	50.6	3.0	434	1	AJ791630	AJ791630 AJ791630
1130	50.8	3.0	707	7	CV520959	CV520959 0089P0052	1203	50.6	3.0	434	1	AL719646	AL719646 AL719646
1131	50.8	3.0	712	7	CF9881073	CF9881073 re02e06.y	1204	50.6	3.0	436	1	AL729450	AL729450 AL729450
1132	50.8	3.0	723	1	AV733682	AV733682 AV733682	1205	50.6	3.0	437	1	AV682737	AV682737 AV682737
1133	50.8	3.0	741	7	CV491293	CV491293 AGENCOURT	1206	50.6	3.0	444	4	BM319186	BM319186 FNPBLC12
1134	50.8	3.0	781	6	CB318685	CB318685 AGENCOURT	1207	50.6	3.0	446	4	BM319186	BM319186 ki69d11.y
1135	50.8	3.0	815	8	B19681	B19681 F4H19-T7.1	1208	50.6	3.0	450	7	CO888261	CO888261 BovGen.16
1136	50.8	3.0	817	8	BH156712	BH156712 ENTSMA9TF	1209	50.6	3.0	451	1	AL721247	AL721247 AL721247
1137	50.8	3.0	820	4	BF968558	BF968558 602271159	1210	50.6	3.0	451	2	BE883021	BE883021 601510028
1138	50.8	3.0	822	5	B0843256	B0843256 AGENCOURT	1211	50.6	3.0	452	7	CF980375	CF980375 re04b03.y
1139	50.8	3.0	822	9	CNS00911	AL052989 Drosophila	1212	50.6	3.0	462	4	BM569326	BM569326 kj59f02.y
1140	50.8	3.0	830	7	CK395910	CK395910 AGENCOURT	1213	50.6	3.0	463	6	CB445238	CB445238 696490.MA
1141	50.8	3.0	832	5	B0842545	B0842545 AGENCOURT	1214	50.6	3.0	464	4	BM517997	BM517997 ki86e09.y
1142	50.8	3.0	835	5	BUS29221	BUS29221 AGENCOURT	1215	50.6	3.0	465	4	BM517871	BM517871 ki83f02.y
1143	50.8	3.0	836	5	BUS65750	BUS65750 AGENCOURT	c1216	50.6	3.0	468	6	CF047285	CF047285 QCK6904.y
1144	50.8	3.0	847	7	CO647224	CO647224 ILLUMIGEN	1217	50.6	3.0	471	4	BI702656	BI702656 fr55h03.y
1145	50.8	3.0	881	7	CK151831	CK151831 FGAS03458	1218	50.6	3.0	475	4	BM567111	BM567111 kj10c09.y
1146	50.8	3.0	886	7	CK157081	CK157081 FGAS03815	1219	50.6	3.0	482	7	CF124659	CF124659 UI-HF-CHO
1147	50.8	3.0	886	7	CK161161	CK161161 FGAS04285	1220	50.6	3.0	501	1	AJ798819	AJ798819 AJ798819
1148	50.8	3.0	891	9	CNS0092J	AL053767 Drosophila	1221	50.6	3.0	509	6	CB080062	CB080062 hp80f10.b
1149	50.8	3.0	905	7	CK322888	CNS22888 AGENCOURT	1222	50.6	3.0	571	5	BP256021	BP256021 BP256021
1150	50.8	3.0	908	7	CV066886	CV066886 WNEL95.W	1223	50.6	3.0	581	5	BP375614	BP375614 BNEL100B9
1151	50.8	3.0	909	7	CK407058	CK407058 AUF IFLvr	1224	50.6	3.0	584	7	CV053519	CV053519 BNEL100B9
1152	50.8	3.0	926	4	BG575702	BG575702 602598774	1225	50.6	3.0	585	7	CO403863	CO403863 AGENCOURT
1153	50.8	3.0	940	6	CD386618	CD386618 AGENCOURT	1226	50.6	3.0	597	4	BG572394	BG572394 602593434
1154	50.8	3.0	955	2	BE890041	BE890041 601512310	1227	50.6	3.0	606	5	BUI14551	BUI14551 603131443
1155	50.8	3.0	956	6	CD512769	CD512769 AGENCOURT	1228	50.6	3.0	614	6	CB980039	CB980039 CAB70001.y
1156	50.8	3.0	975	3	CK733776	CK733776 Tetraodon	1229	50.6	3.0	617	7	CF370504	CF370504 AG50b02.y
1157	50.8	3.0	996	9	CNS04XL6	AG392861 Mus muscu	1230	50.6	3.0	624	5	BP382214	BP382214 BP382214
1158	50.8	3.0	1009	9	AG392861	AG392861 Mus muscu	1231	50.6	3.0	634	7	CK320427	CK320427 L3P07d09
1159	50.8	3.0	1023	5	BUS06457	BUS06457 AGENCOURT	1232	50.6	3.0	638	4	BG218217	BG218217 RST37944
1160	50.8	3.0	1031	9	CNS016YV	AL107380 Drosophila	1233	50.6	3.0	642	7	CK455895	CK455895 921256.MA
1161	50.8	3.0	1098	6	CD049441	CD049441 AGENCOURT	1234	50.6	3.0	717	8	AZ849900	AZ849900 2M0151103
1162	50.8	3.0	1101	9	CNS016TQ	AL107192 Drosophila	1235	50.6	3.0	722	7	CV064765	CV064765 WNEL14H5
1163	50.8	3.0	1151	9	AG324438	AG324438 Mus muscu	1236	50.6	3.0	752	6	CD521791	CD521791 AGENCOURT
1164	50.8	3.0	1227	9	AG361182	AG361182 Mus muscu	c1237	50.6	3.0	771	9	AG517090	AG517090 Mus muscu
1165	50.8	3.0	1274	9	AG341312	AG341312 Mus muscu	1238	50.6	3.0	772	5	BUS958222	BUS958222 AGENCOURT
1166	50.8	3.0	1690	9	CL078351	CL078351 CH216-149	1239	50.6	3.0	801	7	CF289632	CF289632 AGENCOURT
1167	50.8	3.0	4796	3	CK749476	CK749476 Homo sapi	1240	50.6	3.0	803	5	BUS65241	BUS65241 AGENCOURT
1168	50.6	3.0	157	4	BM513623	BM513623 kx97b03.y	1241	50.6	3.0	806	7	CK128745	CK128745 AGENCOURT
1169	50.6	3.0	169	1	AL697897	AL697897 DKE2p686A	1242	50.6	3.0	809	5	BUS43613	BUS43613 AGENCOURT
1170	50.6	3.0	191	4	BI705400	BI705400 fr58g02.y	1243	50.6	3.0	813	5	BUS42611	BUS42611 AGENCOURT
1171	50.6	3.0	193	4	BM530850	BM530850 fy17e12.y	c1244	50.6	3.0	814	7	CK200263	CK200263 FGAS00877
1172	50.6	3.0	194	4	BM154531	BM154531 fv86c02.y	1245	50.6	3.0	816	5	BUS64811	BUS64811 AGENCOURT
1173	50.6	3.0	196	4	BI705266	BI705266 fr55f03.y	1246	50.6	3.0	826	9	CL043364	CL043364 CH216-560
1174	50.6	3.0	210	4	BM154362	BM154362 fv84b10.y	1247	50.6	3.0	827	9	BH182445	BH182445 O21.O.13
1175	50.6	3.0	220	5	BF785757	BF785757 saq87c03.	1248	50.6	3.0	827	9	CNS07N08	AL619394 T7 end of
1176	50.6	3.0	222	7	CF926234	CF926234 laf6e09.	1249	50.6	3.0	829	5	BUS31959	BUS31959 AGENCOURT
1177	50.6	3.0	236	4	BI681181	BI681181 460497.MA	1250	50.6	3.0	832	9	CNS00818	AL051195 Drosophila
1178	50.6	3.0	236	7	CF754919	CF754919 lae09c01.	1251	50.6	3.0	833	5	BUS88052	BUS88052 AGENCOURT
1179	50.6	3.0	252	6	CB043981	CB043981 NISC gc01	1252	50.6	3.0	833	6	CB963986	CB963986 AGENCOURT
1180	50.6	3.0	287	6	CB343712	CB343712 CA32EN000	1253	50.6	3.0	844	9	AG058605	AG058605 Pan trogl
1181	50.6	3.0	291	7	CO195274	CO195274 EC39963.5	1254	50.6	3.0	845	5	BUS537023	BUS537023 AGENCOURT
1182	50.6	3.0	318	6	CB984581	CB984581 AGENCOURT	1255	50.6	3.0	853	5	BUS88997	BUS88997 AGENCOURT
1183	50.6	3.0	337	5	BQ780082	BQ780082 UI-R-PF0-	1256	50.6	3.0	854	5	BUS60392	BUS60392 AGENCOURT
1184	50.6	3.0	345	2	BE878735	BE878735 601492990	1257	50.6	3.0	859	7	CO808031	CO808031 AGENCOURT
1185	50.6	3.0	346	5	BX476056	BX476056 DKE2p686B	c1258	50.6	3.0	868	7	CK200194	CK200194 FGAS00870
1186	50.6	3.0	348	6	CB704554	CB704554 AMGNNUC:S	1259	50.6	3.0	874	6	CB844981	CB844981 M2PN-0547
1187	50.6	3.0	375	3	AY068947	AY068947 Schmidtea	1260	50.6	3.0	876	7	CK323414	CK323414 AGENCOURT
1188	50.6	3.0	377	1	AL722378	AL722378 NISC gc04	1261	50.6	3.0	881	9	AZ200698	AZ200698 SP.1026.A
1189	50.6	3.0	386	6	CB044394	CB044394 NISC gc04	1262	50.6	3.0	883	9	CL067381	CL067381 Drosophila
1190	50.6	3.0	387	1	AA204368	AA204368 mu31c08.r	1263	50.6	3.0	886	9	CNS011SM	AL100672 Drosophila
1191	50.6	3.0	391	4	BJ688931	BJ688931	c1264	50.6	3.0	888	4	BM415362	BM415362 OP20436.M
1192	50.6	3.0	397	5	BQ395470	BQ395470 NISC ng15	c1265	50.6	3.0	888	7	CK160993	CK160993 FGAS04266

1266	50.6	3.0	889	5	BUE51997	AGENCOURT	BUE51997	AGENCOURT	1339	50.4	3.0	762	7	CK397238	AGENCOURT
1267	50.6	3.0	904	4	BI859386	603388113	BI859386	603388113	1340	50.4	3.0	771	5	BUE60352	AGENCOURT
1268	50.6	3.0	915	4	BG518636	602578491	BG518636	602578491	1341	50.4	3.0	777	2	BE875022	601487588
1269	50.6	3.0	915	5	BQ718652	AGENCOURT	BQ718652	AGENCOURT	C1342	50.4	3.0	778	9	AGS86300	Mus muscu
1270	50.6	3.0	916	5	BUS88527	AGENCOURT	BUS88527	AGENCOURT	1343	50.4	3.0	787	5	BUS36254	AGENCOURT
1271	50.6	3.0	936	5	BQ233428	AGENCOURT	BQ233428	AGENCOURT	1344	50.4	3.0	802	6	CD000230	AGENCOURT
1272	50.6	3.0	937	9	CNS00011Q		AL074356	DroboPhill	C1345	50.4	3.0	803	4	BG335466	602403936
1273	50.6	3.0	941	5	BUS34769	AGENCOURT	BUS34769	AGENCOURT	1346	50.4	3.0	818	5	BUS29789	AGENCOURT
1274	50.6	3.0	945	5	BQ431642	AGENCOURT	BQ431642	AGENCOURT	C1347	50.4	3.0	828	8	AZ194425	SP_1026_A
1275	50.6	3.0	955	5	BUS33926	AGENCOURT	BUS33926	AGENCOURT	1348	50.4	3.0	844	9	AG129984	Pan trogl
1276	50.6	3.0	955	5	BUS66880	AGENCOURT	BUS66880	AGENCOURT	1349	50.4	3.0	858	7	CNS01273	DroboPhill
1277	50.6	3.0	956	7	CK423987	AUF_IpSto	CK423987	AUF_IpSto	1350	50.4	3.0	873	7	CF455006	AGENCOURT
1278	50.6	3.0	960	6	CB597408	AGENCOURT	CB597408	AGENCOURT	C1351	50.4	3.0	877	7	CK159921	FGAS04144
1279	50.6	3.0	962	8	AZ680445	ENTMWS07R	AZ680445	ENTMWS07R	1352	50.4	3.0	892	5	BUS960887	AGENCOURT
1280	50.6	3.0	978	4	BF969662	602272040	BF969662	602272040	1353	50.4	3.0	895	6	CB229191	AGENCOURT
1281	50.6	3.0	1005	8	BH164025	ENTOU60TF	BH164025	ENTOU60TF	1354	50.4	3.0	908	6	CD513633	AGENCOURT
1282	50.6	3.0	1054	3	AF130104	Homo sapi	AF130104	Homo sapi	1355	50.4	3.0	912	5	BUS29547	AGENCOURT
1283	50.6	3.0	1063	5	BUS40218	AGENCOURT	BUS40218	AGENCOURT	1356	50.4	3.0	916	9	CNS06VOC	
1284	50.6	3.0	1101	9	BG5000F07		BUS40218	AGENCOURT	1357	50.4	3.0	923	5	BUS33956	AGENCOURT
1285	50.6	3.0	1122	4	CNS001454	602548028	AG070758	DroboPhill	1358	50.4	3.0	972	9	AL078167	DroboPhill
1286	50.6	3.0	1124	9	AG288406	Mus muscu	AG288406	Mus muscu	1359	50.4	3.0	998	6	CD049247	AGENCOURT
1287	50.6	3.0	1150	6	CD249726	AGENCOURT	CD249726	AGENCOURT	1360	50.4	3.0	1011	5	BUS934341	AGENCOURT
1288	50.6	3.0	1165	9	CL051682	CH216-74F	CL051682	CH216-74F	1361	50.4	3.0	1038	6	CD249177	AGENCOURT
1289	50.6	3.0	1178	9	AG430313	Mus muscu	AG430313	Mus muscu	1362	50.4	3.0	1081	5	BUS10236	AGENCOURT
1290	50.6	3.0	1260	3	AY108843	Zea mays	AY108843	Zea mays	C1363	50.4	3.0	1095	9	CNS016E8	DroboPhill
1291	50.6	3.0	1308	6	CD248372	AGENCOURT	CD248372	AGENCOURT	1364	50.4	3.0	1114	4	BM452203	AGENCOURT
1292	50.6	3.0	1308	8	CD230203	CH261-62P	CD230203	CH261-62P	C1365	50.4	3.0	1161	9	AG365964	Mus muscu
1293	50.6	3.0	3517	3	BC030264	Homo sapi	BC030264	Homo sapi	1366	50.4	3.0	1205	4	BM544190	AGENCOURT
1294	50.6	3.0	3443	3	HSW803534		AL832227	Homo sapi	1367	50.4	3.0	1291	5	BQ231056	AGENCOURT
1295	50.4	3.0	141	7	CK467264		AK8467264	938548 MA	1368	50.4	3.0	1504	3	BC023270	Homo sapi
1296	50.4	3.0	213	7	CR548135	DFK2P4591	CR548135	DFK2P4591	1369	50.4	3.0	1651	9	CL0779030	CH216-154
1297	50.4	3.0	164	7	CF118240	f8351.z1	CF118240	f8351.z1	C1370	50.2	3.0	199	5	BQ326520	MR4-CN014
1298	50.4	3.0	261	7	CR763363	DKF2P4701	CR763363	DKF2P4701	C1371	50.2	3.0	201	4	BG981501	MR3-CN014
1299	50.4	3.0	270	4	BM981117	k109f12.y	BM981117	k109f12.y	C1372	50.2	3.0	201	6	CA667413	wlsu1.pk0
1300	50.4	3.0	273	4	BI089282		BI089282	602853209	1373	50.2	3.0	203	7	CN276442	170006001
1301	50.4	3.0	278	5	BQ289284		BQ289284	P127905.y	1374	50.2	3.0	208	6	CA082715	SC441a12.2
1302	50.4	3.0	278	6	CD641261	AGENCOURT	CD641261	AGENCOURT	1375	50.2	3.0	209	7	CO182777	EAU41a12.7
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1304	50.4	3.0	296	1	AI856737	eb41e07.y	AI856737	eb41e07.y	1377	50.2	3.0	214	4	BM265899	fw37b09.y
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1306	50.4	3.0	307	6	CD722153	o106b12.y	AD722153	o106b12.y	1379	50.2	3.0	220	7	CF383239	lac39c02..
1307	50.4	3.0	378	1	AV760102	AV760102	AV760102	AV760102	1380	50.2	3.0	223	5	BQ276953	AGENCOURT
1308	50.4	3.0	382	6	CA987506	AGENCOURT	CA987506	AGENCOURT	1381	50.2	3.0	239	4	BM532471	fy08e08.y
1309	50.4	3.0	408	6	CB770419	AMGNNUC:S	CB770419	AMGNNUC:S	1382	50.2	3.0	241	4	BM186126	fy98c06.y
1310	50.4	3.0	419	5	BUS30428	AGENCOURT	BUS30428	AGENCOURT	1383	50.2	3.0	243	7	CO193787	EC368008.5
1311	50.4	3.0	419	6	CB934821	laa44h01..	CB934821	laa44h01..	1384	50.2	3.0	252	7	CF212181	CGF100066
1312	50.4	3.0	430	6	CB075623	h249c09.b	CB075623	h249c09.b	1385	50.2	3.0	270	7	CK625724	mjl3e12.y
1313	50.4	3.0	435	4	BM283047	K144d10.y	BM283047	K144d10.y	1386	50.2	3.0	271	6	CA802092	sa030a04..
1314	50.4	3.0	466	4	BM567650	bak77a05..	BM567650	bak77a05..	1387	50.2	3.0	296	2	BE059362	sn31g07.y
1315	50.4	3.0	471	5	BUS1050	AGENCOURT	CA836663	NISC_lv03	1388	50.2	3.0	347	6	CB705238	AMGNNUC:Y
1316	50.4	3.0	508	7	CK431061	o157d12.y	CK431061	o157d12.y	1393	50.2	3.0	365	4	BI941631	sc80f10.y
1317	50.4	3.0	531	1	AL712171	DKFZ5686D	AL712171	DKFZ5686D	1395	50.2	3.0	374	7	CO878391	BoyGen_06
1318	50.4	3.0	538	1	AV757416	AV757416	AV757416	AV757416	1396	50.2	3.0	377	7	CO195922	EC43542.5
1319	50.4	3.0	500	2	BF882334	IL3-ET011	BF882334	IL3-ET011	1397	50.2	3.0	378	7	CF124412	UI-HF-CHO
1320	50.4	3.0	571	5	BQ522127	NISC_n114	BQ522127	NISC_n114	1398	50.2	3.0	386	2	BF037097	601456863
1321	50.4	3.0	579	6	CB607201	AMGNNUC:S	CB607201	AMGNNUC:S	1399	50.2	3.0	417	7	CK384549	lah26f05..
1322	50.4	3.0	582	5	BP249933	BP249933	BP249933	BP249933	1400	50.2	3.0	420	1	AL711793	DKFZP686B
1323	50.4	3.0	595	8	BH189680	001_K_11-	BH189680	001_K_11-	1401	50.2	3.0	426	7	CK421093	AUF_IpSpn
1324	50.4	3.0	568	7	CV285468	tak47h02..	CV285468	tak47h02..	1402	50.2	3.0	427	2	BF793360	602254790
1325	50.4	3.0	571	6	BQ522137	NISC_n114	BQ522137	NISC_n114	1403	50.2	3.0	442	1	AV763658	AV763658
1326	50.4	3.0	579	6	CB336663	NISC_lv03	CB336663	NISC_lv03	1404	50.2	3.0	444	7	CF612777	laf06b12..
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1328	50.4	3.0	642	5	BQ747828	UI-M-PAO-	BQ747828	UI-M-PAO-	1406	50.2	3.0	457	8	AQ752942	HS_5231.A
1329	50.4	3.0	663	7	CF350633	r153c08.y	CF350633	r153c08.y	1407	50.2	3.0	471	7	CF307986	ABF--01-J
1330	50.4	3.0	693	7	CG581501	ILLUMIGEN	CG581501	ILLUMIGEN	C1407	50.2	3.0	483	7	CF315792	HD--04-N1
1331	50.4	3.0	732	9	AG546088	Mus muscu	AG546088	Mus muscu	1408	50.2	3.0	490	1	AV756619	AV756619
1332	50.4	3.0	741	9	CN842216	AGENCOURT	CN842216	AGENCOURT	1410	50.2	3.0	525	5	BP683189	BP683189
1333	50.4	3.0	743	9	AG285887	Mus muscu	AG285887	Mus muscu	1411	50.2	3.0	525	7	CV066363	WNL31a1.W

1412	50.2	3.0	538	1	AL727686	AL727686	1485	50	3.0	346	2	BF751308	BF751308 RC3-BN042
1413	50.2	3.0	601	6	CD239085	FNPBK001	1486	50	3.0	350	2	BF806065	BF806065 MR1-CI018
1414	50.2	3.0	603	1	AV732976	AV732976	1487	50	3.0	354	7	CK428760	CK428760 laj16b02
1415	50.2	3.0	604	5	BP271854	BP271854	1488	50	3.0	361	7	CK004628	CK004628 AGENCOURT
1416	50.2	3.0	609	6	CD239279	FNPBMF09	1489	50	3.0	363	7	CV194197	CV194197 SnsSTbaa9
1417	50.2	3.0	609	6	CD239341	FNPEND08	1490	50	3.0	372	7	CF801074	CF801074 rj1ld08.y
1418	50.2	3.0	653	9	CNS02M1D	Tetraodon	1491	50	3.0	375	2	AW827214	AW827214 xn09f12.y
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1420	50.2	3.0	750	5	BUS37749	AGENCOURT	1493	50	3.0	392	5	BQ290505	BQ290505 NXR045.B
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1422	50.2	3.0	759	8	B12963	T23D1-T7.1	1495	50	3.0	405	5	BU055967	BU055967 UI-M-F90-
1423	50.2	3.0	781	9	AG592717	Mus muscu	1496	50	3.0	406	6	CB975383	CB975383 CAB30006
1424	50.2	3.0	782	5	BX422198	BX422198	1497	50	3.0	408	5	BQ126842	BQ126842 i119h05.y
1425	50.2	3.0	802	1	AV757528	AV757528	1498	50	3.0	408	7	CK565162	CK565162 dor12a2.D
1426	50.2	3.0	802	9	AG452709	Mus muscu	1499	50	3.0	424	1	AA597163	AA597163 vo35h02.r
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1428	50.2	3.0	847	6	CD250700	AGENCOURT							
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1434	50.2	3.0	891	7	CK169028	FGAS04363							
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1437	50.2	3.0	927	5	BQ920326	AGENCOURT							
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1446	50.2	3.0	999	5	BU513295	AGENCOURT							
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1460	50.2	3.0	3191	3	HSM804649	AL833336 Homo sapi							
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1480	50	3.0	301	5	BUS63515	AGENCOURT							
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1482	50	3.0	309	9	CF3319405	tigr-gss-							
1483	50	3.0	321	2	CF331988	NACU--08-							
1484	50	3.0	324	2	AW306965	sf51a09.y							

ALIGNMENTS

RESULT 1	AK045973	1808 bp	linear	HTC 03-APR-2004
LOCUS	AK045973	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B230328N06 product:NEUROTRIMIN PRECOURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.		
ACCESSION	AK045973			
VERSION	AK045973.1	GI:26337738		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	1	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Carninci, P. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10149636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, Y., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			
MEDLINE	20530913			
PUBMED	11076861			
REFERENCE	4			
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium			
TITLE	Functional annotation of a full-length mouse cDNA collection			
JOURNAL	Nature 409, 685-690 (2001)			
MEDLINE	11076861			
PUBMED	11076861			
REFERENCE	5			
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.			
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs			
JOURNAL	Nature 420, 563-573 (2002)			
MEDLINE	12053913			
PUBMED	12053913			
REFERENCE	6	(bases 1 to 1808)		

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayata, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/.

FEATURES
source

location/Qualifiers
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/mol_type="mRNA"
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ORIGIN

Query Match 66.7%; Score 1119.4; DB 3; Length 1808;
Best Local Similarity 83.1%; Pred. NO. 1.8e-278;
Matches 1417; Conservative 0; Mismatches 251; Indels 37; Gaps 11;

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Qy 61 AATCTATCAGGAAAGAAAGAAAAAAGAAAAACCGAACCTGACAAAAA-----G 108
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Qy 109 AAGAAAG 168
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Qy 169 CTCTTGGGCAATCTTCAACGGGGCTGGCTGCTGTGTGTCTCTTCAAGAGAGTGCCTGGCG 228
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Db 299 TAGCGAGATGCCACCTTCCCTCCAAAGCTATGGACAAGCTGACCGTCCGGCAGGGGGAGAG 358

Qy 289 CGCCACCTCAGGTGCACTATTGACACCGGTCCACCGGTGGCTGGCTGAAACCGCGAG 348
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Qy 349 CACCATCTCTATGCTGGGAATGACAAAGTGGTGGCTCTCGCGTGGTCTTCTTCTGAG 408
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Qy 409 CAACACCAAGCGGAGTACGATCGAGATCCAGAAAGTGGATGTGTATGACAGAGGGCCC 468
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Qy 589 TATTAGCTCCTGATAGCAATGTGTAGACAGAGCTTACGGTTACTTTGGAGACACAT 648
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Db	1309	AGCACAGTGCAGATCAATGAAATCCGAGATCCAGACC-AATGAGACAGAAATTCG	1367
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Db	1368	AGGGAGGAGGACAAAGCATACTGTGTTAAAGGGGAAAGAGTTTAAAGAAAGGAATTT	1427
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Db	1728	GTGAATTCGAGGAGAAAAA 1752	
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AK046377			
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DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN		
	full-length enriched library, clone:B230377K17 product:NEUROTRIMIN		
ACCESSION	PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.		
VERSION	AK046377.1	GI:26338018	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	Carninci, P. and Hayashizaki, Y.		
JOURNAL	High-efficiency full-length cDNA cloning		
MEDLINE	Meth. Enzymol. 303, 19-44 (1999)		
PUBMED	99279253		
REFERENCE	10349636		
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to		
	prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,		
	Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M.,		
	Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,		
	Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,		
	Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,		
	Yoneda, Y., Ishikawa, I., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,		
	Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
REFERENCE	4		

AUTHORS	
TITLE	The RIKEN Genome Exploration Research Group Phase II Team and the
JOURNAL	FANTOM Consortium.
REFERENCE	Functional annotation of a full-length mouse cDNA collection
AUTHORS	Nature 409, 685-690 (2001)
TITLE	The FANTOM Consortium and the RIKEN Genome Exploration Research
JOURNAL	Group Phase I & II Team.
REFERENCE	Analysis of the mouse transcriptome based on functional annotation
AUTHORS	of 60,770 full-length cDNAs
	Nature 420, 563-573 (2002)
TITLE	6 (bases 1 to 1808)
JOURNAL	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
REFERENCE	Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
AUTHORS	Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
	Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
	Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
	Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
	Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohseto, N.,
	Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
	Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
	Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
	Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
	Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
	Physical and Chemical Research (RIKEN), Laboratory for Genome
	Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
	RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
	Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
	URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
	Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome
	Encyclopedia Project of Genome Exploration Research Group in Riken
	Sciences Center and Genome Science Laboratory in RIKEN.
	Division of Experimental Animal Research in Riken contributed to
	prepare mouse tissues.
	Please visit our web site for further details.
	URL: http://genome.gsc.riken.jp/
	URL: http://fantom.gsc.riken.jp/
FEATURES	Location/Qualifiers
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	Query Match 66.7%; Score 1119.4; DB 3; Length 1808;
	Best Local Similarity 83.1%; Pred. No. 1.8e-278;
	Matches 1417; Conservative 0; Mismatches 251; Indels 37; Gaps 11;
Qy	1 GTTGTGCTCTTCACAAAACAGTGGATTTAAATCTCTTCACAAAGCTTGAGAGCAACAC 60

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RESULT 3
CR602526
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DEFINITION 2512 bp mRNA linear HTC 21-JUL-2004
ACCESSION CR602526
VERSION CR602526.1 GI:50483333
KEYWORDS HTC; CNSLT cdna
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2512)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cdna libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2512)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

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Matches 1145; Conservative		0; Mismatches 4; Indels 118; Gaps 1;
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Qy	1613	GCATTTTGTGTAGTGTGCCACCGCTGTGTGTGAAACGTGAAATAAAAAGAGCAA 1672
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Qy	1673	AAAAAAA 1679
Db	1361	AAAAAAA 1367
RESULT 4		
AY406347		874 bp DNA linear GSS 12-DEC-2003
LOCUS		
DEFINITION		Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
ACCESSION		AY406347
VERSION		AY406347.1 GI:39762321
KEYWORDS		GSS.
SOURCE		Homo sapiens (human)
ORGANISM		Homo sapiens
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE		Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
JOURNAL		Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
PUBMED		Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
REFERENCE		Adams,M.D. and Cargill,M.
AUTHORS		Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
TITLE		Rockville, MD 20850, USA
JOURNAL		This sequence was made by sequencing genomic exons and ordering
COMMENT		them based on alignment.
FEATURES		Location/Qualifiers
source		1..874
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		/mol_type="genomic DNA"
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ORIGIN		
Query Match		50.7%; Score 852; DB 9; Length 874;
Best Local Similarity		99.3%; Pred. No. 2.9e-209;
Matches 868; Conservative		0; Mismatches 0; Indels 6; Gaps 1;

Qy	301	GTGCACCTATTGACAAACCGGCTCACCCGGTGGCTTAAACCGCAGCACATCTCTCTA	360
Db	1	GTGCACCTATTGACAAACCGGCTCACCCGGTGGCTTAAACCGCAGCACATCTCTCTA	60
Qy	361	TGCTGGGAATGACAAGTGGTGGCTTGGATCTCGGTGGCTTCTTGAGCAACACCCAAAC	420
Db	61	TGCTGGGAATGACAAGTGGTGGCTTGGATCTCGGTGGCTTCTTGAGCAACACCCAAAC	120
Qy	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACTGCTC	480
Db	121	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACTGCTC	180
Qy	481	GGTCGAGACAGCAACACCCAAAGACCTCTAGGTGCACCTCATTTGGCAAGTATCTCC	540
Db	181	GGTCGAGACAGCAACACCCAAAGACCTCTAGGTGCACCTCATTTGGCAAGTATCTCC	240
Qy	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	600
Db	241	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC	300
Qy	601	CTGCATAGCAACTGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCAA---	657
Db	301	CTGCATAGCAACTGGTAGACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAACC	360
Qy	658	---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA	714
Db	361	CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA	420
Qy	715	GCAGTACAGGGACTACGAGTGCAGTGCCTCAATGAGCGCGCCCGGTGTTACGGAG	774
Db	421	GCAGTACAGGGACTACGAGTGCAGTGCCTCAATGAGCGCGCCCGGTGTTACGGAG	480
Qy	775	AGTAAAGGTACACCGTGAACCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCCC	834
Db	481	AGTAAAGGTACACCGTGAACCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCCC	540
Qy	835	CGTGGGACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCCA	894
Db	541	CGTGGGACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCCA	600

RESULT 5

AY406348

LOCUS

DEFINITION

ACCESSION

VERSION

SOURCE

ORGANISM

AY406348

Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY406348

GI:39762322

Pan troglodytes (chimpanzee)

Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE	1 (bases 1 to 773)	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Pan.
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios	
JOURNAL	Science 302 (5652), 1960-1963 (2003)	
PUBMED	14671302	
REFERENCE	2 (bases 1 to 773)	
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	
TITLE	Direct Submission	
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA	
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.	
FEATURES	Location/Qualifiers	
source	1..773	
gene	/organism="Pan troglodytes" /mol_type="genomic DNA" /db_xref="taxon:9598"	
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Best Local Similarity	98.4%; Pred. No. 4.3e-181;	
Matches	761; Conservative 0; Mismatches 6; Indels 6; Gaps 1;	
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Db	1	GTGCACCTATTGACAAACCGGCTCACCCGGTGGCTTAAACCGCAGCACATCTCTCTA 60
Qy	361	TGCTGGGAATGACAAGTGGTGGCTTGGATCTCGGTGGCTTCTTGAGCAACACCCAAAC 420
Db	61	TGCTGGGAATGACAAGTGGTGGCTTGGATCTCGGTGGCTTCTTGAGCAACACCCAAAC 120
Qy	421	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACTGCTC 480
Db	121	GCAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACAGGGCCCTTACACTGCTC 180
Qy	481	GGTCGAGACAGCAACACCCAAAGACCTCTAGGTGCACCTCATTTGGCAAGTATCTCC 540
Db	181	GGTCGAGACAGCAACACCCAAAGACCTCTAGGTGCACCTCATTTGGCINNNTATCTCC 240
Qy	541	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 600
Db	241	CAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCAC 300
Qy	601	CTGCATAGCAACTGGTAGACAGCCTACGGTTACTTTGGAGACACATCTCTCCCAA--- 657
Db	301	CTGCATAGCAACTGGTAGACAGCCTACGGTTACTTTGGAGACACATCTCTCCCAAACC 360
Qy	658	---AGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 714
Db	361	CGCAGCGGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGA 420
Qy	715	GCAGTACAGGGACTACGAGTGCAGTGCCTCAATGAGCGCGCCCGGTGTTACGGAG 774
Db	421	GCAGTACAGGGACTACGAGTGCAGTGCCTCAATGAGCGCGCCCGGTGTTACGGAG 480
Qy	775	AGTAAAGGTACACCGTGAACCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCCC 834
Db	481	AGTAAAGGTACACCGTGAACCTATCCACCATACATTTTCAAGAACCAAGGGTACAGGTGTCCC 540
Qy	835	CGTGGGACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCCA 894
Db	541	CGTGGGACAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCCA 600

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Qy 895 GTGGTACAGGATGACAAAAGACTGATTGAAGAGAAAGAAAGGGGTGAAAGTGGAAAACAG 954
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Qy 955 ACCTTTCTCTCAAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGAACTACAC 1014
Db 661 ACCTTTCTCTCAAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGAACTACAC 720
Qy 1015 TTGGGTGGCTCCAAAGCTGGGCGCACCAACCAATGCCAGCATCATGCTATTG 1067
Db 721 TTGGGTGGCTCCAAAGCTGGGCGCACCAACCAATGCCAGCATCATGCTATTG 773

RESULT 6
BM807426 1033 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT_6581928 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5471935
5', mRNA sequence.
ACCESSION BM807426.1 GI:19124249
VERSION BM807426.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1033)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM1981 row: c column: 08
High quality sequence stop: 639.
FEATURES
source
location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="NIH_MGC_41"
/note="Organ: skin; Vector: pOTB7; Site:1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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ORIGIN

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Query Match 43.7%; Score 733.4; DB 4; Length 1033;
Best Local Similarity 92.5%; Pred. No. 1.6e-178;
Matches 830; Conservative 0; Mismatches 26; Indels 41; Gaps 4;

Qy 663 TTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAG 722
Db 1 TTGGCTTTGTGAGTGAAGCAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAG 60
Qy 723 GGGACTACAGTGCAGTGCCTCCCAATGACGTGGCGCGCGCGTGTGACGGAGTAAAGG 782
Db 61 GGGACTACAGTGCAGTGCCTCCCAATGACGTGGCGCGCGCGTGTGACGGAGTAAAGG 120
Qy 783 TCACCGTGAATCTCCACCATACATTTTCAGAGCCCAAGGGTACAGGTGTCTCCCGTGGAC 842
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Db 121 TCACCGTGAATCTCCACCATACATTTTCAGAGCCCAAGGGTACAGGTGTCTCCCGTGGAC 180
Qy 843 AAAAGGGGACACATCGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAGAATTCAGTGGTACA 902
Db 181 AAAAGGGGACACATCGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAGAATTCAGTGGTACA 240
Qy 903 AGGATGACAAAAGACTGATTGAAGAGAAAGAAAGGGGTGAAAGTGGAAAACAGACTTTTC 962
Db 241 AGGATGACAAAAGACTGATTGAAGAGAAAGAAAGGGGTGAAAGTGGAAAACAGACTTTTC 300
Qy 963 TCTCAAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTTGCGTGG 1022
Db 301 TCTCAAAACTCATCTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTTGCGTGG 360
Qy 1023 CCTCCAAAGAGCTGGGCGCACCAACCAATGCCAGCATCATGCTATTTT----- 1066
Db 361 CCTCCAAAGAGCTGGGCGCACCAACCAATGCCAGCATCATGCTATTTGAAAGTGAANAACACAG 420
Qy 1067 -----GGTCCAGGCGCCGTACGAGAGGTGAGCAACGGCACTGTCGAGGA 1109
Db 421 CCCTGACCCCTTTGGAAAAGGTCAGGGCGCGTACGAGAGGTGAGCAACGGCACTGTCGAGGA 480
Qy 1110 GGGCAGGCTCGCTGCTGCTCTCTCTGCTCTTCTGCTCTTGCACCTGCTTCTCAAAATTTTGCAT 1169
Db 481 GGGCAGGCTCGCTGCTGCTCTCTCTGCTCTTCTGCTCTTGCACCTGCTTCTCAAAATTTTGCAT 540
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Db 541 GTGAGTGCCTACTTCCCGCACCCGGGAAAGGCTGCCGCCACCAACCACCAACACACAGC 600
Qy 1230 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAATTTAGAGAAACACAGC 1289
Db 601 AATGGCAACACCGACAGCAACCAATCAGATATATACAAATGAATTTAGAGAAACACAGC 660
Qy 1290 CTCATGGGACAGAAATTTGAGGGAGGGGAAACAAAGAAATCTTTTGGGGGAAAGAGTTT 1349
Db 661 CTCATGGGACAGAAATTTGAGGGAGGGGAAACAAAGAAATCTTTTGGGGGAAAGAGTTT 720
Qy 1350 AAAAAAGAAATTTGAAATTTGCTTTCAGATATATTTAGGTACAAATGGAGTTTCTTTTCCCA 1409
Db 721 AAAAA--GAATTCAAATTCCTTTGAGATATTTAGGTACAAATGGAGTTTCTTTTCCCA 778
Qy 1410 AACGGGAAGAACACAGCACACCCC--GGCTTGGACCCATCGCAAGCTGCAATCGTGAACCTC 1468
Db 779 AACGGGAAGAACACAGCACACCCC--GGCTTGGACCCATCGCAAGCTGCAATCGTGAACCTC 838
Qy 1469 TTTGGTCCAGTGTGGG-----CAAGGGCTCAGCTCTCTGCCACAGAGTGCCCC 1520
Db 839 TTTGGGGGGCAATGGGGGGGCAAGGGGGTTCATCTCTTCTGCCACAGAAATGGCCCC 895

RESULT 7
BM809227 1083 bp mRNA linear EST 05-MAR-2002
LOCUS AGENCOURT_6582414 NIH_MGC_41 Homo sapiens cDNA clone IMAGE:5468221
5', mRNA sequence.
ACCESSION BM809227
VERSION BM809227.1 GI:19126050
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1083)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ruben Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Plate: LICM1971 row: h column: 14

High quality sequence stop: 656.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5468221"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NTH MGC 41"
/notes="Organ: skin; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GCCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 42.9%; Score 720.2; DB 4; Length 1083;
Best Local Similarity 91.7%; Pred. No. 4.3e-175;
Matches 853; Conservative 0; Mismatches 34; Indels 43; Gaps 7;

QY 663 TTGGCTTTGTGAGTGAAGCAAACTCTTGGAAATTCAGGGCATCACCCGGGAGAGTCAG 722
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QY 723 GGGACTAGAGTGAGTCCCTCCATGACGTGGCGGCCCGTGTACGGAGAGTAAAGG 782
DB 61 GGGACTAGAGTGAGTCCCTCCATGACGTGGCGGCCCGTGTACGGAGAGTAAAGG 120

QY 783 TCACCGTGAACATATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGAC 842
DB 121 TCACCGTGAACATATCCACCATACATTTTCAGAAAGCAAGGGTACAGGTGTCCCGTGGGAC 180

QY 843 AAAAGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACA 902
DB 181 AAAAGGGACACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACA 240

QY 903 AGGATGACAAAGACTGATTCGAGGAAAGAGGGGTGAAAGTGGAAACAGACTTTC 962
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QY 963 TCTCAAAACTCATCTTTCTCAATGTCTCTGAACATGACTATGGGAATTCACACTTGGTGG 1022
DB 301 TCTCAAAACTCATCTTTCTCAATGTCTCTGAACATGACTATGGGAATTCACACTTGGTGG 360

QY 1023 CCTCAAAAGAGTGGGACACCAATATGCGAGCATCATCTATTTT----- 1066
DB 361 CCTCAAAAGAGTGGGACACCAATATGCGAGCATCATCTATTTTGAAGTGAAGAACTACAG 420

QY 1067 -----GGTCCAGCGCGCTCAGCGAGTGCAGCAACGGCAGCTCGAGGA 1109
DB 421 CCCTGACCCCTTGGAAAGAGTTCAGCGCGCGTTCAGGAGGTGAGCAACGGCAGCTCGAGGA 480

QY 1110 GGGCAGGCTGGCTGTGGTGTGCTCTTCTGGTCTTGCACCTGTCTTCAAAATTTTGTAT 1169
DB 481 GGGCAGGCTGGCTGTGGTGTGCTCTTCTGGTCTTGCACCTGTCTTCAAAATTTTGTAT 540

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DB 541 GTGAGTGCACATTCCTCCACCCGGGAAAGGCTGCGGCCACACCCACCAACACAGC 600

QY 1230 AATGCAACACCGACAGCAACCAATTCAGATATATACAAATGAAATTAAGAAACACAGC 1289
DB 601 AATGCAACACCGACAGCAACCAATTCAGATATATACAAATGAAATTAAGAAACACAGC 660

QY 1290 CTCATGGGACAGAAATTTTGGAGGAGGGGAAACAAAGAAATATCTTTT-GGGGGGAAAGAGTTT 1348

DB 661 CTCATGGGACAGAAATTTGAGGGAGGGGAACAAAGAATACTTTTGGGGGGAAGAGTTT 720
QY 1349 TAAAAAGAAATTCAAAATTG-CCTTCAGATATTTAGGTACATGAGTTTCTTTTCC 1407
DB 721 TAAAAAGAAATTCAAAATTGCCCCCTTCGACATATTTAGGTACATGAGTTTCTTATT 780
QY 1408 CAAACGGGAAGAACACAGCA----CACCCGGCTTGGACCCCACTCAAGTCATCGTGA 1463
DB 781 CCAAAACGGGAAGAAACACAGCAACCCGGGCTTGGACCCCACTCGAAGTCATCGTGC 840
QY 1464 ACCTCTTTGTGGCAGTGTGG-CAAGGGCTCAGCC-TCTGTGCCACAGAGTGCCCCCA 1521
DB 841 ACCCTCTTGGTGGCAGTGTGGCCCAAGGGCTCAGCCCTTCTGTGCCACAGAAATGGCCCCA 900
QY 1522 --CGTGAACATTTCTGAGCTGGCCATCCC 1549
DB 901 ACGTGAACATTTCTGGAATGGGCCCATCC 930

RESULT 8
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LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406349
VERSION AY406349.1 GI:39762323
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 874)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 874)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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gene

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Best Local Similarity 89.1%; Pred. No. 2.3e-172;
Matches 779; Conservative 0; Mismatches 89; Indels 6; Gaps 1;

QY 301 GTGCACTATTGACAAACCGGTCACCCGGTGGCTTAAACCGCAGCACCATCTCTA 360
DB 1 GTGCACAAATTTGACAAACCGGTCACCCGGTGGCTTAAACCGCAGTACATCTCTA 60

QY 361 TGCTGGGAATGACAAGTGGTGCCTGGATCCTCGGTGGTCTTCTGAGCAACACCCCAAC 420
DB 61 TGCTGGGAATGACAAGTGGTGCCTGATAGTCTCTGTTGGTCTCTCTGATTAACCCAGC 120

QY 421 GCAGTACAGCATCGAGATCCAGAACGTTGATGACGAGGGCCCTTACACCTGCTC 480


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650  CCTGCATAGCAACTGGTAGACGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAAG 709
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660  CGGTTGGCTTTGTGAGTGAAGACGAA 685
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670  CGGTTGGCTTTGTGAGTGAAGACGAA 735
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RESULT 10
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LOCUS
DEFINITION   IMAGp971B1852 ; IMAGE:789137 5', mRNA sequence.
ACCESSION   CR736885
VERSION     CR736885.1 GI:51585450
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 673)
AUTHORS     Ebert,L., Heil,O., Hennig,S., Korn,B., Neubert,P., Partsch,E.,
            Peters,M., Radehof,U. and Schneider,D.
TITLE       I.M.A.G.E. cDNA Clone Collection
JOURNAL     Unpublished (2004)
COMMENT     Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Email: www.rzpd.de
            RZPD; IMAGp971B1852.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Contact: Inge Arlart
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 100
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAACGACTATGAC.

FEATURES             source
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Matches 571; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY  1005  GGAATACACTTGGTGGCTTCCACAGCTGGGGCCACCAATGCCAGCATCTAT 1064
DB  61    GGAATACACTTGGTGGCTTCCACAGCTGGGGCCACCAATGCCAGCATCTAT 120

QY  1065  TTGGTCCAGGCGCCCTCAGCGAGGTGAGCAACGGGACGCTCGAGGAGGCGAGCTGCGTCT 1124
DB  121  TTGGTCCAGGCGCCCTCAGCGAGGTGAGCAACGGGACGCTCGAGGAGGCGAGCTGCGTCT 180

QY  1125  GCGTCTGCCCTTCTGCTGTTCACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCC 1184
DB  181  GCGTCTGCCCTTCTGCTGTTCACCTGCTTCTCAAAATTTGATGTGAGTGCCACTTCC 240

QY  1185  CCACCCGGGAAGGTCGGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCGAC 1244
DB  241  CCACCCGGGAAGGTCGGGCCACCAACCAACCAACCAACCAACCAACCAACCAACCAACCGAC 300
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QY  1245  AGCAACCAATCAGATATATACAAATGAAATTAGAAGAAACACAGCCTCATGGGACAGAA 1304
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QY  1305  TTTGAGGAGGGGNAACAAAGAAATCTTTGGGGGAAAAAGAGTTTAAAAAAGAAATTCAA 1364
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QY  1365  AATTGCCTTCAGATATTTAGGTACAATGAGTTTCTTTTCCCAACGGGAAGAACACA 1424
DB  421  AATTGCCTTCAGATATTTAGGTACAATGAGTTTCTTTTCCCAACGGGAAGAACACA 480

QY  1425  GCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTCAAACTCTTTGGTGCCAGTGTGG 1484
DB  481  GCACACCCGGCTTGGACCCACTGCAAGCTGCATCGTCAAACTCTTTGGTGCCAGTGTGG 540

QY  1485  GCAAGGCTCAGCTCTCTGCCACAGAGTGGCCCGCAGTGCGGACATCTCTGGAGCTGGCC 1544
DB  541  GCAAGGCTCAGCTCTCTGCCACAGAGTGGCCCGCAGTGCGGACATCTCTGGAGCTGGCC 600

QY  1545  ATCCCAAAATCAATCAGTCCATAGAGACGAAACAGAAATGAGACCTTCGCGGCCCAAGCGTGG 1604
DB  601  ATCCCAAAATCAATCAGTCCATAGAGACGAAACAGAAATGAGACCTTCGCGGCCCAAGCGTGG 660

QY  1605  CGCTGCGGGCACT 1617
DB  661  CGCTGCGGGCACT 673

RESULT 11
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LOCUS
DEFINITION   AGENCOURT 7973225 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6166839
            5', mRNA sequence.
ACCESSION   BUI55617
VERSION     BUI55617.1 GI:22669149
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 856)
AUTHORS     NIH-MGC http://mgc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DRP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13527 row: m column: 16
            High quality sequence stop: 593.

FEATURES             source
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         /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
            Average insert size 2 kb. Library constructed by Life
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ORIGIN
Query Match      39.6%; Score 664.8; DB 5; Length 856;
Best Local Similarity 97.6%; Pred. No. 9.2e-161;
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Matches	728;	Conservative	0;	Mismatches	12;	Indels	6;	Gaps	5;
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Qy	274	CCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAACCGGGTACCCGGGTGGC	333						
Db	154	CCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGACAACCGGGTACCCGGGTGGC	213						
Qy	334	CTGGCTAAACCGCAGCACCCTCTATGCTGGGAATGACAAGTGGTGCCTGGATCTCTCG	393						
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Qy	394	CGTGTCTCTCTGAGCAACACCCAAACGACGATACGATCGAGATCCAGAAACGTCGATGT	453						
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Qy	514	GCTCCACCTCATTTGCAAGTATCTCCCAAATTTGTAGAGATTTCTTCAGATATCTCAT	573						
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Qy	574	TAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACTGGTAGACGAGCCTACCGT	633						
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Qy	928	AAAGAAAGGGGTGAAGTGGAAAAACA	953						
Db	814	AAAAAAGGGGTGGAAGGGGGAANA	839						

RESULT 12
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LOCUS
DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cdna clone
ACCESSION CS00N005YD20 5-PRIME, mRNA sequence.
VERSION AL533026.3 GI:45707932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1027)
AUTHORS Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 13, 2001 this sequence version replaced gi:31070858.
Contact: Genoscope

Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6387.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DN005DB10QPl&c=6387.f.
Location/Qualifiers
1.1027
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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

Query Match	38.4%;	Score 645;	DB 1;	Length 1027;
Best Local Similarity	86.8%;	Pred. No. 1.3e-155;		
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Db	222	CTCCAAAGCGTTGGCTTTGTGAGTGAAGCAAGTAATCTTGGAAATTCAGGCGATCACCC	281	
Qy	711	GGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGAGCTGGCGCCCGCTGGTAC	770	
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Qy	771	GGAGAGTAAAGGTACCGTGAACTATCCACATACATTTGAGAGCCAGGGTACAGGTG	830	
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Qy	915	-----	914	
Db	522	AAAGCTTCTCTCCCATGGTGACGAATGGTGTCAAAAACGGCCAGTGGGATCAATCAGCCT	581	
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Qy	1013	ACTTGGTGGCTCCAAAGAGCTGGGCCACCAATGCCAGCATCTGCTATTGTTGGTCCA	1072	

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Qy 1193 GAAAGGTCGCCGCCACCAACCAACCAACAACAAGCAATGGCAACACCGACAGAACCA 1252
Db 881 GAAAGGTCGCCGCCACCAACCAACCAACAACAAGCAATGGCAACACCGACAGAACCA 939
Qy 1253 ATCAGATATACAAATGAAATAGAGAAACACAGCTCATGGACAGAAATTTGAGGG 1312
Db 940 ATCAGATATACAAATGAAATAGAGAAACACAGCTCATGGACAGAAATTTGAGGG 999
Qy 1313 AGGGGAACAAAGATACTTTTGGGGGAAA 1341
Db 1000 AGGGG-ACAAAGATACTTTTGGGGGAAA 1027

RESULT 13
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LOCUS 603197479F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5277115 5',
mRNA sequence.
ACCESSION BI551784
VERSION BI551784.1 GI:154339096
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 732)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM11699 row: m column: 20
High quality sequence stop: 732.
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(gtgag); Oligo-dT primed using primer
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insert size 2.5 kb and normalized to 80T 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by M. Brownstein
(NIH/NHGRI, National Institutes of Health). Note: this
is a NIH_MGC Library."

FEATURES
source

RESULT 14
CN362539
LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
ACCESSION CN362539
VERSION CN362539.1 GI:47362473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 748)
AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Pang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
TITLE Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT Contact: Brandenberger R
Regenerative Medicine
Geron Corporation

Qy	718	GTACGGGACTACGAGTCCAGTGCCTCCAATGA	CGTGGCCCGCCCGTGGTACGGAGAGT	777
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Qy	838	GGGACAAAAGGGGACACTGCGAGTGTGAAGCCT	TCAGCAGTCCCGCTCAGCAGAAATTC	897
Db	605	GGGACAAAAGGGGACACTGCGAGTGTGAAGCCT	TCAGCAGTCCCGCTCAGCAGAAATTC	664
Qy	898	GTACAAGGATGACAAAAGACTGATTTGAAGGAA	---AGAAAAGGGGTGAAAGTGGAAAACAG	954
Db	665	GTACAAGGATGACAAAAGACTGATTTGAAGGAA	CAGAGGGGTGAACAGTTGGAAAACAG	724
Qy	955	ACCTTTCCTCTC	966	
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Search completed: October 30, 2005, 09:21:18
Job time : 6000 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 30, 2005, 06:59:01 ; Search time 308 Seconds
(without alignments)
8919.833 Million cell updates/sec

Title: US-10-017-084A-522

Perfect score: 1679

Sequence: 1 gttgtccttcagcaaac.....ataaaagagcaaaaaaa 1679

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1661.4	99.0	1693	4	US-09-700-397-2
2	1032	61.5	1032	4	US-09-700-397-1
3	939	55.9	939	4	US-09-700-397-5
4	343	20.4	1238	2	US-08-414-657D-3
5	343	20.4	1238	3	US-09-135-080-3
6	341.6	20.3	1195	4	US-09-976-594-403
7	340.6	20.3	924	2	US-08-414-657D-7
8	340.6	20.3	977	2	US-08-414-657D-1
9	340.6	20.3	977	3	US-09-135-080-1
10	340.6	20.3	1014	2	US-08-414-657D-5
11	340.6	20.3	1014	3	US-09-135-080-7
12	338.6	20.2	861	2	US-08-414-657D-9
13	338.6	20.2	912	2	US-08-414-657D-6
14	337.4	20.1	945	2	US-08-414-657D-8
15	333.8	19.9	861	2	US-08-414-657D-10
16	316.2	18.8	333	4	US-09-513-999C-23289
17	303.6	18.1	756	2	US-08-414-657D-17
18	301	17.9	309	4	US-09-621-976-3309
19	298.2	17.8	756	2	US-08-414-657D-18
20	281	16.7	1030	4	US-09-949-016-4587
21	193.6	11.5	352	4	US-09-513-999C-2775
22	174.4	10.4	182	4	US-09-621-976-967
23	146	8.7	200	4	US-09-513-999C-14430
24	105.6	6.3	913	4	US-09-774-528-410
25	100	6.0	219	2	US-08-414-657D-11
26	95.2	5.7	219	2	US-08-414-657D-12
27	87	5.2	438	4	US-09-621-976-8385

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29	77.8	4.6	177	2	US-08-414-657D-13	Sequence 13, Appl
30	77.8	4.6	177	2	US-08-414-657D-14	Sequence 14, Appl
c	76.8	4.6	601	4	US-09-949-016-163724	Sequence 163724, A
32	65.6	3.9	198	2	US-08-414-657D-15	Sequence 15, Appl
33	63.4	3.8	198	2	US-08-414-657D-16	Sequence 16, Appl
34	50.4	3.0	612	4	US-09-902-540-1357	Sequence 1357, Ap
35	50.2	3.0	240	1	US-08-628-417-6	Sequence 6, Appl
36	50.2	3.0	1039	4	US-09-902-540-1280	Sequence 1280, Ap
37	49.8	3.0	1048	4	US-09-489-847-38	Sequence 38, Appl
38	48.8	2.9	1813	3	US-09-071-224-3	Sequence 3, Appl
39	48.4	2.9	147	4	US-09-621-976-10383	Sequence 10383, A
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52	47.8	2.8	4121	4	US-09-601-537-9	Sequence 9, Appl
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54	47.6	2.8	2447	2	US-09-014-969-14	Sequence 14, Appl
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65	46.6	2.8	630	1	US-08-185-414E-1	Sequence 1, Appl
66	46.6	2.8	630	1	US-09-620-405B-465	Sequence 465, App
67	46.6	2.8	674	4	US-09-433-826B-465	Sequence 465, App
68	46.6	2.8	674	4	US-09-604-287A-465	Sequence 465, App
69	46.6	2.8	674	4	US-09-834-759-465	Sequence 465, App
70	46.6	2.8	674	4	US-09-590-751A-465	Sequence 465, App
71	46.6	2.8	674	4	US-09-551-621-465	Sequence 5, Appl
72	46.6	2.8	1411	3	US-08-964-127-5	Sequence 5, Appl
73	46.6	2.8	1411	3	US-09-496-692-5	Sequence 5, Appl
74	46.6	2.8	1411	3	US-10-000-273-5	Sequence 5, Appl
75	46.6	2.8	1411	3	US-09-370-838-151	Sequence 151, App
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77	46.6	2.8	3275	4	US-08-628-417-5	Sequence 5, Appl
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79	46.4	2.8	193	4	US-09-602-877A-95	Sequence 95, Appl
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82	46.4	2.8	1034	4	US-09-363-708-3	Sequence 3, Appl
83	46.4	2.8	2246	3	US-09-083-587-3	Sequence 3, Appl
84	46.4	2.8	2246	3	US-08-813-150-1	Sequence 1, Appl
85	46.4	2.8	2280	3	US-09-546-553-1	Sequence 1, Appl
86	46.4	2.8	2280	4	US-10-164-595-29	Sequence 29, Appl
87	46.4	2.8	3438	4	US-09-902-540-1318	Sequence 1318, Ap
88	46.2	2.8	614	4	US-09-363-970-4	Sequence 4, Appl
89	46.2	2.8	790	3	US-09-328-475C-50	Sequence 50, Appl
90	46.2	2.8	1024	4	US-09-873-737A-3	Sequence 3, Appl
91	46	2.7	4064	4	US-09-621-976-1322	Sequence 1322, Ap
92	45.8	2.7	249	4	US-09-621-976-16042	Sequence 16042, A
93	45.8	2.7	365	4	US-09-949-016-47248	Sequence 47248, A
94	45.8	2.7	601	4	FCT-US95-06406A-21	Sequence 21, Appl
c	45.8	2.7	903	5	US-09-443-041A-27	Sequence 27, Appl
96	45.8	2.7	1447	3	US-09-800-729-33	Sequence 33, Appl
97	45.8	2.7	2394	4	US-09-949-016-12049	Sequence 12049, A
98	45.8	2.7	5481	4	US-09-949-016-15589	Sequence 15589, A
c	45.8	2.7	5484	4	US-09-949-016-13123	Sequence 13123, A
100	45.8	2.7	12797	4		

101	45.8	2.7	96327	4	US-09-949-016-16541	Sequence 16541, A	c 174	44.6	2.7	396	4	US-09-970-966-33	Sequence 33, Appl
102	45.6	2.7	282	4	US-09-621-976-18648	Sequence 18648, A	175	44.6	2.7	601	4	US-09-949-016-204599	Sequence 204599,
c 103	45.4	2.7	260	2	US-08-520-678A-29	Sequence 29, Appl	176	44.6	2.7	601	4	US-09-949-016-204600	Sequence 204600,
c 104	45.4	2.7	260	3	US-08-897-126-29	Sequence 29, Appl	177	44.6	2.7	601	4	US-09-949-016-204601	Sequence 204601,
105	45.4	2.7	1098	3	US-09-248-335-35	Sequence 35, Appl	178	44.6	2.7	601	4	US-09-949-016-204602	Sequence 204602,
106	45.4	2.7	2146	4	US-10-003-332-3	Sequence 3, Appl	179	44.6	2.7	601	4	US-09-949-016-204603	Sequence 204603,
c 107	45.4	2.7	7218	1	US-08-232-463-14	Sequence 14, Appl	180	44.6	2.7	601	4	US-09-949-016-204604	Sequence 204604,
c 108	45.4	2.7	54246	4	US-09-949-016-16206	Sequence 16206, A	181	44.6	2.7	601	4	US-09-949-016-204605	Sequence 204605,
c 109	45.4	2.7	22452	4	US-09-949-016-12968	Sequence 12968, A	182	44.6	2.7	601	4	US-09-949-016-204606	Sequence 204606,
110	45.2	2.7	176	4	US-09-621-976-13903	Sequence 13903, A	183	44.6	2.7	601	4	US-09-949-016-204607	Sequence 204607,
111	45.2	2.7	359	4	US-09-621-976-16008	Sequence 16008, A	184	44.6	2.7	708	4	US-09-270-767-13081	Sequence 13081, A
112	45.2	2.7	359	4	US-09-621-976-16019	Sequence 16019, A	185	44.6	2.7	2184	3	US-08-955-918C-1	Sequence 1, Appl
113	45.2	2.7	362	4	US-09-621-976-16010	Sequence 16010, A	186	44.6	2.7	2184	3	US-08-697-766A-1	Sequence 1, Appl
c 114	45.2	2.7	396	4	US-09-640-173-33	Sequence 53, Appl	187	44.6	2.7	2527	4	US-09-244-805-29	Sequence 29, Appl
c 115	45.2	2.7	396	4	US-09-713-550-53	Sequence 53, Appl	188	44.6	2.7	2806	3	US-09-653-839-9	Sequence 9, Appl
c 116	45.2	2.7	396	4	US-09-825-294-53	Sequence 53, Appl	189	44.6	2.7	2806	4	US-10-202-619-9	Sequence 9, Appl
c 117	45.2	2.7	396	4	US-09-970-966-53	Sequence 53, Appl	190	44.6	2.7	87734	4	US-09-949-016-17521	Sequence 17521, A
c 118	45.2	2.7	537	4	US-09-720-201A-4	Sequence 4, Appl	191	44.6	2.7	118143	4	US-09-949-016-17196	Sequence 17196, A
c 119	45.2	2.7	644	4	US-09-720-201A-6	Sequence 6, Appl	192	44.4	2.6	127	4	US-09-621-976-13933	Sequence 13933, A
c 120	45.2	2.7	1091	4	US-09-328-965-1	Sequence 1, Appl	193	44.4	2.6	196	4	US-09-442-054A-42	Sequence 42, Appl
121	45.2	2.7	1273	4	US-09-270-767-14731	Sequence 14731, A	c 194	44.4	2.6	196	4	US-08-442-054A-42	Sequence 42, Appl
c 122	45.2	2.7	9589	1	US-07-925-695-1	Sequence 1, Appl	c 195	44.4	2.6	356	2	US-08-897-126-22	Sequence 22, Appl
c 123	45.2	2.7	9589	1	US-07-925-695-2	Sequence 2, Appl	c 196	44.4	2.6	356	2	US-08-897-126-22	Sequence 22, Appl
124	45	2.7	371	4	US-09-621-976-16048	Sequence 16048, A	c 197	44.4	2.6	582	4	US-09-787-292-3	Sequence 3, Appl
125	45	2.7	1459	4	US-09-537-654-3	Sequence 3, Appl	198	44.4	2.6	601	4	US-09-949-016-38491	Sequence 38491, A
126	45	2.7	1798	3	US-09-797-906-1	Sequence 1, Appl	199	44.4	2.6	601	4	US-09-949-016-48520	Sequence 48520, A
127	45	2.7	2010	1	US-07-864-475A-4	Sequence 4, Appl	200	44.4	2.6	601	4	US-09-949-016-170716	Sequence 170716,
c 128	45	2.7	2010	2	US-08-468-249A-4	Sequence 4, Appl	201	44.4	2.6	601	4	US-09-949-016-170759	Sequence 170759,
c 129	44.8	2.7	224	2	US-08-731-272A-26	Sequence 26, Appl	202	44.4	2.6	601	4	US-09-949-016-170802	Sequence 170802,
130	44.8	2.7	357	4	US-09-621-976-16058	Sequence 16058, A	203	44.4	2.6	601	4	US-09-949-016-170843	Sequence 170843,
131	44.8	2.7	554	4	US-09-696-169A-14	Sequence 14, Appl	204	44.4	2.6	1051	3	US-09-245-041-10	Sequence 10, Appl
132	44.8	2.7	601	4	US-09-949-016-38490	Sequence 38490, A	205	44.4	2.6	1051	4	US-09-358-055B-10	Sequence 10, Appl
133	44.8	2.7	601	4	US-09-943-016-170715	Sequence 170715, A	206	44.4	2.6	1051	4	US-09-893-238-10	Sequence 10, Appl
134	44.8	2.7	601	4	US-09-949-016-170758	Sequence 170758, A	207	44.4	2.6	1134	3	US-09-248-335-29	Sequence 29, Appl
135	44.8	2.7	601	4	US-09-949-016-170801	Sequence 170801, A	208	44.4	2.6	1141	4	US-09-800-729-78	Sequence 78, Appl
136	44.8	2.7	601	4	US-09-949-016-170842	Sequence 170842, A	209	44.4	2.6	2327	4	US-10-066-130-20	Sequence 20, Appl
137	44.8	2.7	601	4	US-09-949-016-182153	Sequence 182153, A	210	44.4	2.6	2674	4	US-10-066-130-19	Sequence 19, Appl
138	44.8	2.7	601	4	US-09-949-016-182154	Sequence 182154, A	211	44.4	2.6	2771	4	US-10-066-130-18	Sequence 18, Appl
139	44.8	2.7	1000	3	US-09-018-584A-34	Sequence 34, Appl	212	44.4	2.6	4456	3	US-09-095-443-1	Sequence 1, Appl
140	44.8	2.7	1000	4	US-09-199-542B-108	Sequence 108, App	213	44.4	2.6	5860	4	US-10-066-130-17	Sequence 17, Appl
141	44.8	2.7	1000	4	US-09-184-423-34	Sequence 34, Appl	c 214	44.4	2.6	9646	3	US-08-811-566-1	Sequence 1, Appl
142	44.8	2.7	1212	3	US-09-782-145-34	Sequence 34, Appl	c 215	44.4	2.6	9646	3	US-09-034-756-1	Sequence 1, Appl
c 143	44.8	2.7	1212	3	US-09-182-145-35	Sequence 35, Appl	c 216	44.4	2.6	12980	3	US-08-811-566-5	Sequence 5, Appl
144	44.8	2.7	1641	1	US-08-300-903A-8	Sequence 8, Appl	c 217	44.4	2.6	12980	3	US-09-034-756-5	Sequence 5, Appl
145	44.8	2.7	1641	4	US-08-988-157-8	Sequence 8, Appl	218	44.2	2.6	12980	3	US-09-621-976-18062	Sequence 18062, A
146	44.8	2.7	1641	4	US-10-385-072-8	Sequence 8, Appl	219	44.2	2.6	195	4	US-09-621-976-18062	Sequence 18062, A
147	44.8	2.7	1771	4	US-09-907-794A-158	Sequence 158, App	220	44.2	2.6	272	4	US-09-270-767-11902	Sequence 11902, A
148	44.8	2.7	1771	4	US-09-866-028-36	Sequence 36, Appl	221	44.2	2.6	318	4	US-09-621-976-10247	Sequence 10247, A
149	44.8	2.7	1771	4	US-09-905-135A-158	Sequence 158, App	222	44.2	2.6	1066	1	US-08-157-101A-4	Sequence 4, Appl
150	44.8	2.7	1771	4	US-09-902-775A-158	Sequence 158, App	223	44.2	2.6	1193	3	US-09-372-422A-23	Sequence 23, Appl
151	44.8	2.7	1771	4	US-09-906-700-158	Sequence 158, App	224	44.2	2.6	1801	4	US-09-709-103-3	Sequence 3, Appl
152	44.8	2.7	1771	4	US-09-944-457-36	Sequence 36, Appl	225	44.2	2.6	1801	4	US-09-439-410A-3	Sequence 3, Appl
153	44.8	2.7	1771	4	US-09-903-603A-158	Sequence 158, App	226	44.2	2.6	1925	4	US-09-148-545-128	Sequence 128, App
154	44.8	2.7	1771	4	US-09-904-920A-158	Sequence 158, App	227	44.2	2.6	2202	3	US-09-465-558-59	Sequence 59, Appl
155	44.8	2.7	1771	4	US-09-909-064-158	Sequence 158, App	c 228	44.2	2.6	670689	4	US-09-949-016-12505	Sequence 12505, A
156	44.8	2.7	1771	4	US-09-905-381A-158	Sequence 158, App	c 229	44.2	2.6	670689	4	US-09-949-016-14207	Sequence 14207, A
157	44.8	2.7	1771	4	US-09-906-618-158	Sequence 158, App	230	44	2.6	123	4	US-09-621-976-12330	Sequence 12330, A
158	44.8	2.7	6671	1	US-08-280-443-1	Sequence 1, Appl	231	44	2.6	186	4	US-09-531-999C-18897	Sequence 18897, A
159	44.8	2.7	6671	1	US-08-457-459-1	Sequence 1, Appl	232	44	2.6	240	4	US-09-621-976-1324	Sequence 1324, Ap
160	44.8	2.7	6671	1	US-08-555-678-1	Sequence 1, Appl	233	44	2.6	601	4	US-09-949-016-204598	Sequence 204598,
161	44.8	2.7	6671	5	PCT-US95-02275-1	Sequence 1, Appl	234	44	2.6	882	4	US-09-311-021-107	Sequence 107, App
162	44.8	2.7	36075	4	US-09-949-016-16571	Sequence 16571, A	235	44	2.6	1342	4	US-09-489-847-89	Sequence 89, Appl
163	44.8	2.7	36075	4	US-09-949-016-16572	Sequence 16572, A	236	44	2.6	1882	3	US-09-370-253-1	Sequence 1, Appl
164	44.8	2.7	3625	4	US-09-949-016-12788	Sequence 12788, A	237	44	2.6	1921	2	US-08-557-128-11	Sequence 11, Appl
165	44.8	2.7	37133	4	US-09-949-016-16569	Sequence 16569, A	238	44	2.6	2269	3	US-09-394-645-1	Sequence 1, Appl
166	44.8	2.7	37133	4	US-09-949-016-16570	Sequence 16570, A	239	44	2.6	2269	3	US-09-243-560B-1	Sequence 1, Appl
167	44.8	2.7	74881	4	US-09-949-016-15545	Sequence 15545, A	240	44	2.6	6409	4	US-09-967-908A-1	Sequence 1, Appl
168	44.8	2.7	74914	4	US-09-949-016-12286	Sequence 12286, A	241	44	2.6	6409	4	US-10-159-151-1	Sequence 1, Appl
c 169	44.8	2.7	133358	4	US-09-949-016-15964	Sequence 15964, A	242	43.8	2.6	1248	4	US-09-489-847-101	Sequence 101, App
c 170	44.8	2.7	133360	4	US-09-949-016-12651	Sequence 12651, A	243	43.8	2.6	1636	4	US-09-578-194-6	Sequence 6, Appl
c 171	44.6	2.7	396	4	US-09-640-173-33	Sequence 33, Appl	244	43.8	2.6	1781	4	US-09-818-512-1	Sequence 1, Appl
c 172	44.6	2.7	396	4	US-09-713-550-33	Sequence 33, Appl	245	43.8	2.6	1872	4	US-09-801-052-1	Sequence 1, Appl
c 173	44.6	2.7	396	4	US-09-825-294-33	Sequence 33, Appl	246	43.8	2.6	1872	4	US-10-020-121-1	Sequence 1, Appl

247	43.8	2.6	2082	2	US-08-785-310A-2	Sequence 2, Appli	320	42.6	2.5	558	4	US-09-043-861-3	Sequence 3, Appli
248	43.8	2.6	2262	4	US-09-311-021-171	Sequence 171, App	321	42.6	2.5	601	4	US-09-949-016-161729	Sequence 161729,
c 249	43.8	2.6	31842	4	US-09-949-016-15123	Sequence 15123, A	322	42.6	2.5	2218	4	US-09-016-434-1157	Sequence 1157, Ap
250	43.6	2.6	121	3	US-09-297-535-20	Sequence 20, Appl	323	42.6	2.5	2218	4	US-10-329-668-7	Sequence 7, Appli
251	43.6	2.6	246	4	US-09-621-976-13617	Sequence 13617, A	324	42.6	2.5	2276	4	US-09-205-258-183	Sequence 183, App
c 252	43.6	2.6	396	4	US-09-640-173-16	Sequence 16, Appl	325	42.6	2.5	3334	4	US-09-668-119-2	Sequence 2, Appli
c 253	43.6	2.6	396	4	US-09-713-550-16	Sequence 16, Appl	326	42.6	2.5	5096	4	US-09-949-016-15105	Sequence 15105, A
c 254	43.6	2.6	396	4	US-09-825-294-16	Sequence 16, Appl	c 327	42.6	2.5	17836	4	US-09-949-016-16167	Sequence 16167, A
c 255	43.6	2.6	396	4	US-09-970-966-16	Sequence 16, Appl	c 328	42.6	2.5	39690	4	US-09-949-016-16167	Sequence 15079, A
256	43.6	2.6	550	4	US-09-010-147B-5	Sequence 5, Appli	329	42.4	2.5	194	4	US-09-621-976-9596	Sequence 9596, Ap
257	43.6	2.6	1507	3	US-09-453-323-1	Sequence 1, Appli	330	42.4	2.5	331	4	US-09-621-976-16100	Sequence 16100, A
258	43.6	2.6	2407	3	US-09-370-807-7	Sequence 7, Appli	331	42.4	2.5	1445	3	US-09-814-951A-1	Sequence 1, Appli
259	43.6	2.6	2407	3	US-09-921-259-7	Sequence 7, Appli	332	42.4	2.5	1474	3	US-08-821-994-64	Sequence 64, Appli
260	43.6	2.6	2634	3	US-09-463-238-3	Sequence 3, Appli	333	42.4	2.5	4548	4	US-09-571-479C-5	Sequence 5, Appli
261	43.6	2.6	18026	4	US-09-949-016-13309	Sequence 13309, A	c 334	42.4	2.5	44848	4	US-09-435-739-42	Sequence 42, Appl
262	43.6	2.6	41736	4	US-09-949-016-17091	Sequence 17091, A	c 335	42.4	2.5	44848	4	US-09-988-113-42	Sequence 42, Appl
263	43.4	2.6	552	4	US-09-461-325-111	Sequence 111, App	336	42.4	2.5	61664	4	US-09-949-016-13308	Sequence 13308, A
264	43.4	2.6	552	4	US-10-012-542-111	Sequence 111, App	c 337	42.4	2.5	113379	4	US-09-949-016-17561	Sequence 17561, A
265	43.4	2.6	552	4	US-10-115-123-111	Sequence 111, App	c 338	42.4	2.5	113379	4	US-09-949-016-17562	Sequence 17562, A
266	43.4	2.6	1296	4	US-09-461-325-29	Sequence 29, Appl	339	42.2	2.5	105	4	US-09-621-976-13820	Sequence 13820, A
267	43.4	2.6	1296	4	US-10-012-542-29	Sequence 29, Appl	340	42.2	2.5	298	4	US-09-621-976-3871	Sequence 3871, Ap
268	43.4	2.6	1296	4	US-10-115-123-29	Sequence 29, Appl	c 341	42.2	2.5	370	4	US-09-513-999C-497	Sequence 497, App
269	43.4	2.6	2625	4	US-09-270-767-10080	Sequence 10080, A	c 342	42.2	2.5	370	4	US-09-471-276-222	Sequence 222, App
270	43.4	2.6	2665	3	US-08-971-089-5	Sequence 5, Appli	c 343	42.2	2.5	601	4	US-09-949-016-168357	Sequence 168357,
271	43.4	2.6	3715	4	US-09-234-245-1	Sequence 1, Appli	c 344	42.2	2.5	601	4	US-09-949-016-168358	Sequence 168358,
272	43.4	2.6	49931	4	US-09-949-016-13727	Sequence 13727, A	345	42.2	2.5	601	4	US-09-949-016-193087	Sequence 193087,
273	43.4	2.6	49931	4	US-09-949-016-13728	Sequence 13728, A	346	42.2	2.5	601	4	US-09-949-016-193088	Sequence 193088,
274	43.4	2.6	49931	4	US-09-949-016-13729	Sequence 13729, A	347	42.2	2.5	601	4	US-09-949-016-193180	Sequence 193180,
275	43.4	2.6	225127	4	US-09-949-016-16480	Sequence 16480, A	348	42.2	2.5	601	4	US-09-949-016-193181	Sequence 193181,
c 276	43.2	2.6	196	4	US-09-644-460-40	Sequence 40, Appl	349	42.2	2.5	601	4	US-09-949-016-193273	Sequence 193273,
277	43.2	2.6	358	4	US-09-621-976-927	Sequence 927, App	350	42.2	2.5	601	4	US-09-949-016-193274	Sequence 193274,
278	43.2	2.6	601	4	US-09-949-016-48516	Sequence 48516, A	351	42.2	2.5	601	4	US-09-949-016-193366	Sequence 193366,
279	43.2	2.6	601	4	US-09-949-016-48521	Sequence 48521, A	352	42.2	2.5	601	4	US-09-949-016-193367	Sequence 193367,
c 280	43.2	2.6	601	4	US-09-949-016-186016	Sequence 186016,	353	42.2	2.5	746	3	US-09-013-810-1	Sequence 1, Appli
281	43.2	2.6	763	4	US-09-743-207-3	Sequence 3, Appli	354	42.2	2.5	990	4	US-09-800-729-79	Sequence 79, Appl
282	43.2	2.6	812	3	US-09-091-097-7	Sequence 7, Appli	355	42.2	2.5	1023	1	US-08-252-566B-16	Sequence 16, Appl
283	43.2	2.6	931	4	US-09-482-273-31	Sequence 31, Appl	356	42.2	2.5	1114	3	US-09-152-060-41	Sequence 41, Appl
284	43.2	2.6	2434	4	US-09-489-847-67	Sequence 67, Appl	357	42.2	2.5	1277	4	US-09-270-767-25838	Sequence 25838, A
c 285	43.2	2.6	4419	4	US-09-620-312D-187	Sequence 187, App	358	42.2	2.5	1454	3	US-09-372-422A-19	Sequence 19, Appl
286	43.2	2.6	16600	4	US-09-949-016-13332	Sequence 13332, A	359	42.2	2.5	3116	4	US-09-311-021-187	Sequence 187, App
287	43.2	2.6	16600	4	US-09-949-016-13333	Sequence 13333, A	360	42.2	2.5	3556	4	US-09-270-767-10439	Sequence 10439, A
c 288	43.2	2.6	16600	4	US-09-949-016-13334	Sequence 13334, A	361	42.2	2.5	86213	4	US-09-949-016-17240	Sequence 17240, A
289	43.2	2.6	90724	4	US-09-949-016-13175	Sequence 13175, A	362	42.2	2.5	86213	4	US-09-949-016-17241	Sequence 17241, A
c 290	43.2	2.6	96922	4	US-09-949-016-16601	Sequence 16601, A	363	42.2	2.5	86213	4	US-09-949-016-17242	Sequence 17242, A
291	43	2.6	144	1	US-08-702-344-26	Sequence 26, Appl	364	42.2	2.5	86213	4	US-09-949-016-17243	Sequence 17243, A
292	43	2.6	166	4	US-09-621-976-18390	Sequence 18390, A	365	42.2	2.5	118868	4	US-09-949-016-15746	Sequence 15746, A
293	43	2.6	347	4	US-09-621-976-16026	Sequence 16026, A	c 366	42.2	2.5	225127	4	US-09-949-016-16480	Sequence 16480, A
294	43	2.6	635	1	US-08-455-633A-35	Sequence 35, Appl	c 367	42.2	2.5	678533	4	US-09-949-016-14577	Sequence 14577, A
295	43	2.6	635	1	US-08-416-336-5	Sequence 35, Appli	c 368	42.2	2.5	563	4	US-09-949-016-14578	Sequence 14578, A
296	43	2.6	635	5	PCT-US94-05354-35	Sequence 35, Appl	369	42	2.5	639	4	US-09-621-976-19183	Sequence 19183, A
297	43	2.6	711	4	US-09-270-767-9609	Sequence 9609, Ap	370	42	2.5	639	4	US-09-482-273-49	Sequence 49, Appl
c 298	43	2.6	711	4	US-09-270-767-9609	Sequence 9609, Ap	371	42	2.5	1013	4	US-09-322-409-6	Sequence 6, Appli
c 299	43	2.6	1545	4	US-09-559-023-1	Sequence 1, Appli	c 372	42	2.5	1013	4	US-09-322-409-6	Sequence 8, Appli
300	43	2.6	1733	3	US-09-073-569-1	Sequence 1, Appli	373	42	2.5	1013	4	US-09-451-527-8	Sequence 6, Appli
301	43	2.6	2091	3	US-09-813-818-1	Sequence 1, Appli	c 374	42	2.5	1013	4	US-09-451-527-8	Sequence 8, Appli
302	43	2.6	2091	3	US-10-199-333-1	Sequence 1, Appli	375	42	2.5	1582	3	US-08-545-196B-10	Sequence 10, Appl
303	43	2.6	2091	3	US-10-199-333-1	Sequence 1, Appli	376	42	2.5	1582	3	US-08-545-196B-12	Sequence 12, Appl
304	43	2.6	2186	3	US-09-360-545-66	Sequence 66, Appl	377	42	2.5	1736	3	US-09-182-816-22	Sequence 22, Appl
305	43	2.6	2233	1	US-08-496-631-1	Sequence 1, Appli	c 378	42	2.5	1736	3	US-09-182-816-22	Sequence 24, Appl
306	43	2.6	4086	4	US-09-703-705-1801	Sequence 1801, Ap	379	42	2.5	1736	3	US-09-471-528-22	Sequence 22, Appl
307	43	2.6	4086	4	US-09-736-457-1801	Sequence 1801, Ap	c 380	42	2.5	1736	3	US-09-471-528-22	Sequence 24, Appl
308	43	2.6	4086	4	US-09-671-325-15981	Sequence 15981, Ap	381	42	2.5	1736	3	US-09-634-530-22	Sequence 22, Appl
309	43	2.6	12521	4	US-09-949-016-15988	Sequence 15988, A	c 382	42	2.5	1736	3	US-09-634-530-24	Sequence 24, Appl
310	42.8	2.5	177	4	US-09-621-976-1047	Sequence 1047, Ap	383	42	2.5	1927	3	US-09-336-536-66	Sequence 66, Appl
311	42.8	2.5	194	4	US-09-621-976-801	Sequence 801, App	384	42	2.5	5749	4	US-09-949-016-15441	Sequence 15441, A
312	42.8	2.5	601	4	US-09-949-016-48517	Sequence 48517, A	385	42	2.5	5749	4	US-09-949-016-15442	Sequence 15442, A
313	42.8	2.5	601	4	US-09-949-016-48518	Sequence 48518, A	386	42	2.5	13184	4	US-09-949-016-16573	Sequence 16573, A
314	42.8	2.5	601	4	US-09-949-016-48519	Sequence 48519, A	387	42	2.5	101349	4	US-09-949-016-17433	Sequence 17433, A
315	42.8	2.5	1378	3	US-09-149-476-208	Sequence 208, App	388	41.8	2.5	130	4	US-09-621-976-12892	Sequence 12892, A
316	42.8	2.5	2271	4	US-09-205-258-243	Sequence 243, App	c 389	41.8	2.5	227	2	US-08-520-678A-28	Sequence 28, Appl
317	42.8	2.5	2323	3	US-09-149-476-24	Sequence 24, Appl	c 390	41.8	2.5	227	3	US-08-520-678A-28	Sequence 28, Appl
c 318	42.8	2.5	209210	4	US-09-949-016-15094	Sequence 15094, A	391	41.8	2.5	250	4	US-09-621-976-18893	Sequence 18893, A
319	42.6	2.5	323	4	US-09-621-976-10374	Sequence 10374, A	392	41.8	2.5	601	4	US-09-949-016-184918	Sequence 184918,

333	41.8	2.5	601	4	US-09-949-016-185073	Sequence 185073,	466	41.4	2.5	3410	4	US-09-688-489-110	Sequence 110, App
334	41.8	2.5	601	4	US-09-949-016-201490	Sequence 201490,	467	41.4	2.5	3410	4	US-09-679-426-110	Sequence 110, App
335	41.8	2.5	1008	4	US-09-780-641-1	Sequence 1, Appli	468	41.4	2.5	3410	4	US-09-759-143-110	Sequence 110, App
336	41.8	2.5	1192	4	US-09-439-554-23	Sequence 23, Appl	469	41.4	2.5	3410	4	US-09-651-236-110	Sequence 110, App
337	41.8	2.5	1361	4	US-09-489-847-64	Sequence 64, Appl	c 470	41.4	2.5	123778	4	US-09-949-016-12191	Sequence 12191, A
338	41.8	2.5	1461	3	US-08-722-126A-4	Sequence 4, Appli	c 471	41.4	2.5	123778	4	US-09-949-016-17075	Sequence 17075, A
339	41.8	2.5	1461	5	PCT-US95-04258-4	Sequence 4, Appli	472	41.4	2.5	123438	4	US-09-949-016-14349	Sequence 14349, A
340	41.8	2.5	1558	4	US-08-467-607-2	Sequence 2, Appli	473	41.4	2.5	132438	4	US-09-949-016-14350	Sequence 14350, A
401	41.8	2.5	1558	2	US-08-469-362-2	Sequence 2, Appli	474	41.4	2.5	151089	4	US-09-949-016-14348	Sequence 14348, A
402	41.8	2.5	1558	2	US-08-850-392-2	Sequence 1, Appli	c 475	41.4	2.5	151295	4	US-09-949-016-14568	Sequence 14568, A
403	41.8	2.5	1662	4	US-09-668-037A-13	Sequence 13, Appl	c 476	41.4	2.5	151295	4	US-09-949-016-14569	Sequence 14569, A
c 404	41.8	2.5	15666	4	US-09-949-016-15929	Sequence 15929, A	c 477	41.4	2.5	151295	4	US-09-949-016-14570	Sequence 14570, A
c 405	41.8	2.5	149543	4	US-09-949-016-15947	Sequence 15947, A	c 478	41.4	2.5	151295	4	US-09-949-016-14571	Sequence 14571, A
406	41.8	2.5	194937	4	US-09-949-016-17032	Sequence 17032, A	c 479	41.4	2.5	151295	4	US-09-949-016-14572	Sequence 14572, A
407	41.8	2.5	194937	4	US-09-949-016-17033	Sequence 17033, A	c 480	41.4	2.5	154605	4	US-09-949-016-11894	Sequence 11894, A
408	41.6	2.5	117	1	US-08-702-344-3	Sequence 3, Appli	481	41.4	2.5	237241	4	US-09-949-016-16101	Sequence 16101, A
409	41.6	2.5	164	4	US-09-621-976-16692	Sequence 16692, A	c 482	41.4	2.5	333753	4	US-09-949-016-14573	Sequence 14573, A
410	41.6	2.5	231	4	US-09-621-976-16317	Sequence 16317, A	c 483	41.4	2.5	333753	4	US-09-949-016-14574	Sequence 14574, A
411	41.6	2.5	242	4	US-09-621-976-16320	Sequence 16320, A	484	41.4	2.5	524032	4	US-09-949-016-16928	Sequence 16928, A
412	41.6	2.5	242	4	US-09-621-976-16324	Sequence 16324, A	485	41.4	2.5	524032	4	US-09-949-016-16929	Sequence 16929, A
c 413	41.6	2.5	253	2	US-08-520-678A-25	Sequence 25, Appl	486	41.4	2.5	524032	4	US-09-949-016-16930	Sequence 16930, A
c 414	41.6	2.5	253	3	US-08-897-126-25	Sequence 25, Appl	487	41.4	2.5	524032	4	US-09-949-016-16931	Sequence 16931, A
c 415	41.6	2.5	270	2	US-08-520-678A-30	Sequence 30, Appl	488	41.4	2.5	529885	4	US-09-949-016-14340	Sequence 14340, A
c 416	41.6	2.5	270	3	US-08-897-126-30	Sequence 30, Appl	489	41.4	2.5	529885	4	US-09-949-016-14341	Sequence 14341, A
c 417	41.6	2.5	601	4	US-09-949-016-37086	Sequence 37086, A	490	41.4	2.5	529885	4	US-09-949-016-14342	Sequence 14342, A
c 418	41.6	2.5	601	4	US-09-949-016-37087	Sequence 37087, A	491	41.4	2.5	529885	4	US-09-949-016-14343	Sequence 14343, A
c 419	41.6	2.5	601	4	US-09-949-016-161063	Sequence 161063, A	492	41.4	2.5	529885	4	US-09-949-016-14344	Sequence 14344, A
c 420	41.6	2.5	601	4	US-09-949-016-161064	Sequence 161064, A	493	41.4	2.5	529885	4	US-09-949-016-14345	Sequence 14345, A
421	41.6	2.5	664	4	US-09-904-615-66	Sequence 66, Appl	494	41.4	2.5	529885	4	US-09-949-016-14346	Sequence 14346, A
422	41.6	2.5	949	4	US-09-489-847-35	Sequence 35, Appl	495	41.4	2.5	529885	4	US-09-949-016-14347	Sequence 14347, A
423	41.6	2.5	1297	4	US-09-800-729-80	Sequence 80, Appl	c 496	41.4	2.5	818128	4	US-09-949-016-14546	Sequence 14546, A
424	41.6	2.5	1308	4	US-10-151-832-1	Sequence 1, Appli	c 497	41.4	2.5	818128	4	US-09-949-016-14547	Sequence 14547, A
425	41.6	2.5	1414	4	US-09-501-115-5	Sequence 5, Appli	c 498	41.4	2.5	818128	4	US-09-949-016-14548	Sequence 14548, A
426	41.6	2.5	1746	4	US-09-485-529-57	Sequence 57, Appl	c 499	41.4	2.5	818128	4	US-09-949-016-14549	Sequence 14549, A
427	41.6	2.5	1768	4	US-09-485-529-13	Sequence 13, Appl	c 500	41.4	2.5	818128	4	US-09-949-016-14550	Sequence 14550, A
428	41.6	2.5	1817	1	US-08-473-981A-5	Sequence 5, Appli	c 501	41.4	2.5	818128	4	US-09-949-016-14551	Sequence 14551, A
429	41.6	2.5	1817	2	US-08-474-087-5	Sequence 5, Appli	c 502	41.4	2.5	818128	4	US-09-949-016-14552	Sequence 14552, A
430	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	c 503	41.4	2.5	818128	4	US-09-949-016-14553	Sequence 14553, A
c 431	41.6	2.5	2671	6	5168051-9	Patent No. 5168051	c 504	41.4	2.5	818128	4	US-09-949-016-14554	Sequence 14554, A
c 432	41.6	2.5	18877	4	US-09-674-311-1	Sequence 1, Appli	c 505	41.4	2.5	818128	4	US-09-949-016-14555	Sequence 14555, A
c 433	41.6	2.5	18107	4	US-09-949-016-13674	Sequence 13674, A	c 506	41.4	2.5	818128	4	US-09-949-016-14556	Sequence 14556, A
434	41.6	2.5	20721	4	US-09-949-016-16257	Sequence 16257, A	c 507	41.4	2.5	818128	4	US-09-949-016-14557	Sequence 14557, A
435	41.6	2.5	26684	4	US-09-949-016-15109	Sequence 15109, A	c 508	41.4	2.5	818128	4	US-09-949-016-14558	Sequence 14558, A
436	41.6	2.5	26684	4	US-09-949-016-15110	Sequence 15110, A	c 509	41.4	2.5	818128	4	US-09-949-016-14559	Sequence 14559, A
437	41.6	2.5	26684	4	US-09-949-016-17409	Sequence 17409, A	c 510	41.4	2.5	818128	4	US-09-949-016-14560	Sequence 14560, A
438	41.6	2.5	26684	4	US-09-949-016-17410	Sequence 17410, A	c 511	41.4	2.5	818128	4	US-09-949-016-14561	Sequence 14561, A
439	41.6	2.5	46823	4	US-09-949-016-12723	Sequence 12723, A	c 512	41.4	2.5	818128	4	US-09-949-016-14562	Sequence 14562, A
440	41.6	2.5	46940	4	US-09-949-016-16252	Sequence 16252, A	c 513	41.4	2.5	818128	4	US-09-949-016-14564	Sequence 14564, A
441	41.6	2.5	53332	4	US-09-801-861-3	Sequence 3, Appli	c 514	41.4	2.5	818128	4	US-09-949-016-14565	Sequence 14565, A
c 442	41.6	2.5	53332	4	US-10-224-562-3	Sequence 3, Appli	c 515	41.4	2.5	818128	4	US-09-949-016-14566	Sequence 14566, A
c 443	41.6	2.5	151088	4	US-09-949-016-16240	Sequence 16240, A	c 516	41.4	2.5	818128	4	US-09-949-016-14567	Sequence 14567, A
444	41.4	2.5	111	3	US-09-297-535-23	Sequence 23, Appl	517	41.2	2.5	250	4	US-09-621-976-11744	Sequence 11744, A
445	41.4	2.5	111	4	US-09-621-976-14677	Sequence 14677, A	518	41.2	2.5	250	4	US-09-621-976-17371	Sequence 17371, A
446	41.4	2.5	351	4	US-09-621-976-15134	Sequence 15134, A	519	41.2	2.5	333	3	US-09-018-584A-27	Sequence 27, Appl
447	41.4	2.5	510	4	US-09-248-796A-13735	Sequence 13735, A	520	41.2	2.5	333	4	US-09-784-423-27	Sequence 27, Appl
c 448	41.4	2.5	601	4	US-09-949-016-149677	Sequence 149677, A	c 521	41.2	2.5	396	4	US-09-640-173-10	Sequence 10, Appl
c 449	41.4	2.5	601	4	US-09-949-016-186673	Sequence 186673, A	c 522	41.2	2.5	396	4	US-09-713-550-10	Sequence 10, Appl
c 450	41.4	2.5	601	4	US-09-949-016-186674	Sequence 186674, A	c 523	41.2	2.5	396	4	US-09-825-294-10	Sequence 10, Appl
c 451	41.4	2.5	601	4	US-09-949-016-186675	Sequence 186675, A	c 524	41.2	2.5	396	4	US-09-970-966-10	Sequence 10, Appl
c 452	41.4	2.5	844	4	US-09-690-942-3	Sequence 3, Appli	c 525	41.2	2.5	1335	4	US-09-270-767-13052	Sequence 13052, A
453	41.4	2.5	890	4	US-09-621-976-2725	Sequence 2725, Ap	526	41.2	2.5	1508	3	US-09-039-046-1	Sequence 1, Appli
454	41.4	2.5	2239	3	US-09-196-390-1	Sequence 1, Appli	527	41.2	2.5	1544	4	US-09-187-999-14	Sequence 14, Appli
455	41.4	2.5	2239	4	US-09-952-677-1	Sequence 1, Appli	528	41.2	2.5	1835	3	US-09-485-549-1	Sequence 1, Appli
456	41.4	2.5	3410	3	US-09-020-956-110	Sequence 110, App	529	41.2	2.5	2599	4	US-09-949-016-4676	Sequence 4676, Ap
457	41.4	2.5	3410	3	US-09-030-607-110	Sequence 110, App	530	41.2	2.5	2633	4	US-09-023-655-90	Sequence 90, App
458	41.4	2.5	3410	3	US-09-439-313-110	Sequence 110, App	531	41.2	2.5	2852	3	US-09-027-137-2	Sequence 2, Appli
459	41.4	2.5	3410	3	US-09-352-616A-110	Sequence 110, App	532	41.2	2.5	2852	3	US-09-344-441-2	Sequence 2, Appli
460	41.4	2.5	3410	3	US-09-602-877A-100	Sequence 100, App	533	41.2	2.5	5807	4	US-09-976-594-245	Sequence 245, App
461	41.4	2.5	3410	3	US-09-232-149A-110	Sequence 110, App	c 534	41.2	2.5	23222	4	US-09-949-016-15949	Sequence 15949, A
462	41.4	2.5	3410	4	US-09-159-812-110	Sequence 110, App	c 535	41.2	2.5	25922	4	US-09-949-016-11874	Sequence 11874, A
463	41.4	2.5	3410	4	US-09-636-215-110	Sequence 110, App	536	41.2	2.5	72604	3	US-09-268-992-7	Sequence 7, Appli
464	41.4	2.5	3410	4	US-09-685-166A-110	Sequence 110, App	537	41.2	2.5	72604	3	US-09-657-474-7	Sequence 7, Appli
465	41.4	2.5	3410	4	US-09-115-453-110	Sequence 110, App	c 538	41.2	2.5	87780	4	US-09-949-016-17011	Sequence 17011, A

C 539	41.2	2.5	90428	4	US-09-949-016-12564	Sequence 13564, A	612	40.6	2.4	2718	4	US-09-667-135-1	Sequence 1, Appli
C 540	41.2	2.5	145928	4	US-09-949-016-15444	Sequence 15444, A	613	40.6	2.4	2989	6	5378464-1	Patent No. 5378464
C 541	41.2	2.5	251672	4	US-09-949-016-17296	Sequence 17296, A	614	40.6	2.4	2989	6	5378464-1	Patent No. 5378464
C 542	41.2	2.5	251682	4	US-09-949-016-11973	Sequence 11973, A	615	40.6	2.4	8353	3	US-08-611-587-1	Sequence 1, Appli
C 543	41	2.4	163	4	US-09-621-976-9608	Sequence 9608, Ap	C 616	40.6	2.4	8638	4	US-10-029-907-6	Sequence 6, Appli
C 544	41	2.4	257	2	US-08-520-678A-24	Sequence 24, Appl	C 617	40.6	2.4	8643	4	US-10-029-907-6	Sequence 6, Appli
C 545	41	2.4	257	3	US-08-897-126-24	Sequence 24, Appl	C 618	40.6	2.4	13146	2	US-08-724-354D-3	Sequence 3, Appli
C 546	41	2.4	601	4	US-09-949-016-193621	Sequence 193621,	C 619	40.6	2.4	13146	2	US-09-270-984A-3	Sequence 3, Appli
C 547	41	2.4	985	4	US-09-322-409-25	Sequence 25, Appl	620	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 17806, A
C 548	41	2.4	985	4	US-09-322-409-27	Sequence 27, Appl	621	40.6	2.4	15108	4	US-09-949-016-11786	Sequence 17806, A
C 549	41	2.4	985	4	US-09-451-527-25	Sequence 25, Appl	622	40.6	2.4	15661	4	US-09-949-016-13161	Sequence 13161, A
C 550	41	2.4	985	4	US-09-451-527-27	Sequence 27, Appl	623	40.6	2.4	15661	4	US-09-949-016-13161	Sequence 13161, A
C 551	41	2.4	1406	4	US-10-000-489-81	Sequence 81, Appl	624	40.6	2.4	29321	4	US-09-949-016-14258	Sequence 14258, A
C 552	41	2.4	1493	1	US-08-340-820-24	Sequence 24, Appl	625	40.6	2.4	50000	3	US-09-146-053-3	Sequence 3, Appli
C 553	41	2.4	1493	1	US-08-593-535-24	Sequence 24, Appl	626	40.6	2.4	55298	4	US-09-491-356C-1	Sequence 1, Appli
C 554	41	2.4	2311	4	US-09-800-729-66	Sequence 66, Appl	627	40.6	2.4	82178	4	US-09-949-016-13394	Sequence 13394, A
C 555	41	2.4	2311	4	US-09-720-317A-19	Sequence 19, Appl	628	40.6	2.4	83708	4	US-09-949-016-17207	Sequence 17207, A
C 556	41	2.4	2320	3	US-09-202-904A-13	Sequence 13, Appl	C 629	40.6	2.4	87752	4	US-09-949-016-16807	Sequence 16807, A
C 557	41	2.4	2406	4	US-09-594-506-37	Sequence 37, Appl	C 630	40.6	2.4	175265	4	US-09-949-016-16089	Sequence 16089, A
C 558	41	2.4	6200	3	US-09-439-923-1	Sequence 1, Appli	631	40.6	2.4	268449	4	US-09-949-016-17244	Sequence 17244, A
C 559	41	2.4	6200	4	US-09-711-202A-1	Sequence 1, Appli	632	40.6	2.4	268449	4	US-09-949-016-17244	Sequence 17244, A
C 560	41	2.4	6200	4	US-09-711-205A-1	Sequence 1, Appli	633	40.4	2.4	390416	4	US-09-949-016-16923	Sequence 16923, A
C 561	41	2.4	7286	3	US-09-331-581-3	Sequence 3, Appli	C 634	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 562	41	2.4	7938	3	US-09-331-581-14	Sequence 14, Appl	635	40.4	2.4	124	6	5185243-1	Patent No. 5185243
C 563	41	2.4	54033	4	US-09-949-016-12091	Sequence 12091, A	636	40.4	2.4	190	4	US-09-621-976-16784	Sequence 16784, A
C 564	41	2.4	54033	4	US-09-949-016-14325	Sequence 14325, A	637	40.4	2.4	326	4	US-09-621-976-16034	Sequence 16034, A
C 565	41	2.4	68283	4	US-09-949-016-12261	Sequence 12261, A	638	40.4	2.4	334	4	US-09-621-976-16044	Sequence 16044, A
C 566	41	2.4	113701	4	US-09-949-016-13214	Sequence 13214, A	639	40.4	2.4	335	4	US-09-621-976-16061	Sequence 16061, A
C 567	41	2.4	124264	4	US-09-949-016-16396	Sequence 16396, A	640	40.4	2.4	336	4	US-09-621-976-16013	Sequence 16013, A
C 568	41	2.4	128175	4	US-09-949-016-16268	Sequence 16268, A	641	40.4	2.4	336	4	US-09-621-976-16051	Sequence 16051, A
C 569	40.8	2.4	84	4	US-09-621-976-14571	Sequence 14571, A	C 642	40.4	2.4	389	4	US-09-621-976-16041	Sequence 16041, A
C 570	40.8	2.4	102	4	US-09-621-976-14804	Sequence 14804, A	643	40.4	2.4	593	4	US-09-513-999C-420	Sequence 420, App
C 571	40.8	2.4	179	4	US-09-621-976-9575	Sequence 9575, Ap	644	40.4	2.4	601	4	US-09-904-615-59	Sequence 59, Appl
C 572	40.8	2.4	188	4	US-09-621-976-10364	Sequence 10364, A	645	40.4	2.4	1052	4	US-09-489-016-189988	Sequence 189988,
C 573	40.8	2.4	273	4	US-09-809-545A-31	Sequence 31, Appl	646	40.4	2.4	1052	4	US-09-489-016-189988	Sequence 189988,
C 574	40.8	2.4	283	4	US-09-621-976-16989	Sequence 16989, A	647	40.4	2.4	1503	4	US-09-907-794A-220	Sequence 220, App
C 575	40.8	2.4	1129	3	US-09-227-357-40	Sequence 40, Appl	648	40.4	2.4	1503	4	US-09-905-125A-220	Sequence 220, App
C 576	40.8	2.4	1214	4	US-09-780-717-28	Sequence 28, Appl	649	40.4	2.4	1503	4	US-09-902-775A-220	Sequence 220, App
C 577	40.8	2.4	1683	3	US-09-347-803-11	Sequence 11, Appl	650	40.4	2.4	1503	4	US-09-906-700-220	Sequence 220, App
C 578	40.8	2.4	2488	4	US-09-816-093-1	Sequence 1, Appli	651	40.4	2.4	1503	4	US-09-903-603A-220	Sequence 220, App
C 579	40.8	2.4	3124	3	US-09-734-030-1	Sequence 1, Appli	652	40.4	2.4	1503	4	US-09-904-920A-220	Sequence 220, App
C 580	40.8	2.4	3124	4	US-10-153-921-1	Sequence 1, Appli	653	40.4	2.4	1503	4	US-09-909-064-220	Sequence 220, App
C 581	40.8	2.4	3124	4	US-10-669-689-1	Sequence 1, Appli	654	40.4	2.4	1503	4	US-09-905-381A-220	Sequence 220, App
C 582	40.8	2.4	15722	4	US-09-949-016-16709	Sequence 16709, A	655	40.4	2.4	1503	4	US-09-906-618-220	Sequence 220, App
C 583	40.8	2.4	61124	4	US-09-949-016-11914	Sequence 11914, A	656	40.4	2.4	1512	2	US-08-909-965C-8	Sequence 8, Appli
C 584	40.8	2.4	61140	4	US-09-949-016-15771	Sequence 15771, A	657	40.4	2.4	1542	4	US-09-205-258-123	Sequence 123, App
C 585	40.8	2.4	65744	4	US-09-949-016-12591	Sequence 12591, A	658	40.4	2.4	1685	4	US-09-907-794A-83	Sequence 83, Appl
C 586	40.8	2.4	65745	4	US-09-949-016-13871	Sequence 13871, A	659	40.4	2.4	1685	4	US-09-905-125A-83	Sequence 83, Appl
C 587	40.8	2.4	76269	4	US-09-949-016-14603	Sequence 14603, A	660	40.4	2.4	1685	4	US-09-902-775A-83	Sequence 83, Appl
C 588	40.8	2.4	100836	4	US-09-949-016-12871	Sequence 12871, A	661	40.4	2.4	1685	4	US-09-906-700-83	Sequence 83, Appl
C 589	40.8	2.4	100837	4	US-09-949-016-17063	Sequence 17063, A	662	40.4	2.4	1685	4	US-09-903-603A-83	Sequence 83, Appl
C 590	40.8	2.4	321022	4	US-09-949-016-17063	Sequence 17063, A	663	40.4	2.4	1685	4	US-09-904-920A-83	Sequence 83, Appl
C 591	40.8	2.4	321022	4	US-09-949-016-11852	Sequence 11852, A	664	40.4	2.4	1685	4	US-09-909-064-83	Sequence 83, Appl
C 592	40.8	2.4	1684976	4	US-09-949-016-14166	Sequence 14166, A	665	40.4	2.4	1685	4	US-09-905-381A-83	Sequence 83, Appl
C 593	40.8	2.4	1684976	4	US-08-916-421B-1	Sequence 1, Appli	666	40.4	2.4	1685	4	US-09-906-618-83	Sequence 83, Appl
C 594	40.6	2.4	147	4	US-09-621-976-8551	Sequence 8551, Ap	667	40.4	2.4	1718	4	US-09-778-510-5	Sequence 5, Appli
C 595	40.6	2.4	189	4	US-09-621-976-14761	Sequence 14761, A	668	40.4	2.4	1820	4	US-09-778-510-1	Sequence 1, Appli
C 596	40.6	2.4	376	2	US-08-623-906A-18	Sequence 18, Appl	669	40.4	2.4	2233	1	US-08-257-073-4	Sequence 4, Appli
C 597	40.6	2.4	601	4	US-09-949-016-47249	Sequence 47249, A	670	40.4	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli
C 598	40.6	2.4	601	4	US-09-949-016-47327	Sequence 47327, A	671	40.4	2.4	3200	1	US-08-444-405-1	Sequence 1, Appli
C 599	40.6	2.4	601	4	US-09-949-016-57131	Sequence 57131, A	672	40.4	2.4	192700	4	US-09-949-016-11820	Sequence 11820, A
C 600	40.6	2.4	601	4	US-09-949-016-57132	Sequence 57132, A	673	40.4	2.4	192704	4	US-09-949-016-17182	Sequence 17182, A
C 601	40.6	2.4	601	4	US-09-949-016-57133	Sequence 57133, A	C 674	40.4	2.4	202001	4	US-09-734-674-3	Sequence 3, Appli
C 602	40.6	2.4	601	4	US-09-949-016-88560	Sequence 88560, A	C 675	40.4	2.4	422592	4	US-09-949-016-14182	Sequence 14182, A
C 603	40.6	2.4	601	4	US-09-949-016-88565	Sequence 88565, A	676	40.2	2.4	454	2	US-08-623-906A-6	Sequence 6, Appli
C 604	40.6	2.4	601	4	US-09-949-016-193622	Sequence 193622,	677	40.2	2.4	572	3	US-09-342-653-5	Sequence 5, Appli
C 605	40.6	2.4	601	4	US-09-949-016-193623	Sequence 193623,	678	40.2	2.4	601	4	US-09-949-016-17855	Sequence 17855, A
C 606	40.6	2.4	601	4	US-09-949-016-193624	Sequence 193624,	679	40.2	2.4	601	4	US-09-949-016-41735	Sequence 41735, A
C 607	40.6	2.4	795	4	US-09-270-767-14068	Sequence 14068, A	680	40.2	2.4	601	4	US-09-949-016-56224	Sequence 56224, A
C 608	40.6	2.4	1147	1	US-08-665-716-1	Sequence 1, Appli	C 681	40.2	2.4	601	4	US-09-949-016-84943	Sequence 84943, A
C 609	40.6	2.4	1198	3	US-09-248-335-27	Sequence 27, Appl	682	40.2	2.4	601	4	US-09-949-016-162251	Sequence 162251,
C 610	40.6	2.4	1878	3	US-09-465-558-39	Sequence 39, Appl	683	40.2	2.4	601	4	US-09-949-016-162252	Sequence 162252,
C 611	40.6	2.4	2458	3	US-08-611-587-6	Sequence 6, Appli	C 684	40.2	2.4	601	4	US-09-949-016-204750	Sequence 204750,

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688	40.2	2.4	958	3	US-09-135-988-5	Sequence 5, Appli	761	39.8	2.4	588	4	US-09-205-258-64	Sequence 64, Appli
689	40.2	2.4	958	3	US-09-277-716-5	Sequence 5, Appli	762	39.8	2.4	601	4	US-09-949-016-29142	Sequence 29142, A
690	40.2	2.4	958	3	US-08-597-274A-5	Sequence 5, Appli	763	39.8	2.4	601	4	US-09-949-016-29143	Sequence 29143, A
691	40.2	2.4	958	3	US-08-908-909-5	Sequence 5, Appli	764	39.8	2.4	601	4	US-09-949-016-29144	Sequence 29144, A
692	40.2	2.4	958	3	US-09-609-161B-5	Sequence 5, Appli	765	39.8	2.4	601	4	US-09-949-016-29145	Sequence 29145, A
693	40.2	2.4	958	3	US-08-990-103-5	Sequence 5, Appli	766	39.8	2.4	601	4	US-09-949-016-41097	Sequence 41097, A
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696	40.2	2.4	958	4	US-10-126-798-5	Sequence 5, Appli	769	39.8	2.4	601	4	US-09-949-016-41100	Sequence 41100, A
697	40.2	2.4	958	4	US-10-126-777-5	Sequence 5, Appli	770	39.8	2.4	601	4	US-09-949-016-161232	Sequence 161232, A
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700	40.2	2.4	1359	3	US-09-387-574-11	Sequence 11, Appli	773	39.8	2.4	1046	1	US-08-361-467B-4	Sequence 4, Appli
701	40.2	2.4	1359	3	US-09-668-096-11	Sequence 11, Appli	774	39.8	2.4	1046	1	US-08-484-332C-4	Sequence 4, Appli
702	40.2	2.4	1606	4	US-09-820-004-1	Sequence 1, Appli	775	39.8	2.4	1172	1	US-07-945-288-9	Sequence 9, Appli
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704	40.2	2.4	2065	2	US-08-968-751-1	Sequence 1, Appli	777	39.8	2.4	1172	1	US-08-461-809-9	Sequence 9, Appli
705	40.2	2.4	5506	4	US-09-976-534-530	Sequence 530, App	778	39.8	2.4	1172	1	US-08-461-441-9	Sequence 9, Appli
706	40.2	2.4	5083	4	US-09-949-016-17600	Sequence 17600, A	779	39.8	2.4	1172	5	PCT-US93-08518-9	Sequence 9, Appli
c 707	40.2	2.4	53769	4	US-09-949-016-17527	Sequence 17527, A	780	39.8	2.4	1602	1	US-08-530-950-3	Sequence 3, Appli
c 708	40.2	2.4	86639	4	US-09-949-016-17397	Sequence 17397, A	781	39.8	2.4	1602	3	US-08-888-429A-3	Sequence 3, Appli
c 709	40.2	2.4	89240	4	US-09-949-016-16279	Sequence 16279, A	782	39.8	2.4	1602	3	US-09-149-879-3	Sequence 3, Appli
710	40.2	2.4	89844	4	US-09-949-016-12346	Sequence 12346, A	783	39.8	2.4	1602	4	US-09-057-009-3	Sequence 3, Appli
711	40.2	2.4	89844	4	US-09-949-016-13656	Sequence 13656, A	784	39.8	2.4	1602	4	US-09-593-653-3	Sequence 3, Appli
c 712	40.2	2.4	93398	4	US-09-949-016-14167	Sequence 14167, A	785	39.8	2.4	1692	4	US-09-821-803A-5	Sequence 5, Appli
c 713	40.2	2.4	144158	4	US-09-949-016-11755	Sequence 11755, A	786	39.8	2.4	1725	4	US-09-668-097A-21	Sequence 21, Appli
c 714	40.2	2.4	144158	4	US-09-949-016-12936	Sequence 12936, A	787	39.8	2.4	2239	4	US-10-380-105-7	Sequence 7, Appli
c 715	40.2	2.4	256287	4	US-09-949-016-14608	Sequence 14608, A	788	39.8	2.4	4860	4	US-09-949-016-296	Sequence 296, App
716	40	2.4	92	4	US-09-621-976-13620	Sequence 13620, A	789	39.8	2.4	5173	1	US-08-242-677-1	Sequence 1, Appli
717	40	2.4	146	4	US-09-621-976-8550	Sequence 8550, Ap	790	39.8	2.4	10502	4	US-09-949-016-16708	Sequence 16708, A
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720	40	2.4	289	2	US-08-911-020-3	Sequence 3, Appli	c 793	39.8	2.4	19557	5	PCT-US92-06300-1	Sequence 1, Appli
721	40	2.4	293	4	US-09-621-976-16965	Sequence 16965, A	794	39.8	2.4	25175	4	US-09-949-016-16247	Sequence 16247, A
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725	40	2.4	601	4	US-09-949-016-40845	Sequence 40845, A	c 798	39.8	2.4	36159	4	US-10-135-687-3	Sequence 3, Appli
726	40	2.4	601	4	US-09-949-016-40846	Sequence 40846, A	799	39.8	2.4	38772	4	US-09-949-016-12382	Sequence 12382, A
727	40	2.4	1578	3	US-09-416-050A-1	Sequence 1, Appli	800	39.8	2.4	38772	4	US-09-949-016-12729	Sequence 12729, A
728	40	2.4	1578	3	US-09-664-800-1	Sequence 1, Appli	c 801	39.8	2.4	83178	4	US-09-949-016-14606	Sequence 14606, A
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731	40	2.4	2065	3	US-09-370-473-5	Sequence 5, Appli	c 804	39.8	2.4	260247	4	US-09-949-016-13358	Sequence 13358, A
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734	40	2.4	6243	2	US-09-056-075-1	Sequence 1, Appli	807	39.6	2.4	339	4	US-09-621-976-16015	Sequence 16015, A
735	40	2.4	7224	4	US-08-486-049-1	Sequence 1, Appli	c 808	39.6	2.4	516	3	US-09-018-584A-24	Sequence 24, Appli
736	40	2.4	8100	4	US-09-554-337-4	Sequence 4, Appli	c 809	39.6	2.4	516	4	US-09-784-423-24	Sequence 24, Appli
737	40	2.4	15538	4	US-09-949-016-13046	Sequence 1, Appli	c 810	39.6	2.4	593	3	US-09-385-982-262	Sequence 262, App
c 738	40	2.4	28555	4	US-09-949-016-12778	Sequence 13046, A	811	39.6	2.4	601	4	US-09-949-016-160808	Sequence 160808, A
c 739	40	2.4	35064	4	US-09-949-016-13196	Sequence 12778, A	812	39.6	2.4	633	4	US-09-270-767-6288	Sequence 6288, Ap
c 740	40	2.4	35065	4	US-09-949-016-13196	Sequence 13196, A	813	39.6	2.4	633	4	US-09-270-767-21570	Sequence 21570, A
c 741	40	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	814	39.6	2.4	711	4	US-09-621-976-17854	Sequence 17854, A
c 742	40	2.4	43323	4	US-09-949-016-16142	Sequence 16142, A	815	39.6	2.4	796	1	US-08-104-073-2	Sequence 2, Appli
c 743	40	2.4	137046	4	US-09-949-016-12427	Sequence 12427, A	816	39.6	2.4	1210	3	US-09-443-041A-29	Sequence 29, Appli
c 744	40	2.4	137048	4	US-09-949-016-13438	Sequence 13438, A	817	39.6	2.4	1332	2	US-09-057-762-1	Sequence 1, Appli
c 745	40	2.4	462589	4	US-09-949-016-12900	Sequence 12900, A	818	39.6	2.4	1332	3	US-08-326-119A-1	Sequence 1, Appli
c 746	40	2.4	476044	4	US-09-949-016-12412	Sequence 12412, A	819	39.6	2.4	1559	4	US-09-489-847-42	Sequence 42, Appli
747	40	2.4	786431	4	US-09-751-389-3	Sequence 3, Appli	820	39.6	2.4	1740	4	US-09-709-103-45	Sequence 45, Appli
748	39.8	2.4	92	4	US-09-621-976-14689	Sequence 14689, A	821	39.6	2.4	1740	4	US-09-439-410A-45	Sequence 45, Appli
749	39.8	2.4	97	4	US-09-621-976-12430	Sequence 12430, A	822	39.6	2.4	2445	4	US-09-949-016-781	Sequence 781, App
750	39.8	2.4	98	1	US-08-088-658-42	Sequence 42, Appli	823	39.6	2.4	2539	4	US-10-144-198-21	Sequence 21, Appli
751	39.8	2.4	98	2	US-08-471-907A-42	Sequence 42, Appli	824	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
752	39.8	2.4	98	4	US-09-621-976-12160	Sequence 12160, A	825	39.6	2.4	2550	6	5258287-23	Patent No. 5258287
753	39.8	2.4	98	4	US-09-621-976-15091	Sequence 15091, A	826	39.6	2.4	3366	4	US-09-596-141C-6	Sequence 6, Appli
754	39.8	2.4	159	4	US-09-621-976-17448	Sequence 17448, A	827	39.6	2.4	3366	4	US-09-595-526C-6	Sequence 6, Appli
755	39.8	2.4	179	4	US-09-621-976-18054	Sequence 18054, A	828	39.6	2.4	4239	4	US-09-815-048-1	Sequence 1, Appli
c 756	39.8	2.4	200	3	US-09-014-416-64	Sequence 64, Appli	829	39.6	2.4	10442	4	US-09-596-141C-1	Sequence 1, Appli
757	39.8	2.4	329	4	US-09-621-976-16012	Sequence 16012, A	830	39.6	2.4	10442	4	US-09-595-526C-1	Sequence 1, Appli

831	39.6	2.4	10474	4	US-09-596-141C-7	Sequence 7, Appli	904	39.2	2.3	3080	4	US-09-865-364-25	Sequence 25, Appli
832	39.6	2.4	10474	4	US-09-596-141C-9	Sequence 9, Appli	c 905	39.2	2.3	5852	1	US-07-867-106-2	Sequence 2, Appli
833	39.6	2.4	10474	4	US-09-595-526C-7	Sequence 7, Appli	c 906	39.2	2.3	6370	3	US-09-306-595C-2	Sequence 2, Appli
834	39.6	2.4	10474	4	US-09-595-536C-9	Sequence 9, Appli	c 907	39.2	2.3	6370	4	US-09-925-388-2	Sequence 2, Appli
835	39.6	2.4	16595	3	US-09-146-053-7	Sequence 7, Appli	c 908	39.2	2.3	16549	4	US-09-949-016-16456	Sequence 16456, A
836	39.6	2.4	21193	4	US-09-949-016-17215	Sequence 17215, A	c 909	39.2	2.3	44453	3	US-09-146-053-5	Sequence 5, Appli
837	39.6	2.4	80246	3	US-09-078-294-3	Sequence 4, Appli	c 910	39.2	2.3	46698	4	US-09-949-016-17323	Sequence 17323, A
838	39.6	2.4	80595	3	US-09-078-294-3	Sequence 3, Appli	c 911	39.2	2.3	54382	4	US-09-949-016-12139	Sequence 12139, A
839	39.6	2.4	85369	4	US-09-949-016-12171	Sequence 12171, A	c 912	39.2	2.3	61932	4	US-09-949-016-15338	Sequence 15338, A
840	39.6	2.4	117001	4	US-09-949-016-15684	Sequence 15684, A	c 913	39.2	2.3	61922	4	US-09-949-016-11772	Sequence 11772, A
841	39.6	2.4	250958	4	US-09-949-016-16061	Sequence 16061, A	c 914	39.2	2.3	68580	4	US-09-949-016-15844	Sequence 15844, A
842	39.6	2.4	312474	4	US-09-949-016-17434	Sequence 17434, A	c 915	39.2	2.3	73519	4	US-09-949-016-16344	Sequence 16344, A
843	39.4	2.3	169	4	US-09-621-976-11249	Sequence 11249, A	c 916	39.2	2.3	105919	4	US-09-949-016-11769	Sequence 11769, A
844	39.4	2.3	196	4	US-09-270-767-23094	Sequence 23094, A	c 917	39.2	2.3	112219	4	US-09-949-016-12453	Sequence 12453, A
845	39.4	2.3	601	4	US-09-949-016-120672	Sequence 120672, A	c 918	39.2	2.3	112222	4	US-09-949-016-14324	Sequence 14324, A
846	39.4	2.3	624	4	US-09-949-016-175160	Sequence 175160, A	c 919	39.2	2.3	113186	4	US-09-949-016-17512	Sequence 17512, A
847	39.4	2.3	624	4	US-09-270-767-13424	Sequence 13424, A	c 920	39.2	2.3	113701	4	US-09-949-016-13214	Sequence 13214, A
848	39.4	2.3	647	4	US-09-495-050A-54	Sequence 54, Appli	c 921	39.2	2.3	158841	4	US-09-949-016-16192	Sequence 16192, A
849	39.4	2.3	1509	3	US-09-149-476-179	Sequence 179, App	c 922	39.2	2.3	187595	4	US-09-949-016-15546	Sequence 15546, A
850	39.4	2.3	12703	4	US-09-949-016-16685	Sequence 16685, A	c 923	39.2	2.3	260286	4	US-09-949-016-17037	Sequence 17037, A
851	39.4	2.3	19601	4	US-09-949-016-15629	Sequence 15629, A	c 924	39.2	2.3	260293	4	US-09-949-016-12106	Sequence 12106, A
852	39.4	2.3	24645	4	US-09-949-016-14062	Sequence 14062, A	c 925	39.2	2.3	392000	4	US-10-027-983-11	Sequence 11, Appli
853	39.4	2.3	25659	4	US-09-949-016-15052	Sequence 15052, A	c 926	39	2.3	127	3	US-09-014-416-59	Sequence 59, Appli
854	39.4	2.3	29927	4	US-09-949-016-11814	Sequence 11814, A	c 927	39	2.3	176	3	US-09-014-416-60	Sequence 60, Appli
855	39.4	2.3	29927	4	US-09-949-016-11814	Sequence 11814, A	c 928	39	2.3	183	3	US-09-014-416-60	Sequence 60, Appli
856	39.4	2.3	29927	4	US-09-949-016-17474	Sequence 17474, A	c 929	39	2.3	185	4	US-09-621-976-16779	Sequence 16779, A
857	39.4	2.3	31111	4	US-09-949-016-15628	Sequence 15628, A	c 930	39	2.3	204	4	US-09-621-976-1323	Sequence 1323, Ap
858	39.4	2.3	34372	4	US-09-949-016-13098	Sequence 13098, A	c 931	39	2.3	266	4	US-09-621-976-16813	Sequence 16813, A
859	39.4	2.3	34875	4	US-09-949-016-13099	Sequence 13099, A	c 932	39	2.3	299	4	US-09-621-976-16226	Sequence 16226, A
860	39.4	2.3	37802	4	US-09-949-016-12639	Sequence 12639, A	c 933	39	2.3	321	2	US-08-520-678A-23	Sequence 23, Appli
861	39.4	2.3	44393	4	US-09-949-016-14944	Sequence 14944, A	c 934	39	2.3	332	4	US-09-621-976-16031	Sequence 6031, A
862	39.4	2.3	44393	4	US-09-949-016-14945	Sequence 14945, A	c 935	39	2.3	348	2	US-08-623-906A-14	Sequence 14, Appli
863	39.4	2.3	44393	4	US-09-949-016-14946	Sequence 14946, A	c 936	39	2.3	536	1	US-08-341-568-1	Sequence 1, Appli
864	39.4	2.3	44393	4	US-09-949-016-16911	Sequence 16911, A	c 937	39	2.3	536	2	US-08-911-020-1	Sequence 1, Appli
865	39.4	2.3	55841	4	US-09-949-016-16602	Sequence 16602, A	c 938	39	2.3	599	3	US-09-328-111-147	Sequence 147, App
866	39.4	2.3	64788	4	US-09-949-001-37	Sequence 37, Appli	c 939	39	2.3	601	4	US-09-949-016-19754	Sequence 19754, A
867	39.4	2.3	83851	4	US-09-949-016-13847	Sequence 13847, A	c 940	39	2.3	601	4	US-09-949-016-43955	Sequence 43955, A
868	39.4	2.3	86936	4	US-09-949-016-17314	Sequence 17314, A	c 941	39	2.3	601	4	US-09-949-016-71483	Sequence 71483, A
869	39.4	2.3	94877	4	US-09-949-016-16114	Sequence 16114, A	c 942	39	2.3	601	4	US-09-949-016-80449	Sequence 80449, A
870	39.4	2.3	116592	4	US-09-818-512-3	Sequence 11809, A	c 943	39	2.3	601	4	US-09-949-016-80451	Sequence 80451, A
871	39.4	2.3	137949	4	US-09-949-016-12196	Sequence 12196, A	c 944	39	2.3	601	4	US-09-949-016-81973	Sequence 81973, A
872	39.4	2.3	137956	4	US-09-949-016-17260	Sequence 17260, A	c 945	39	2.3	601	4	US-09-949-016-152093	Sequence 152093, A
873	39.4	2.3	236341	4	US-09-949-016-13978	Sequence 13978, A	c 946	39	2.3	601	4	US-09-949-016-152166	Sequence 152166, A
874	39.4	2.3	253345	4	US-09-949-016-12656	Sequence 12656, A	c 947	39	2.3	601	4	US-09-949-016-152239	Sequence 152239, A
875	39.4	2.3	253364	4	US-09-949-016-13639	Sequence 13639, A	c 948	39	2.3	601	4	US-09-949-016-152312	Sequence 152312, A
876	39.4	2.3	253364	4	US-09-949-016-13639	Sequence 13639, A	c 949	39	2.3	601	4	US-09-949-016-159398	Sequence 159398, A
877	39.2	2.3	85	4	US-09-621-976-13395	Sequence 13395, A	c 950	39	2.3	601	4	US-09-949-016-159471	Sequence 159471, A
878	39.2	2.3	85	4	US-09-621-976-14949	Sequence 14949, A	c 951	39	2.3	601	4	US-09-949-016-159544	Sequence 159544, A
879	39.2	2.3	89	4	US-09-621-976-14974	Sequence 14974, A	c 952	39	2.3	601	4	US-09-949-016-159617	Sequence 159617, A
880	39.2	2.3	89	4	US-09-621-976-14974	Sequence 14974, A	c 953	39	2.3	601	4	US-09-949-016-160807	Sequence 160807, A
881	39.2	2.3	91	4	US-09-621-976-12161	Sequence 12161, A	c 954	39	2.3	601	4	US-09-949-016-161983	Sequence 161983, A
882	39.2	2.3	208	1	US-08-686-878A-37	Sequence 37, Appli	c 955	39	2.3	1069	3	US-09-372-422A-7	Sequence 7, Appli
883	39.2	2.3	208	3	US-09-175-928-37	Sequence 37, Appli	c 956	39	2.3	1133	4	US-09-916-204-1	Sequence 1, Appli
884	39.2	2.3	271	4	US-09-621-976-10380	Sequence 10380, A	c 957	39	2.3	1133	4	US-10-282-048-1	Sequence 1, Appli
885	39.2	2.3	505	4	US-09-621-976-15639	Sequence 15639, A	c 958	39	2.3	1249	4	US-09-461-325-128	Sequence 128, App
886	39.2	2.3	601	4	US-09-949-016-126414	Sequence 126414, A	c 959	39	2.3	1249	4	US-10-012-542-128	Sequence 128, App
887	39.2	2.3	601	4	US-09-949-016-126417	Sequence 126417, A	c 960	39	2.3	1249	4	US-10-012-542-93	Sequence 93, Appli
888	39.2	2.3	601	4	US-09-949-016-145250	Sequence 145250, A	c 961	39	2.3	1260	4	US-10-115-123-93	Sequence 93, Appli
889	39.2	2.3	601	4	US-09-949-016-145251	Sequence 145251, A	c 962	39	2.3	1260	4	US-09-248-796A-928	Sequence 928, App
890	39.2	2.3	601	4	US-09-949-016-159061	Sequence 159061, A	c 963	39	2.3	1798	2	US-08-557-128-12	Sequence 12, Appli
891	39.2	2.3	756	4	US-09-949-016-159061	Sequence 93, Appli	c 964	39	2.3	2378	3	US-08-802-805D-20	Sequence 20, Appli
892	39.2	2.3	803	3	US-09-270-767-28941	Sequence 28941, A	c 965	39	2.3	2378	4	US-08-860-370-1	Sequence 1, Appli
893	39.2	2.3	960	3	US-09-248-335-57	Sequence 57, Appli	c 966	39	2.3	2485	4	US-09-889-463A-9	Sequence 9, Appli
894	39.2	2.3	1476	4	US-09-248-796A-5437	Sequence 5437, Ap	c 967	39	2.3	2744	3	US-09-071-101-1	Sequence 1, Appli
895	39.2	2.3	1700	2	US-08-897-340-4	Sequence 4, Appli	c 968	39	2.3	2744	3	US-09-369-618-1	Sequence 1, Appli
896	39.2	2.3	1700	3	US-08-252-329-4	Sequence 4, Appli	c 969	39	2.3	2744	3	US-09-369-617-1	Sequence 1, Appli
897	39.2	2.3	2045	3	US-09-152-060-22	Sequence 22, Appli	c 970	39	2.3	3450	4	US-09-902-540-9001	Sequence 9001, Ap
898	39.2	2.3	2291	4	US-09-220-132-114	Sequence 114, App	c 971	39	2.3	3527	2	US-08-909-965C-7	Sequence 7, Appli
899	39.2	2.3	2291	4	US-09-814-915A-95	Sequence 95, Appli	c 972	39	2.3	7305	4	US-09-902-540-961	Sequence 961, App
900	39.2	2.3	3080	3	US-09-095-041A-25	Sequence 25, Appli	c 973	39	2.3				
901	39.2	2.3	3080	3	US-09-245-281-25	Sequence 25, Appli	c 974	39	2.3				
902	39.2	2.3	3080	3	US-09-207-359B-25	Sequence 25, Appli	c 975	39	2.3				
903	39.2	2.3	3080	4	US-09-340-620A-25	Sequence 25, Appli	c 976	39	2.3				

c 977	39	2.3	7989	4	US-09-539-601-10	Sequence 10, Appl	1050	38.8	2.3	225	4	US-09-248-796A-10883	Sequence 10883, A
c 978	39	2.3	8001	4	US-09-539-601-7	Sequence 7, Appl	1051	38.8	2.3	259	4	US-09-621-976-16294	Sequence 16294, A
c 979	39	2.3	8001	4	US-09-539-601-16	Sequence 16, Appl	1052	38.8	2.3	371	4	US-09-621-976-16294	Sequence 16294, A
c 980	39	2.3	8001	4	US-09-539-601-22	Sequence 22, Appl	c1053	38.8	2.3	599	4	US-09-270-767-13708	Sequence 13708, A
c 981	39	2.3	8001	4	US-09-539-601-28	Sequence 28, Appl	1054	38.8	2.3	601	4	US-09-949-016-67114	Sequence 67114, A
c 982	39	2.3	8637	4	US-09-539-601-4	Sequence 4, Appl	1055	38.8	2.3	601	4	US-09-949-016-67114	Sequence 67114, A
c 983	39	2.3	8638	4	US-10-029-907-7	Sequence 7, Appl	1056	38.8	2.3	601	4	US-09-949-016-76961	Sequence 76961, A
c 984	39	2.3	8638	4	US-10-029-907-24	Sequence 24, Appl	1057	38.8	2.3	601	4	US-09-949-016-76962	Sequence 76962, A
c 985	39	2.3	8638	4	US-10-029-907-25	Sequence 25, Appl	1058	38.8	2.3	601	4	US-09-949-016-76963	Sequence 76963, A
c 986	39	2.3	8639	4	US-10-029-907-1	Sequence 1, Appl	1059	38.8	2.3	601	4	US-09-949-016-76964	Sequence 76964, A
c 987	39	2.3	8649	4	US-09-539-601-13	Sequence 13, Appl	1060	38.8	2.3	601	4	US-09-949-016-109665	Sequence 109665, A
c 988	39	2.3	8905	4	US-09-949-016-11761	Sequence 11761, A	1061	38.8	2.3	601	4	US-09-949-016-113694	Sequence 113694, A
c 989	39	2.3	8907	4	US-09-949-016-16261	Sequence 16261, A	1062	38.8	2.3	601	4	US-09-949-016-113695	Sequence 113695, A
c 990	39	2.3	9595	3	US-09-014-416-4	Sequence 4, Appl	c1063	38.8	2.3	601	4	US-09-949-016-126415	Sequence 126415, A
c 991	39	2.3	9595	3	US-09-014-416-2	Sequence 2, Appl	c1064	38.8	2.3	601	4	US-09-949-016-127893	Sequence 127893, A
c 992	39	2.3	9599	3	US-09-014-416-6	Sequence 6, Appl	c1065	38.8	2.3	601	4	US-09-949-016-128230	Sequence 128230, A
c 993	39	2.3	9740	4	US-09-949-016-15833	Sequence 15833, A	c1066	38.8	2.3	601	4	US-09-949-016-145252	Sequence 145252, A
c 994	39	2.3	11076	4	US-09-539-601-1	Sequence 1, Appl	1067	38.8	2.3	601	4	US-09-949-016-201489	Sequence 201489, A
c 995	39	2.3	11076	4	US-09-539-601-19	Sequence 19, Appl	1068	38.8	2.3	1492	4	US-09-369-247-23	Sequence 23, Appl
c 996	39	2.3	11076	4	US-09-539-601-25	Sequence 25, Appl	1069	38.8	2.3	1843	4	US-09-328-925-49	Sequence 49, Appl
c 997	39	2.3	11076	4	US-09-539-601-31	Sequence 31, Appl	1070	38.8	2.3	1843	4	US-09-949-016-50	Sequence 50, Appl
c 998	39	2.3	11517	3	US-07-920-281C-1	Sequence 1, Appl	1071	38.8	2.3	1844	4	US-10-003-392-7	Sequence 7, Appl
c 999	39	2.3	11517	3	US-08-466-277-1	Sequence 1, Appl	1072	38.8	2.3	4773	4	US-09-270-767-14129	Sequence 14129, A
c1000	39	2.3	11517	4	US-09-688-842-1	Sequence 1, Appl	1073	38.8	2.3	5009	1	US-08-487-890A-3	Sequence 3, Appl
c1001	39	2.3	11641	4	US-09-949-016-11906	Sequence 11906, A	1074	38.8	2.3	5009	2	US-08-478-435-3	Sequence 3, Appl
c1002	39	2.3	11643	4	US-09-949-016-14931	Sequence 14931, A	1075	38.8	2.3	5009	2	US-08-337-483-3	Sequence 3, Appl
c1003	39	2.3	17879	4	US-09-949-016-12992	Sequence 12992, A	1076	38.8	2.3	5009	2	US-08-478-373-3	Sequence 3, Appl
c1004	39	2.3	23319	4	US-09-949-016-14407	Sequence 14407, A	1077	38.8	2.3	5009	3	US-08-474-671-3	Sequence 3, Appl
c1005	39	2.3	23431	4	US-09-949-016-12234	Sequence 12234, A	1078	38.8	2.3	5009	3	US-08-483-577A-3	Sequence 3, Appl
c1006	39	2.3	37215	4	US-09-949-016-15526	Sequence 15526, A	1079	38.8	2.3	5009	3	US-08-897-438-3	Sequence 3, Appl
c1007	39	2.3	45427	4	US-09-949-016-16243	Sequence 16243, A	1080	38.8	2.3	5009	3	US-08-637-654-3	Sequence 3, Appl
c1008	39	2.3	45467	3	US-09-146-053-6	Sequence 6, Appl	1081	38.8	2.3	5033	1	US-08-649-518-3	Sequence 3, Appl
c1009	39	2.3	50383	4	US-09-949-016-17600	Sequence 17600, A	1082	38.8	2.3	5033	2	US-08-487-890A-2	Sequence 2, Appl
c1010	39	2.3	51698	4	US-09-949-016-12671	Sequence 12671, A	1083	38.8	2.3	5033	2	US-08-478-435-2	Sequence 2, Appl
c1011	39	2.3	78846	4	US-09-949-016-12396	Sequence 12396, A	1084	38.8	2.3	5033	2	US-08-337-483-2	Sequence 2, Appl
c1012	39	2.3	78846	4	US-09-949-016-12791	Sequence 12791, A	1085	38.8	2.3	5033	2	US-08-478-373-2	Sequence 2, Appl
c1013	39	2.3	78846	4	US-09-949-016-12792	Sequence 12792, A	1086	38.8	2.3	5033	2	US-08-474-671-2	Sequence 2, Appl
c1014	39	2.3	78846	4	US-09-949-016-12793	Sequence 12793, A	1087	38.8	2.3	5033	3	US-08-483-577A-2	Sequence 2, Appl
c1015	39	2.3	78850	4	US-09-949-016-16013	Sequence 16013, A	1088	38.8	2.3	5033	3	US-08-897-438-2	Sequence 2, Appl
c1016	39	2.3	78850	4	US-09-949-016-16014	Sequence 16014, A	1089	38.8	2.3	5033	3	US-08-637-654-2	Sequence 2, Appl
c1017	39	2.3	78850	4	US-09-949-016-16015	Sequence 16015, A	1090	38.8	2.3	5033	3	US-08-649-518-2	Sequence 2, Appl
c1018	39	2.3	78850	4	US-09-949-016-16016	Sequence 16016, A	1091	38.8	2.3	20445	4	US-09-949-016-14875	Sequence 14875, A
c1019	39	2.3	78850	4	US-09-949-016-16201	Sequence 16201, A	c1092	38.8	2.3	20852	4	US-09-949-016-14974	Sequence 14974, A
c1020	39	2.3	78850	4	US-09-949-016-16202	Sequence 16202, A	1093	38.8	2.3	31469	4	US-09-949-016-13722	Sequence 13722, A
c1021	39	2.3	78850	4	US-09-949-016-16203	Sequence 16203, A	c1094	38.8	2.3	41454	4	US-09-949-016-17107	Sequence 17107, A
c1022	39	2.3	78850	4	US-09-949-016-16204	Sequence 16204, A	1095	38.8	2.3	45469	4	US-09-949-016-13398	Sequence 13398, A
c1023	39	2.3	118382	4	US-09-949-016-15996	Sequence 15996, A	c1096	38.8	2.3	55195	4	US-09-949-016-15854	Sequence 15854, A
c1024	39	2.3	118382	4	US-09-949-016-15997	Sequence 15997, A	c1097	38.8	2.3	65990	4	US-09-949-016-11830	Sequence 11830, A
c1025	39	2.3	134140	4	US-09-949-016-12672	Sequence 12672, A	1098	38.8	2.3	74177	4	US-09-949-016-11988	Sequence 11988, A
c1026	39	2.3	134241	4	US-09-949-016-12673	Sequence 12673, A	1099	38.8	2.3	74177	4	US-09-949-016-17388	Sequence 17388, A
c1027	39	2.3	134242	4	US-09-949-016-15813	Sequence 15813, A	c1100	38.8	2.3	118067	4	US-09-497-855A-32	Sequence 32, Appl
c1028	39	2.3	134242	4	US-09-949-016-15814	Sequence 15814, A	c1101	38.8	2.3	113559	4	US-09-949-016-15845	Sequence 15845, A
c1029	39	2.3	134242	4	US-09-949-016-15815	Sequence 15815, A	1102	38.6	2.3	83	4	US-09-621-976-12087	Sequence 12087, A
c1030	39	2.3	177797	4	US-09-949-016-14125	Sequence 14125, A	1103	38.6	2.3	83	4	US-09-621-976-12175	Sequence 12175, A
c1031	39	2.3	186950	4	US-09-949-016-13125	Sequence 13125, A	1104	38.6	2.3	83	4	US-09-621-976-12429	Sequence 12429, A
c1032	39	2.3	192506	4	US-09-949-016-15830	Sequence 15830, A	1105	38.6	2.3	83	4	US-09-621-976-12450	Sequence 12450, A
c1033	39	2.3	227979	4	US-09-949-016-11842	Sequence 11842, A	1106	38.6	2.3	84	1	US-08-664-596B-3	Sequence 3, Appl
c1034	39	2.3	235064	4	US-09-949-016-15390	Sequence 15390, A	1107	38.6	2.3	84	1	US-08-738-367-3	Sequence 3, Appl
c1035	39	2.3	238815	4	US-09-949-016-16274	Sequence 16274, A	1108	38.6	2.3	91	4	US-09-621-976-14925	Sequence 14925, A
c1036	39	2.3	258775	4	US-09-949-016-16435	Sequence 16435, A	1109	38.6	2.3	102	4	US-09-621-976-1436	Sequence 11436, A
c1037	39	2.3	421491	4	US-09-949-016-12805	Sequence 12805, A	1110	38.6	2.3	299	4	US-09-621-976-10211	Sequence 10211, A
c1038	39	2.3	421494	4	US-09-949-016-14060	Sequence 14060, A	1111	38.6	2.3	300	4	US-09-621-976-16227	Sequence 16227, A
c1039	38.8	2.3	84	4	US-09-621-976-14577	Sequence 14577, A	1112	38.6	2.3	327	4	US-09-621-976-16018	Sequence 16018, A
c1040	38.8	2.3	91	3	US-09-404-879A-201	Sequence 201, App	1113	38.6	2.3	344	2	US-08-623-906A-8	Sequence 8, Appl
c1041	38.8	2.3	91	4	US-09-338-933-201	Sequence 201, App	1114	38.6	2.3	443	3	US-09-936-885A-1	Sequence 1, Appl
c1042	38.8	2.3	91	4	US-09-215-681-201	Sequence 201, App	c1115	38.6	2.3	500	4	US-09-270-767-3118	Sequence 3118, Ap
c1043	38.8	2.3	91	4	US-09-216-003A-201	Sequence 201, App	c1116	38.6	2.3	500	4	US-09-270-767-18400	Sequence 18400, A
c1044	38.8	2.3	91	4	US-09-667-857-201	Sequence 201, App	1117	38.6	2.3	601	4	US-09-949-016-59330	Sequence 59330, A
c1045	38.8	2.3	101	3	US-09-404-879A-293	Sequence 293, App	1118	38.6	2.3	601	4	US-09-949-016-126899	Sequence 126899, A
c1046	38.8	2.3	101	4	US-09-338-933-293	Sequence 293, App	1119	38.6	2.3	601	4	US-09-949-016-180024	Sequence 180024, A
c1047	38.8	2.3	101	4	US-09-215-681-293	Sequence 293, App	1120	38.6	2.3	700	3	US-09-152-060-26	Sequence 26, Appl
c1048	38.8	2.3	101	4	US-09-216-003A-293	Sequence 293, App	c1121	38.6	2.3	986	4	US-09-328-475C-141	Sequence 141, Appl
c1049	38.8	2.3	101	4	US-09-667-857-293	Sequence 293, App	1122	38.6	2.3	1027	3	US-09-465-558-57	Sequence 57, Appl

1123	38.6	2.3	1279	3	US-09-248-335-25	Sequence 25, Appl	1196	38.4	2.3	71119	4	US-09-949-016-15358	Sequence 15358, A
c1124	38.6	2.3	1447	4	US-09-976-594-338	Sequence 338, App	c1197	38.4	2.3	78630	4	US-09-949-016-16790	Sequence 16790, A
1125	38.6	2.3	2031	4	US-09-417-251A-9	Sequence 9, Appl	c1198	38.4	2.3	129415	4	US-09-949-016-16937	Sequence 16937, A
1126	38.6	2.3	5021	4	US-09-949-016-786	Sequence 786, App	c1199	38.4	2.3	137394	4	US-09-949-016-13872	Sequence 13872, A
c1127	38.6	2.3	23569	4	US-09-949-016-12153	Sequence 12153, A	c1200	38.4	2.3	137743	4	US-09-949-016-12178	Sequence 12178, A
c1128	38.6	2.3	23574	4	US-09-949-016-15351	Sequence 15351, A	c1201	38.4	2.3	150780	4	US-09-949-016-14711	Sequence 14711, A
1129	38.6	2.3	28643	4	US-09-949-016-17208	Sequence 17208, A	c1202	38.4	2.3	176373	3	US-09-128-155-17	Sequence 17, Appl
c1130	38.6	2.3	32922	4	US-09-949-016-15382	Sequence 15382, A	c1203	38.4	2.3	181429	4	US-09-949-016-12372	Sequence 12372, A
1131	38.6	2.3	43255	4	US-09-949-016-11909	Sequence 11909, A	c1204	38.4	2.3	181430	4	US-09-949-016-15772	Sequence 15772, A
1132	38.6	2.3	43507	4	US-09-949-016-13297	Sequence 13297, A	c1205	38.4	2.3	211049	4	US-09-949-016-15770	Sequence 15770, A
c1133	38.6	2.3	46841	4	US-09-949-016-13466	Sequence 13466, A	c1206	38.4	2.3	211769	4	US-09-949-016-13185	Sequence 13185, A
1134	38.6	2.3	51259	3	US-08-781-891-209	Sequence 209, App	c1207	38.4	2.3	231769	4	US-09-949-016-13186	Sequence 13186, A
c1135	38.6	2.3	51259	4	US-09-618-166-209	Sequence 209, App	c1208	38.4	2.3	2326748	4	US-09-949-016-13187	Sequence 13187, A
c1136	38.6	2.3	56326	4	US-09-949-016-16468	Sequence 16468, A	c1209	38.4	2.3	256748	4	US-09-949-016-13188	Sequence 13188, A
c1137	38.6	2.3	95648	4	US-09-949-016-13139	Sequence 13139, A	c1210	38.4	2.3	266748	4	US-09-949-016-14033	Sequence 14033, A
1138	38.6	2.3	152331	3	US-09-128-155-16	Sequence 16, Appl	c1211	38.4	2.3	784019	4	US-09-949-016-12777	Sequence 12777, A
c1139	38.6	2.3	173992	4	US-09-949-016-13379	Sequence 13379, A	c1212	38.2	2.3	828152	4	US-09-949-016-12777	Sequence 12777, A
1140	38.4	2.3	80	1	US-07-920-281C-25	Sequence 25, Appl	c1213	38.2	2.3	83	4	US-09-621-976-12795	Sequence 12195, A
1141	38.4	2.3	80	3	US-08-466-277-25	Sequence 25, Appl	c1214	38.2	2.3	83	4	US-09-621-976-14751	Sequence 14751, A
1142	38.4	2.3	80	3	US-08-688-842-25	Sequence 25, Appl	c1215	38.2	2.3	83	4	US-09-621-976-14959	Sequence 14959, A
1143	38.4	2.3	106	4	US-09-621-976-12079	Sequence 12079, A	c1216	38.2	2.3	138	4	US-09-621-976-9595	Sequence 9595, Ap
c1144	38.4	2.3	141	3	US-08-737-078A-1	Sequence 1, Appl	c1217	38.2	2.3	232	4	US-09-621-976-17701	Sequence 17701, A
c1145	38.4	2.3	141	5	PCT-US94-04706-1	Sequence 1, Appl	c1218	38.2	2.3	253	4	US-09-621-976-12799	Sequence 12799, A
1146	38.4	2.3	234	4	US-09-621-976-16557	Sequence 16557, A	c1219	38.2	2.3	271	2	US-08-731-272A-29	Sequence 29, Appl
1147	38.4	2.3	250	4	US-09-621-976-18363	Sequence 18363, A	c1220	38.2	2.3	333	4	US-09-248-796A-13	Sequence 1241, A
1148	38.4	2.3	366	4	US-09-252-991A-620	Sequence 620, App	c1221	38.2	2.3	388	2	US-08-623-906A-13	Sequence 13, Appl
1149	38.4	2.3	366	4	US-09-134-000C-11	Sequence 13, Appl	c1222	38.2	2.3	601	4	US-09-949-016-32559	Sequence 32559, A
c1150	38.4	2.3	591	1	US-09-134-000C-11	Sequence 11, Appl	c1223	38.2	2.3	601	4	US-09-949-016-32561	Sequence 32561, A
1151	38.4	2.3	601	4	US-09-949-016-48846	Sequence 48846, A	c1224	38.2	2.3	601	4	US-09-949-016-66245	Sequence 66245, A
1152	38.4	2.3	601	4	US-09-949-016-49018	Sequence 49018, A	c1225	38.2	2.3	601	4	US-09-949-016-80104	Sequence 80104, A
1153	38.4	2.3	601	4	US-09-949-016-49190	Sequence 49190, A	c1226	38.2	2.3	601	4	US-09-949-016-94321	Sequence 94321, A
c1154	38.4	2.3	601	4	US-09-949-016-49366	Sequence 49366, A	c1227	38.2	2.3	601	4	US-09-949-016-126059	Sequence 126059, A
c1155	38.4	2.3	601	4	US-09-949-016-127053	Sequence 127053, A	c1228	38.2	2.3	601	4	US-09-949-016-132201	Sequence 132201, A
1156	38.4	2.3	601	4	US-09-949-016-127054	Sequence 127054, A	c1229	38.2	2.3	601	4	US-09-949-016-13406	Sequence 13406, A
c1157	38.4	2.3	601	4	US-09-949-016-127055	Sequence 127055, A	c1230	38.2	2.3	601	4	US-09-949-016-140018	Sequence 140018, A
c1158	38.4	2.3	601	4	US-09-949-016-127056	Sequence 127056, A	c1231	38.2	2.3	601	4	US-09-949-016-155055	Sequence 155055, A
c1159	38.4	2.3	601	4	US-09-949-016-127058	Sequence 127058, A	c1232	38.2	2.3	601	4	US-09-949-016-155362	Sequence 155362, A
c1160	38.4	2.3	601	4	US-09-949-016-127059	Sequence 127059, A	c1233	38.2	2.3	601	4	US-09-949-016-155364	Sequence 155364, A
c1161	38.4	2.3	601	4	US-09-949-016-127060	Sequence 127060, A	c1234	38.2	2.3	601	4	US-09-949-016-173108	Sequence 173108, A
c1162	38.4	2.3	601	4	US-09-949-016-127061	Sequence 127061, A	c1235	38.2	2.3	601	4	US-09-949-016-173109	Sequence 173109, A
1163	38.4	2.3	601	4	US-09-949-016-161233	Sequence 161233, A	c1236	38.2	2.3	832	4	US-09-949-016-179952	Sequence 179952, A
1164	38.4	2.3	601	4	US-09-949-016-205887	Sequence 205887, A	c1237	38.2	2.3	1074	3	US-09-621-976-2813	Sequence 2813, Ap
c1165	38.4	2.3	730	4	US-09-270-767-14600	Sequence 14600, A	c1238	38.2	2.3	1100	3	US-09-248-335-67	Sequence 67, Appl
1166	38.4	2.3	912	4	US-09-252-991A-774	Sequence 774, App	c1239	38.2	2.3	1325	1	US-07-861-458C-4	Sequence 4, Appl
1167	38.4	2.3	948	4	US-09-252-991A-643	Sequence 643, App	c1240	38.2	2.3	1325	1	US-08-306-691B-51	Sequence 51, Appl
1168	38.4	2.3	997	4	US-09-907-794A-376	Sequence 376, App	c1241	38.2	2.3	1325	2	US-08-464-517-1	Sequence 1, Appl
1169	38.4	2.3	997	4	US-09-905-125A-376	Sequence 376, App	c1242	38.2	2.3	1325	2	US-08-246-361A-1	Sequence 1, Appl
1170	38.4	2.3	997	4	US-09-902-775A-376	Sequence 376, App	c1243	38.2	2.3	1325	3	US-08-463-772-1	Sequence 1, Appl
1171	38.4	2.3	997	4	US-09-906-700-376	Sequence 376, App	c1244	38.2	2.3	1325	5	PCT-US93-05000-1	Sequence 1, Appl
1172	38.4	2.3	997	4	US-09-903-603A-376	Sequence 376, App	c1245	38.2	2.3	1663	4	US-09-464-535-43	Sequence 43, Appl
1173	38.4	2.3	997	4	US-09-904-920A-376	Sequence 376, App	c1246	38.2	2.3	1872	3	US-09-291-922-27	Sequence 27, Appl
1174	38.4	2.3	997	4	US-09-905-064-376	Sequence 376, App	c1247	38.2	2.3	2445	6	5215909-9	Patent No. 5215909
1175	38.4	2.3	997	4	US-09-905-381A-376	Sequence 376, App	c1248	38.2	2.3	2460	6	5215909-9	Patent No. 5215909
1176	38.4	2.3	997	4	US-09-906-618-376	Sequence 376, App	c1249	38.2	2.3	2460	6	5215909-9	Patent No. 5215909
1177	38.4	2.3	1518	4	US-09-614-912-191	Sequence 376, App	c1250	38.2	2.3	9157	4	US-09-270-767-12063	Sequence 12063, A
1178	38.4	2.3	1810	4	US-09-800-729-77	Sequence 73, Appl	c1251	38.2	2.3	9558	4	US-09-949-016-16185	Sequence 16185, A
1179	38.4	2.3	1811	4	US-09-800-729-77	Sequence 77, Appl	c1252	38.2	2.3	10451	4	US-09-949-016-13026	Sequence 13026, A
c1180	38.4	2.3	1972	4	US-09-403-861A-1	Sequence 1, Appl	c1253	38.2	2.3	12047	3	US-09-949-016-12192	Sequence 12192, A
1181	38.4	2.3	3243	4	US-09-949-016-12186	Sequence 12186, A	c1254	38.2	2.3	12047	3	US-09-033-556-3	Sequence 3, Appl
1182	38.4	2.3	4890	4	US-09-677-046A-3	Sequence 3, Appl	c1255	38.2	2.3	12047	4	US-09-474-699-11	Sequence 11, Appl
1183	38.4	2.3	4943	4	US-09-677-046A-7	Sequence 7, Appl	c1256	38.2	2.3	12047	4	US-09-814-351-11	Sequence 11, Appl
1184	38.4	2.3	5170	4	US-09-677-046A-5	Sequence 5, Appl	c1257	38.2	2.3	15575	4	US-09-949-016-12634	Sequence 12634, A
1185	38.4	2.3	6124	3	US-08-213-419B-3	Sequence 3, Appl	c1258	38.2	2.3	15575	4	US-09-949-016-16568	Sequence 16568, A
c1186	38.4	2.3	8642	3	US-10-029-907-2	Sequence 2, Appl	c1259	38.2	2.3	20229	4	US-09-949-016-16649	Sequence 16649, A
1187	38.4	2.3	17656	3	US-09-433-579-3	Sequence 3, Appl	c1260	38.2	2.3	23907	4	US-09-949-016-13772	Sequence 13772, A
c1188	38.4	2.3	36171	4	US-09-943-016-13876	Sequence 13876, A	c1261	38.2	2.3	23907	4	US-09-949-016-15323	Sequence 15323, A
c1189	38.4	2.3	36274	4	US-09-949-016-12389	Sequence 12389, A	c1262	38.2	2.3	32327	4	US-09-949-016-14108	Sequence 14108, A
c1190	38.4	2.3	38009	4	US-09-949-016-13617	Sequence 13617, A	c1263	38.2	2.3	33099	4	US-09-949-016-16094	Sequence 16094, A
1191	38.4	2.3	41708	3	US-09-470-512A-3	Sequence 3, Appl	c1264	38.2	2.3	38983	4	US-09-949-016-15700	Sequence 15700, A
1192	38.4	2.3	41708	4	US-09-676-519-18	Sequence 18, Appl	c1265	38.2	2.3	41639	4	US-09-949-016-15471	Sequence 15471, A
1193	38.4	2.3	41798	4	US-09-949-016-16058	Sequence 16058, A	c1266	38.2	2.3	53336	4	US-09-949-016-12500	Sequence 12500, A
c1194	38.4	2.3	42348	4	US-09-949-016-17157	Sequence 17157, A	c1267	38.2	2.3	53337	4	US-09-949-016-16092	Sequence 16092, A
1195	38.4	2.3	67479	4	US-09-949-016-11804	Sequence 11804, A	c1268	38.2	2.3	58397	4	US-09-949-016-14469	Sequence 14469, A

c1269	38.2	2.3	59076	4	US-09-949-016-15097	Sequence 15097, A	c1342	38	2.3	84587	4	US-09-949-016-15733	Sequence 15733, A
1270	38.2	2.3	62072	4	US-09-949-016-16076	Sequence 16076, A	c1343	38	2.3	117838	4	US-09-949-016-17595	Sequence 17595, A
c1271	38.2	2.3	82000	4	US-09-949-016-15595	Sequence 15595, A	c1344	38	2.3	124110	4	US-09-949-016-13353	Sequence 13353, A
1272	38.2	2.3	89689	4	US-09-949-016-13089	Sequence 13089, A	c1345	38	2.3	145812	4	US-09-949-016-15698	Sequence 15698, A
c1273	38.2	2.3	101356	4	US-09-949-016-12364	Sequence 12364, A	c1346	38	2.3	152070	4	US-09-949-016-15402	Sequence 15402, A
c1274	38.2	2.3	101357	4	US-09-949-016-16924	Sequence 16924, A	c1347	38	2.3	152486	4	US-09-949-016-12869	Sequence 12869, A
1275	38.2	2.3	106746	4	US-09-326-402C-1	Sequence 1, Appl	c1348	38	2.3	192700	4	US-09-949-016-11820	Sequence 11820, A
1276	38.2	2.3	106746	4	US-09-326-402C-12	Sequence 12, Appl	c1349	38	2.3	192704	4	US-09-949-016-17182	Sequence 17182, A
1277	38.2	2.3	107980	4	US-09-949-016-14370	Sequence 14370, A	c1350	38	2.3	205044	4	US-09-949-016-15851	Sequence 15851, A
1278	38.2	2.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c1351	38	2.3	205044	4	US-09-949-016-15852	Sequence 15852, A
1279	38.2	2.3	113876	4	US-09-949-016-14828	Sequence 14828, A	c1352	38	2.3	205044	4	US-09-949-016-15853	Sequence 15853, A
1280	38.2	2.3	115508	4	US-09-949-016-11800	Sequence 11800, A	c1353	38	2.3	223471	4	US-09-949-016-12387	Sequence 12387, A
1281	38.2	2.3	115508	4	US-09-949-016-14826	Sequence 14826, A	c1354	38	2.3	223471	4	US-09-949-016-12724	Sequence 12724, A
1282	38.2	2.3	115508	4	US-09-949-016-14826	Sequence 14827, A	c1355	38	2.3	223471	4	US-09-949-016-12725	Sequence 12725, A
1283	38.2	2.3	142508	4	US-09-949-016-13693	Sequence 13693, A	c1356	38	2.3	300598	4	US-09-949-016-11868	Sequence 11868, A
1284	38.2	2.3	142506	4	US-09-949-016-12474	Sequence 12474, A	c1357	38	2.3	302604	4	US-09-949-016-14598	Sequence 14598, A
c1285	38.2	2.3	149971	4	US-09-949-016-13590	Sequence 13590, A	c1358	38	2.3	302604	4	US-09-949-016-14599	Sequence 14599, A
c1286	38.2	2.3	157822	4	US-09-949-016-16723	Sequence 16723, A	c1359	38	2.3	308362	4	US-09-949-016-17119	Sequence 17119, A
1287	38.2	2.3	161124	4	US-09-949-016-11760	Sequence 11760, A	c1360	38	2.3	389504	4	US-09-949-016-11774	Sequence 11774, A
c1288	38.2	2.3	183770	4	US-09-949-016-15494	Sequence 15494, A	c1361	37.8	2.3	165	4	US-09-621-976-8127	Sequence 8127, Ap
c1289	38.2	2.3	191433	4	US-09-949-016-16144	Sequence 16144, A	c1362	37.8	2.3	233	4	US-09-621-976-16559	Sequence 16559, A
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ALIGNMENTS

US-09-700-397-2

Patent No. 6664383

Patent No. 6664383

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd.

TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of t

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NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 1693

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Clone OC001 derived from human brain

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LOCATION: (130)..(1161)

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US-09-700-397-2

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Best Local Similarity

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QY 785 ACCGTGAATCTCCACCATACATTTCAAGCCAGGCTACAGGTGTCCTCGTGGCAAA 844
Db |||||
QY 781 ACCGTGAATCTCCACCATACATTTCAAGCCAGGCTACAGGTGTCCTCGTGGCAAA 840
Db |||||
QY 845 AAGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAA 904
Db |||||
QY 841 AAGGGACACTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAA 900
Db |||||
QY 905 GATGACAAAGACTGATTTGAAGGAAAGAGGGTGAAGTGGAAACACAGACCTTTCTC 964
Db |||||
QY 901 GATGACAAAGACTGATTTGAAGGAAAGAGGGTGAAGTGGAAACACAGACCTTTCTC 960
Db |||||
QY 965 TCBAACACTCATCTTCTCAATGTCTCTGAACATGACTATGGNACTACACTTGGTGCC 1024
Db |||||
QY 961 TCBAACACTCATCTTCTCAATGTCTCTGAACATGACTATGGNACTACACTTGGTGCC 1020
Db |||||
QY 1025 TCCAAACAGCTGGGCCACACCAATGCCAGCATCATGTCTATTGGTCCAGGGCCGTACG 1084
Db |||||
QY 1021 TCCAAACAGCTGGGCCACACCAATGCCAGCATCATGTCTATTGGTCCAGGGCCGTACG 1080
Db |||||
QY 1085 GAGGTGAGCAACGGCACTGAGGAGGAGCGAGTGCCTTCCCGACCCGGGAAAGGTCGCG 1144
Db |||||
QY 1081 GAGGTGAGCAACGGCACTGAGGAGGAGCGAGTGCCTTCCCGACCCGGGAAAGGTCGCG 1140
Db |||||
QY 1145 TTGACCTGCTTCTCAAAATTTTGTATGTAGTGCCACTTCCCGACCCGGGAAAGGTCGCG 1204
Db |||||
QY 1141 TTGACCTGCTTCTCAAAATTTTGTATGTAGTGCCACTTCCCGACCCGGGAAAGGTCGCG 1200
Db |||||
QY 1205 CCACCACCAACCAACACAGCAATGGCAACACCGACAGCAACCAATCAGATATATA 1264
Db |||||
QY 1201 CCACCACCAACCAACAGCAATGGCAACACCGACAGCAACCAATCAGATATATA 1260
Db |||||
QY 1265 CAATGAAATTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAG 1324
Db |||||
QY 1261 CAATGAAATTAGAGAAACACAGCCTCATGGGACAGAAATTTGAGGAGGGGAAACAAAG 1320
Db |||||
QY 1325 AATACCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCCCTTGAGATATTTA 1384
Db |||||
QY 1321 AATACCTTTGGGGGAAAGAGTTTTTAAAGAAATTTGAAATTTGCCCTTGAGATATTTA 1380
Db |||||
QY 1385 GGTACAAATGGAGTTTCTTTTCCCAACCGGGGAAAGAACACAGCACACCGCGGCTTGACCCA 1444
Db |||||
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Db 1381 GGTACAATGGAGTTTCTTTTCCCAACCGGGGAAAGAACACAGCACACCGGGCTTGACCCA 1440
QY 1445 CTGCAAGCTGCATCGTCAACCTCTTTGGTGCCAGTGTGGCAAGGCTCAGCCTCTCTG 1504
Db 1441 CTGCAAGCTGCATCGTCAACCTCTTTGGTGCCAGTGTGGCAAGGCTCAGCCTCTCTG 1500
QY 1505 CCCACAGAGTGGCCCCACAGTGGAAATTTCTGGAGCTGGCCATCCAAATTCATCAGTCC 1564
Db 1501 CCCACAGAGTGGCCCCACAGTGGAAATTTCTGGAGCTGGCCATCCAAATTCATCAGTCC 1560
QY 1565 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCTGGCGCTGCGGCACTTTGGTAG 1624
Db 1561 ATAGAGACGAACAGAATGAGACCTTCCGGCCCAAGCTGGCGCTGCGGCACTTTGGTAG 1620
QY 1625 ACTGTGCCACACCGCGCTGTGTGTGAACGTGAAATTAAGAGACCAAAAAA 1679
Db 1621 ACTGTGCCACACCGCGCTGTGTGTGAACGTGAAATTAAGAGACCAAAAAA 1675

RESULT 2
US-09-700-397-1
; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of t
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1

Query Match 61.5%; Score 1032; DB 4; Length 1032;
Best Local Similarity 100.0%; Pred. No. 4.3e-273;
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 134 ATGAAAACCATCCAGCCAAATAATGCACAAATTCATCTTTGGGCAATCTTCACGGGGCTG 193
Db 1 ATGAAAACCATCCAGCCAAATAATGCACAAATTCATCTTTGGGCAATCTTCACGGGGCTG 60
QY 194 GCTGCTCTGTGCTCTTCCAGGAGTGCCCGTGGCGAGGATGCCACCTTCCCAAA 253
Db 61 GCTGCTCTGTGCTCTTCCAGGAGTGCCCGTGGCGAGGATGCCACCTTCCCAAA 120
QY 254 GCTATGACAACAGTGAAGTCCCGCAGGGGAGAGCGCACCTCAGGTGCACTATTGAC 313
Db 121 GCTATGACAACAGTGAAGTCCCGCAGGGGAGAGCGCACCTCAGGTGCACTATTGAC 180
QY 314 AACCGGGTCAACCGGGTGGCTTGGCTAAACCGCAGACCATCTCTATGCTGGGAATGAC 373
Db 181 AACCGGGTCAACCGGGTGGCTTGGCTAAACCGCAGACCATCTCTATGCTGGGAATGAC 240
QY 374 AAGTGGTGCCTGGATCTCTCGCGTGGTCTCTTGAGCAACCCCAACCCAGTACAGCATC 433
Db 241 AAGTGGTGCCTGGATCTCTCGCGTGGTCTCTTGAGCAACCCCAACCCAGTACAGCATC 300
QY 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
Db 301 GAGATCCAGAAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 360
QY 494 AACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG 553
Db 361 AACCAACCAAGACCTCTAGGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTGAGAG 420
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Qy 554 ATTTCTTCAGATATCTCATTAATTAAGGGGAAACAATATTAGCCTCAGCTGATGCAACT 613
Db 421 ATTTCTTCAGATATCTCATTAATTAAGGGGAAACAATATTAGCCTCAGCTGATGCAACT 480
Qy 614 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
Db 481 GGTAGACAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
Qy 674 AGTGAAGACGAATATTCTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
Db 541 AGTGAAGACGAATATTCTGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 600
Qy 734 TGCAGTGCTCCAATGACGTGGCCGCGCCCTGTGTGTAACGAGATGAAGGTCAACGTAAC 793
Db 601 TGCAGTGCTCCAATGACGTGGCCGCGCCCTGTGTGTAACGAGATGAAGGTCAACGTAAC 660
Qy 794 TATCCACCATACATTTCAAGGCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
Db 661 TATCCACCATACATTTCAAGGCCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 720
Qy 854 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGTACAGGATGACAAA 913
Db 721 CTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGATTTCCAGTGTGTACAGGATGACAAA 780
Qy 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
Db 781 AGACTGATTGAAGGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 840
Qy 974 ATCTTCTCAATGTCTCGAATCATGATGATGAGGAACTACATTTGGTGGGCTTCCAAAG 1033
Db 841 ATCTTCTCAATGTCTCGAATCATGATGATGAGGAACTACATTTGGTGGGCTTCCAAAG 900
Qy 1034 CTGGGCGACACAAATGCCAGCATCATGTATTTGGTCCAGGCGCGTCAGGAGGTGAGC 1093
Db 901 CTGGGCGACACAAATGCCAGCATCATGTATTTGGTCCAGGCGCGTCAGGAGGTGAGC 960
Qy 1094 AACGGCAGCTCGAGAGGGCAGGTGCGTCTGGTGTGCTCTTCTGCTTCTGCTGCTG 1153
Db 961 AACGGCAGCTCGAGAGGGCAGGTGCGTCTGGTGTGCTCTTCTGCTGCTGCTGCTG 1020
Qy 1154 CTTCTCAAAATTT 1165
Db 1021 CTTCTCAAAATTT 1032

RESULT 3

US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-5

Query Match 55.9%; Score 939; DB 4; Length 939;
Best Local Similarity 100.0%; Pred. No. 1.4e-247;
Matches 939; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 227 CGCAGCGGAGATGCCACCTTCCCAAGCTATGGACACGTGACGGTCCGGCAGGGGAG 286

Db 1 CGCAGCGGAGATGCCACCTTCCCAAGCTATGGACACGTGACGGTCCGGCAGGGGAG 60
Qy 287 AGGCCACACCTCAGGTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGC 346
Db 61 AGGCCACACCTCAGGTGCACTATTGACAAACCGGGTCAACCGGGTGGCTGGCTAAACCGC 120
Qy 347 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTCTGATCTCCGCTGGTCTCTCTG 406
Db 121 AGCACCATCTCTATGCTGGGAATGACAAAGTGGTCTGATCTCCGCTGGTCTCTCTG 180
Qy 407 AGCAACACCCAAAGCGAGTACAGATCGAGATCCAGAACCTGGATGTGTATGACAGGGC 466
Db 181 AGCAACACCCAAAGCGAGTACAGATCGAGATCCAGAACCTGGATGTGTATGACAGGGC 240
Qy 467 CTTTACACCTCTCGGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCAT 526
Db 241 CTTTACACCTCTCGGTGACAGACAAACCAACCAAGACCTCTAGGGTCCACCTCAT 300
Qy 527 GTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAA 586
Db 301 GTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTTCAGATATCTCCATTAATGAAGGAA 360
Qy 587 AATATTAGCTCAGCTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 646
Db 361 AATATTAGCTCAGCTCAGTACAGTACAGTACAGTACAGTACAGTACAGTACAGTACAG 420
Qy 647 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATTAATTTGGAAATTTACAGGGATC 706
Db 421 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATTAATTTGGAAATTTACAGGGATC 480
Qy 707 ACCGGGAGCAGTCAGGGGACTACAGTGTGAGTGTGCTTCCATGACGTGGCGCCCGCTG 766
Db 481 ACCGGGAGCAGTCAGGGGACTACAGTGTGAGTGTGCTTCCATGACGTGGCGCCCGCTG 540
Qy 767 GTACGGAGATTAAGTCAAGTGAATATCCACCATACATTTTCAGAGCCCAAGGGTACA 826
Db 541 GTACGGAGATTAAGTGAAGTGAATATCCACCATACATTTTCAGAGCCCAAGGGTACA 600
Qy 827 GGTGTCCCGCTGGGACAAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCA 886
Db 601 GGTGTCCCGCTGGGACAAAAGGGGACACTGCAAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660
Qy 887 GAATTCAGTGTGTAACAAGGATGACAAAGACTGATTAAGAGAAAGAGGGGTGAAAAGTG 946
Db 661 GAATTCAGTGTGTAACAAGGATGACAAAGACTGATTAAGAGAAAGAGGGGTGAAAAGTG 720
Qy 947 GAAAAAGACCTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 1006
Db 721 GAAAAAGACCTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGG 780
Qy 1007 AACTTACACTTTCGTGGCTCCCAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 1066
Db 781 AACTTACACTTTCGTGGCTCCCAAGCTGGGCCACACCAATGCCAGCATCATGCTATTT 840
Qy 1067 GGTCCAGGCGCGCTCAGCAGAGGTGAGCAACGGCAGCTCGAGAGGGGAGGCTGCTCTGG 1126
Db 841 GGTCCAGGCGCGCTCAGCAGAGGTGAGCAACGGCAGCTCGAGAGGGGAGGCTGCTCTGG 900
Qy 1127 CTGCTGCTCTTCTGCTGCTTTCGACCTGCTTCTCAAAATTT 1165
Db 901 CTGCTGCTCTTCTGCTGCTTTCGACCTGCTTCTCAAAATTT 939

RESULT 4

US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria

;; TITLE OF INVENTION: Limbic System-Associated Membrane
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FASTSEQ for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1238 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; FEATURE:
;; NAME/KEY: Coding Sequence
;; LOCATION: 56...1069
;; OTHER INFORMATION:
US-08-414-657D-3

Query Match 20.4%; Score 343; DB 2; Length 1238;
Best Local Similarity 62.0%; Pred. No. 9,5e-84;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;
QY 205 TCTCTTCCAGAGATGCGCGTGGCGAGATGCCACCTTCCCAAGCTATGGACAA 264
DB 121 TCTTCCACAGACTGCCCGTTTCGACGGTGGAT-----TTTAAACCGAGGCGACGGACAA 174
QY 265 CGTGACGGTCCGCGAGGCGGAGCGCCACCTCAGGTGCACCTATTGACAAACCGGTCAC 324
DB 175 CATCACCGTGGAGGCGGAGCGCCATCTCTCAGGTGTGTGGTAGAAGACAAGAACTC 234
QY 325 CCGGTGCGCTGGCTTAACCGCAGACCACTCTCTATGCTGGGAATGACAAAGTGGTGCCT 384
DB 235 GAAAGTGCGCTGGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGACAAAGTGGTCTCT 294
QY 385 GGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGCGATACAGCATCGAGATCCAGAA 444
DB 295 GGACCTCGGGTTGAGCTGGAGAAACGCGCATGCTCTGGAATACAGCTCCGAAATCCAGAA 354
QY 445 CGTGATCTGTATGACGAGGCGCTTACACCTGCTCGGTGGAGACAGACCAACCCCAAA 504
DB 355 GGTGGATGTCTATGATGAAGGATCTTACATGCTCAGTTCTGAGACACAGCATGAGCCCAA 414
QY 505 GACCTCTAGGTCACCTCATTTGTCAAGTATCTCCCAAAATGTAGAGATTTCTTTCAGA 564
DB 415 GACCTCTCAAGTTTACTTGTATGTACAGTTCCACCAAGATCTCCAACATCTCTCGGA 474
QY 565 TATCTCCATTAATGAAGGGAACAATATTAGCTCACTACCTGCTAGCAATCTGGTAGACAGA 624
DB 475 TGTACTGTGAATGAGGCGAGCAATGTAAACCTTGTCTGCATGGCCAAATGGGCGCCCTGA 534

QY 625 GCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTGAGTGAAGCGA 684
DB 535 ACTGTTATCACCTGGAGACACCTTACACCACTTGGAGAGAAATTTGAAGGAGAAGA 594
QY 685 ATACTTGGAAATTCAGGGCATACCCGGGAGCAGTCAAGGAGCTACAGAGTCACTGCTC 744
DB 595 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCAAGGCAAAATATGAGTCAAGGCTGC 654
QY 745 CAATGACGTGGCGCGCGCTGGTACGAGAGTAAAGGTCAACGATCAAGGTCACTGTGAAC 804
DB 655 CAACGAGGTCTCTCTCCGCGGATGTCAAAAGTCAAGGTCACTGTGAACATATCCACC 714
QY 805 CATTTCAAGAACCAAGGGTACAGGTGCCCGTGGGACAAAGGGGACACTGCGAGTGTGA 864
DB 715 CATCACAGAGTCTTAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCCCTCAAT 774
QY 865 AGCCTCAGCAGTCCCCTCAGCAGAAATTCAGATGGTGAACAAGATGACAAAGACTGATT 924
DB 775 AGCCTCAGCGTGCCTGCACCTGACTTTGAGTGGTACCGGGATGACACCAG---GATA 831
QY 925 AGGAAAGAAAGGGGTGAAGTGGGAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAA 984
DB 832 CAGTGAACACGGCCTTGAGATTAAGAGCATGAGGGCCAGTCTCTCCCTGACGGTGACC 891
QY 985 TGTCTCTGAACATGACTATGGGAACACTACACTTGGCGTGGCTCCCAACAGCTGGGCCAC 1044
DB 892 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGGTCCCAACAGCTCGGCGTCA 951
QY 1045 CAATGCCAGCATCATGTATTGTTGTCAGGCGCGCTCAGGAGGTGAGCAACGGCACGTC 1104
DB 952 CAATGCCAGCCTAGTCTCTTTTCAGACCGGGTCGGTGAG---AGGAATCAACGGATCC 1008
QY 1105 GAGGAGGCGAGGCTGCGTCTGGCTGCTGCTCTTCTGGTCTTGACACCTGCTTCTCAA 1164
DB 1009 CAGTCTGGCGGTACCACACTGTGGTGTCTGGGACGCTCCTGTCTCTGAGCAAAATG 1069
QY 1165 TTGAT 1169
DB 1069 TTAAT 1073
RESULT 5
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995

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;
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
;
;
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
;
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
;
; US-09-135-080-3

Query Match 20.4%; Score 343; DB 3; Length 1238;
Best Local Similarity 62.0%; Pred. No. 9.5e-84;
Matches 598; Conservative 0; Mismatches 355; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAGCTATG3ACAA 264
Db 121 TCTTCCCAAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAGCTATG3ACAA 174
Qy 265 CGTGACGCTGCGGAGCGGAGAGCGCCACCTCAGGTGCACTATTGACACCGGTCAC 324
Db 175 CATCAGCTGAGGAGCGGAGAGCGCCATCTCAGGTGCTGTTGGTAGAAGCAAGATC 234
Qy 325 CCGGCTGCGCTGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAAGTGTGCT 384
Db 235 GAAAGTGCCTGTTGAACCGCTCTGGCATCATCTTCGTGACACAGCAAGTGTCTCT 294
Qy 385 GGATCTCGCTGCTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db 295 GGACCTCGGCTTGAGCTGGAGAAACGCGATGCTTGGAAATACAGCCTCCGAATCCAGAA 354
Qy 445 CGTGATGTGTATGACGAGGCGCTTACACCTGCTCGGTGCGAGACAGACACACCCAAA 504
Db 355 GGTGATGTCTATGATGAAGATCTCTACATGCTCAGTTTCCAGATCAGACAGATGAGCCCAA 414
Qy 505 GACCTCTAGGCTCAACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAGTTCTTCAGA 564
Db 415 GACCTCTCAAGTTTACTTGTATGATGTTCCACCAAGATCTCCAAACATCTCTCGGA 474
Qy 565 TATCTCCATTAATGAGGGAACAATAATTAGCTCACCCTGCAATAGCACTGGTAGACCA 624
Db 475 TGTCACTGTGAATGAGGCGCAATGTAAACCTGCTCTGATGCGCAATGGCGCCCTGA 534
Qy 625 GCCTACGGTTACTTGGAGACATCTCTCCCAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
Db 535 ACCTGTTATACCTTGGAGACACTTTACACCACTTGGAAAGAAATTTGAAGGAGAAGAGA 594
Qy 685 ATACTTGGAAATTCAGGCGCATCACCCGCGGAGCAGTTCAGGCGACTACAGAGTCAGTGCCT 744
Db 595 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCCAGCAATATATGATGCAAGGCTGC 654
Qy 745 CAATGACGTGCGCGCCCGCTGGTACCGGAGAGTAAAGGTACCGGTAACTATCCACATA 804
Db 655 CAACGAGGTCTCTCCGCGGATGTCAAAACAAAGTCAAGGTCACTGTGAACTATCCACCCAC 714
Qy 805 CATTTCAAGCCAGGTAAGGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGA 864
Db 715 CATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAAAGCTTCCCTCAATGTGA 774
Qy 865 AGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGTACAAAAGACTGATGA 924
Db 775 AGCCTCAGCGGTGCTGACCTGACTTTGATGGTATCGGAGTACACCCAG---GATAAA 831
Qy 925 AGGAAAGAAAGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTCATCTTCTTCAA 984
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Db 832 CAGTCAAACGGCCTTGAGATTAAAGACACTGAGGCGCAGTCTCTCCCTGACGGTGACCAA 891
Qy 985 TGTCTCTGAACATGACTATGGAACACTTGTGCTGCTCCCAACAAAGCTGGGCGCACAC 1044
Db 892 CGTCACTAGGAACACTACGCAACTATCTCTGTGCTGCCAACAAAGCTCGGCGTCAC 951
Qy 1045 CAATGCCAGCATCATGCTATTGCTCCAGGCGCGCTCAGCAGAGGTGAGCAACGGCACGTC 1104
Db 952 CAATGCCAGCTAGTCTCTTTTCAGACCCGGTGGTGAG---AGGAATCAACGGATCCAT 1008
Qy 1105 GAGGAGGCGCAGGCTGCTGCTGCTGCTCTCTCTGCTTGTGACCTGCTTCTCAAAAT 1164
Db 1009 CAGTCTGCGCGTACCACTGTGCTGCTGCGCAGCGTCCCTGTTCTGCTTCTCAGCAAAAT 1068
Qy 1165 TTGAT 1169
Db 1069 TTAAT 1073

RESULT 6
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE OF INVENTION: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CBI
;
; US-09-976-594-403

Query Match 20.3%; Score 341.6; DB 4; Length 1195;
Best Local Similarity 60.1%; Pred. No. 2.3e-83;
Matches 626; Conservative 0; Mismatches 404; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATG3ACAA 264
Db 66 TCTTCCCAAGGACTGCTGTTCCAGCGTGGAT-----TTTAAACCGAGCGACGGACAA 119
Qy 265 CGTGACCGTCCGCGAGGGGAGAGCGCCACCTCAGGTGCACTATTTCACACCGGTCAC 324
Db 120 CATCACCGTGAAGGAGGGGAGACAGCCATCTCCTCAGGTGCGTTCTAGAAGACAAGAACTC 179
Qy 325 CCGGCTGCGCTGCTTAAACCGCAGCACCATCTCTATGCTGGGAATGACAAGTGGTGCCT 384
Db 180 AAGGTGCGCTGCTTGAACCGCTTCTGCAATCATTTTTGCTGGACATGACAAAGTGGTCTCT 239
Qy 385 GGATCTCTGCGTGGTCTCTCTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db 240 GGACCCACGGGTTGAGCTGGAGAAAACGCCATTTCTTGGAAATACAGCCTCCGAAATCCAGAA 299
Qy 445 CGTGATGTGTATGACGAGGCGCTTACACCTGCTCGGTGCGAGACAGACACACCCCAA 504
Db 300 GGTGGATGTCTATGATGAGGGTTCTTACACTTGTCTCAGTTCTCAGACACAGCATGAGCCCAA 359
Qy 505 GACCTCTAGGCTCCACCTCTATTGTGCAAGTATCTCCCAAAATTTGTAGAGATTTCTTCTAGA 564
Db 360 GACCTCCCAAGTTTACTTGTATGATCGTACAGTCCCAACCAAGATCTCCCAATATCTCTCGGA 419
Qy 565 TATCTCAATTAATGAAGGGAAACAATATTAGCCTCACCTGCAATAGCAACTGCTAGACACCA 624
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Db 420 TGTCACTGTGAATGAGGCGACGACGCTGCTGTCTGCTGCAATGCGCGCTCTCTGA 479
QY 625 GCCTACGTTACTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTAGTGAAGACGA 684
Db 480 ACCTGTTATACCTCGGAGACACCTTACACCAACTGGAAAGGAAATTTGAAGGAGAAGA 539
QY 685 ATACTTGGAAATTCAGGGCATCACCGGGAGCAGTACAGGAGCTACAGTGCAGTGCCTC 744
Db 540 ATATCTGGAGATCCTTGGCATCACCGGAGAGCTCAGGCAATATGAGTCAAGCTGC 599
QY 745 CAATGACGTGCGCGCGCTGGTACGAGAGATGAAGTCAACGTGAACTATCCACCATA 804
Db 600 CAACGAGGTCTCTCGCGGATGTCAACAAAGTCAAGGTCACTGTGAATCTCTCCACC 659
QY 805 CATTTGAGAACCAAGGTGACAGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGA 864
Db 660 TATCACAGAAATCCAAGAGCAATGAAGCCACACAGGACGACAGCTTCACTCAAAATGTGA 719
QY 865 AGCTTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGATGACAAAAGACTGATTGA 924
Db 720 GGCCTCGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGATGACACTAG---GATAAA 776
QY 925 AGGAAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTCATCTTTCTCAA 984
Db 777 TAGTGCCAAATGGCTTGAGATTAAGAGCACGAGGGCCAGTCTTCCCTGACGGTGACCAA 836
QY 985 TGTCTCTGAACATGACTATGGAATACACTTGGTGGCTCCAAAGCTGGGCGCAC 1044
Db 837 CGTCACTGAGGAGCACTACGCGCACTACACCTGTGTGGCTGCCAACAAAGCTGGGGGTAC 896
QY 1045 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCGAGGTGACAAACGGCAGCTC 1104
Db 897 CAATGCCAGCTAGTCTCTTTTCAGACCTGGTGGTGAG---AGGAATAATGATCCAT 953
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Db 954 CAGTCTGCGCGTACCACCTGTGGCTGTGGCAGCATCTCTGCTGTGCTTCTCAGCAAAATG 1013
QY 1165 TTGATGTAGTGCCACTTCCCAACCGGGAAGGCTGCGGCGCACCAACACCAACACCA 1224
Db 1014 TTAATAGAAATAAAATTTTAAATAATTTTAAATAACACACAAAAATGCGTCACACAGAT 1073
QY 1225 ACAGCAATGGCAACACCGACAG 1246
Db 1074 ACAGAGAGAGAGACAGAGAG 1095

RESULT 7

US-08-414-657D-7
; Sequence 7, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...924
; OTHER INFORMATION:
; US-08-414-657D-7

Query Match 20,3%; Score 340.6; DB 2; Length 924;
Best Local Similarity 63.3%; Pred. No. 3.7e-83;
Matches 558; Conservative 0; Mismatches 314; Indels 9; Gaps 2;

QY 205 TCTCTTCCAAAGGAGTGGCGTGGCGAGGAGATGCCACCTTCCCCAAAGCTATGGACAA 264
Db 45 TCTTCCACACAGGACTGCTGTTCGACGCTGGAT-----TTTAAACGAGGACGACGAA 98
QY 265 CGTGAACGCTCGGAGGAGGAGCGGCCACCTCAGGTGCACTATTGACACCGGCTCAC 324
Db 99 CATCACGCTGAGGAGGAGGAGCACAGCCATCTCTCAGGTGCGTTCTAGAAGAACAAGAACTC 158
QY 325 CCGGCTGCGCTGGCTTAAACGCGACACCTCTCTATGCTGGGAATGACAAAGTGGTGCCT 384
Db 159 AAGGTGGCTGGTTGAACGCTTCTGGCATCATTTTCTGGACATGACAAAGTGGTCTCT 218
QY 385 GGATCCTCGGTGGTCTCTCTTGAGCAACACCCAAACGACGTACAGCATCGAGATCCAGAA 444
Db 219 GGACCCACGGGTTGAGCTGGAGAAACGCAATCTCTGGAAATACAGCCTCCGAATCCAGAA 278
QY 445 CGTGGATGTATGACGAGGCGCTTACACCTGCTCGGTGACAGACACACCCCAAA 504
Db 279 GGTGGATGTCTATGATGAGGGTTCCTACACTTGTCTCAGATTCAGACACAGCATGAGCCCAA 338
QY 505 GACCTCTAGGCTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGAGAGATTTCTTCAGA 564
Db 339 GACCTCCCAAGTTTACTTGTATCGTACAAAGTCCCAACCAAGATCTCCAATATATCTCTCGGA 398
QY 565 TATCTCCATTAATGAAGGGAAACAATATTAGCTCTCACCTGCTATAGCAACTGGTAGACCAGA 624
Db 399 TGTCACTGTGAATGAGGCGACCAAGTGACTCTGTGCTGTCATGGCCAATGGCCGCTCTGA 458
QY 625 GCCTACGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTGAGTGAAGACGA 684
Db 459 ACCTGTTATCACCTGGAGACACCTTTACACCAACTGGAAAGGGAATTTGAAGGAGAAGAAGA 518
QY 685 ATACTTGGAAATTCAGGCGCATCACCGGAGCAGTACAGGAGCTACAGAGTGCAGTGCCTC 744
Db 519 ATATCTGGAGATCCTTGGCATCACCGGAGCAGTACAGGCAATATATGAGTGCAGAGCTGC 578
QY 745 CAATGACGTGCGCGCGCTGGTACCGGAGATGAAGGTCAACCGTGAATATCCACCATA 804
Db 579 CAACGAGGTCTCTCGCGGATGTCAACAAAGTCAAGGTCACTGTGAATATCTCTCCACC 638
QY 805 CATTTGAGAGCCCAAGGTGACAGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGA 864
Db 639 TATCACAGAAATCCAAGAGCAATGAAGCCACACAGGAGCAAGCTTCACTCAAAATGTGA 698


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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1014
; OTHER INFORMATION:
; US-08-414-657D-5

Query Match      20.3%; Score 340.6; DB 2; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 205 TCTCTTCCAAAGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAGCTATGGACAA 264
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCCAAGAGTCCGCTGTCGCGAGGAGATGCCACCTTCCCAAGCTATGGACAA 119
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
265 CGTGACGCTCCGCGAGGAGGAGCGCCACCTCAGGTGCACTATTGACACCGGTCAC 324
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGGCGAGGAGGAGCGCCATCCTCAGGTGTCGTGTAGAGACAAAGACTC 179
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325 CCGGTGCGCTGGCTTAACCCGAGCACCATCCTCTATGCTGGGAATGACAAAGTGTGCT 384
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180 GAAAGTGGCTGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGCAAGTGTCTCT 239
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385 GGATCCTCGCGTGTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 GGACCTCGGTGAGCTGGAGAAACGCGCATGCTCTGGAATACAGCCTCCGGAATCCAGAA 299
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
445 CGTGATGTATGACGAGGCGCTTACACCTGCTCGGTGAGACAGACACACCCCAAA 504
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 GGTGATGTCTATGATGAAGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCA 359
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505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCA 564
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
360 GACCTCTCAAGTTACTTGTATGTTGACAGTTCCACCAAGATCTCCACATCTCTCGGA 419
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
565 TATCTCCATTAATGAAGGAAACAATATTAGCTCACCTGCAATAGCAACTGCTAGACCA 624
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420 TGTCACTGTAATGAGGCGAGCAATGTAACCTGCTGCAATGGCGGCGCCCTGA 479
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
625 GCCTACGCTTACTTGGAGACACATCTCTCCAAAGCGTTTGGCTTTGTGAGTGAAGCA 684
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
480 ACCTGTTATCACTCGTGAGACACCTTACACCACTTTGGAAGAAATTTGAAGGAGAA 539
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685 ATACTTGAATTCAGGGCATCACCGGGAGCAGTCAGGCGACTACAGTGCAGTGCCTC 744
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
540 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCAGGCAATATATGATGCAAGGCTGC 599
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745 CAATGACGTGCGCGCGCTGGTACGGAGAGTAAAGGTCAACGTCACCGTGAATCCACCA 804
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
600 CAACGAGGTCTCTCCGCGGATGTCAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659
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805 CATTTCAAGCAAGGATGACAGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGA 864
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660 CATCACAGGTCTAAGACAAATGAAGCCACACAGGACGACAAGCTTCCCTCAAAATGTA 719
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865 AGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGATGACAAAAGACTGATTGA 924
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
720 AGCCTCAGCGGTGCTGCACTGACTTTGAGTGGTACCGGATGACACCG---GATAAA 776
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925 AGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTCATCTTTCTCAA 984
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777 CAGTGCAAAAGCGCTTGAGATTAAGAGCACTGAGGGCCAGTCTCTCCCTGACGGTGACCA 836
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985 TGTCTCTGAAACATGATATGGAACATACTTGTGGTGGCTCCCAAGAGCTGGGCGACAC 1044
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
837 CGTCACTAGGAAACACTACGGCAACTATACCTGTGTGGCTGCCAACAGCTCGGCGTCA 896
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1045 CAATGCCAGCATATGCTATTGTTGTCAGGCGCGCTCAGCGAGTGAACAGCGCAGTGC 1104
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
897 CAATGCCAGCCTAGTCTCTTTTACAGACCCGGGTGCGGTGAG---AGGAATCAACGGATCCAT 953
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Qy 1105 GAGAGGGCAGGCTGCGTCTGTGGTGTGCTCTTCTGTGCTTGGACCTGTCTCAAATT 1164
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
954 CAGTCTGCGCGTACCACCTGTGGTGTGCTGGCAGCGTCCCTGCTTCTCAGCAAATG 1013
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Qy 1165 T 1165
Db 1014 T 1014

RESULT 11
US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1014 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1014
; OTHER INFORMATION:
; US-09-135-080-7

Query Match      20.3%; Score 340.6; DB 3; Length 1014;
Best Local Similarity 61.9%; Pred. No. 3.9e-83;
Matches 595; Conservative 0; Mismatches 354; Indels 12; Gaps 3;

Qy 205 TCTTTTCCAGGAGTCCCGTGGCGCAGGAGATGCCACCTTCCCAAGCTATGGACAA 264
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
66 TCTTCCACAGGACTGCCCGTTCGACGCTGGAT-----TTTAAACGAGGACGAGCAA 119
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265 CGTGACGCTCCGCGAGGCGGAGCGCCACCTCAGGTGCACTATTGCAACCGGTCAC 324
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
120 CATCACCGTGAGGCGAGGAGGAGACCGGCCATCTCAGGTGTGTGTGTAGAGACAAAGACTC 179
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325 CCGGTGCGCTGGCTTAAACCCGAGCACCATCCTCTATGCTGGGAATGACAAAGTGTGCT 384
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180 GAAAGTGGCTGTTGAACCGCTCTGGCATCATCTTCGCTGGACACGCAAGTGTCTCT 239
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
385 GGATCCTCGCGTGTCTTCTTGAGCAACACCCAAACGAGTACAGCATCGAGATCCAGAA 444
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
240 GGACCTCGGTGAGCTGGAGAAACGCGCATGCTCTGGAATACAGCCTCCGGAATCCAGAA 299
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445 CGTGATGTATGACGAGGCGCTTACACCTGCTCGGTGAGACAGACACACCCCAAA 504
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
300 GGTGATGTCTATGATGAAGATCCTACACATGCTCAGTTCAGACACAGCATGAGCCCA 359
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505 GACCTCTAGGGTCCACCTCATTGTGCAAGTATCTCCCAAAATTTAGAGATTTCTTCA 564
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
360 GACCTCTCAAGTTACTTGTATGTTGACAGTTCCACCAAGATCTCCACATCTCTCGGA 419
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
565 TATCTCCATTAATGAAGGAAACAATATTAGCTCACCTGCAATAGCAACTGCTAGACCA 624
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420 TGTCACTGTAATGAGGCGAGCAATGTAACCTGCTGCAATGGCGGCGCCCTGA 479
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625 GCCTACGCTTACTTGGAGACACATCTCTCCAAAGCGTTTGGCTTTGTGAGTGAAGCA 684
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480 ACCTGTTATCACTCGTGAGACACCTTACACCACTTTGGAAGAAATTTGAAGGAGAA 539
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685 ATACTTGAATTCAGGGCATCACCGGGAGCAGTCAGGCGACTACAGTGCAGTGCCTC 744
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540 ATATCTGGAGATCTTAGGCATCACAGGGAACAGTCAGGCAATATATGATGCAAGGCTGC 599
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745 CAATGACGTGCGCGCGCTGGTACGGAGAGTAAAGGTCAACGTCACCGTGAATCCACCA 804
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
600 CAACGAGGTCTCTCCGCGGATGTCAACAAGTCAAGGTCACTGTGAACTATCCACCCAC 659
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805 CATTTCAAGCAAGGATGACAGTGTCCCGTGGGACAAAGGGGACACTGCAAGTGA 864
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865 AGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGGTACAAAGATGACAAAAGACTGATTGA 924
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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925 AGGAAAGAAAGGGGTGAAGTGGAAAAACAGACCTTTCTCTCAAAACTCATCTTTCTCAA 984
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
777 CAGTGCAAAAGCGCTTGAGATTAAGAGCACTGAGGGCCAGTCTCTCCCTGACGGTGACCA 836
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985 TGTCTCTGAAACATGATATGGAACATACTTGTGGTGGCTCCCAAGAGCTGGGCGACAC 1044
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837 CGTCACTAGGAAACACTACGGCAACTATACCTGTGTGGCTGCCAACAGCTCGGCGTCA 896
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1045 CAATGCCAGCATATGCTATTGTTGTCAGGCGCGCTCAGCGAGTGAACAGCGCAGTGC 1104
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897 CAATGCCAGCCTAGTCTCTTTTACAGACCCGGGTGCGGTGAG---AGGAATCAACGGATCCAT 953
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```


APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
NUMBER OF SEQUENCES: 60

ADDRESS: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/414,657D
FILING DATE: 31-MAR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-102
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 945 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 1...945
OTHER INFORMATION:
US-08-414-657D-8

Query Match 20.1%; Score 337.4; DB 2; Length 945;

Best Local Similarity 63.1%; Pred. No. 2.8e-82;

Matches 556; Conservative 0; Mismatches 316; Indels 9; Gaps 2;

QY 205 TCTCTTCCAGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCCAAAGCTATGGCAA 264

Db 66 TCTTCCACAGACTGCCCGTTCGCAGCGTGGAT-----TTTAAACCGAGGCACGGCAA 119

QY 265 CGTGACGTCGGCAGGGGGAGAGCGCCACCTCAGGTGCACATTGACAAACCGGTAC 324

Db 120 CATCACCGTGAGCGAGGGGGACACGGCCATCTCAGGTGTGTGGTGAAGAACAAGACTC 179

QY 325 CCGGTGCGCTGGCTTAACCGCAGCACCATCTCTATCTGGGAATGACAAGTGTGCT 384

Db 180 GAAAGTGCCTGGTTGAACCGCTCTGGCATCATCTTCGTGACACGACAAGTGTCTCT 239

QY 385 GGATCCTCGCGTGTCTTCTTGAGCAACACCCAAACGCGAGTACAGCATCGAGATCCAGAA 444

Db 240 GGACCTCGGTGTAGCTGGAGAAACGCATGCTCTGGAATACAGCTCCGGAATCCAGAA 299

QY 445 CGTGATGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAACCCCAAA 504

Db 300 GGTGGATGTATGATGAAGGATCTTACACATGCTCAGTTTCCAGACACAGCATGAGCCCAA 359

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QY 625 GCCTACCGTTACTTGGAGACACATCTCTCCCAACGCGTGTGGCTTTGTGAGTGAAGACGA 684

Db 480 ACCTGTTATCACCTGGAGACACCTTTACACCACTTTGGAAGAGAAATTTGAAGAGAGAAGA 539

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Db 660 CATCACAGAGTCTTAAGAGCAATGAAGCCACCAAGGAGGACAGCTTCCCTCAATGTGA 719

QY 865 AGCCTCAGCAGTCCCTCCTCAGCAGAAATTCAGTGTGTACAAAGGATGACAAAGACTGATTGA 924

Db 720 AGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACCGGATGACACCCAG--GATAAA 776

QY 925 AGAAAGAAAGGGGTGAAGTGGAAACAGACACCTTTCTCTCAAAACATCATCTTCTTCAA 984

Db 777 CAGTCAAAACGGCCTTGAGATTTAAGAGCACTGAGGGCCAGTCTCTCCCTGACCGTGACCA 836

QY 985 TGTCTCTGAACATGACTATGGAACATACACTTGTGCGTCCCAACAGCTGGGGCCACAC 1044

Db 837 CGTCACTGAGGAACACTACGGCAACTATACCTGTGTGCTGCCAACAAAGCTCGGGTGCAC 896

QY 1045 CAATGCCAGCATCATGCTATTGTTGTCAGGCGCGCTCAGCG 1085

Db 897 CAATGCCAGCTAGTCTCTTTTCAGACCCCGGTGCGTGAGAG 937

RESULT 15

US-08-414-657D-10
; Sequence 10, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259

TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
; OTHER INFORMATION:
US-08-414-657D-10

Search completed: October 30, 2005, 11:29:30
Job time : 403 secs

Query Match 19.9%; Score 333.8; DB 2; Length 861;
Best Local Similarity 63.4%; Pred. No. 2.6e-81;
Matches 528; Conservative 0; Mismatches 302; Indels 3; Gaps 1;

QY	253	AGCTATGACAAAGTGGCGTCCGGCAGGGGAGAGCCACCTCAGGTGCACTATTGA	312
DB	24	AGGCACGGACAACATCACCGTGAGCGCAGGGGACACGGCCATCTCAGGTGTGTGTA	83
QY	313	CAACCGGGTCAACCGGGTGGCTAAACCGGAGCACCCTCTATGCTGGGAATGA	372
DB	84	AGACAAGAACTCGAAGTGGCTGTGTAACCGCTCTGGCATCATCTTCGCTGGACAGA	143
QY	373	CAAGTGGTGCCTGGATCCTCGCGTGTCTTCTGAGCAACACCCAAACGCAGTACAGCAT	432
DB	144	CAAGTGGTCTCTGGACCTCGGGTTAGCTGGAGAAACGCCATGCTCTGGAATACAGCT	203
QY	433	CGAGATCAGAAAGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGACAGAGA	492
DB	204	CCGAATCCAGAAAGTGGATGTCTATGATGAAGGATCTTACACATGCTCAGTTCAGACACA	263
QY	493	CAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGA	552
DB	264	GCATGAGCCCAAGACCTCTCAAGTTTCTGATTTGTAAGTTTCCACCAAGATCTCAA	323
QY	553	GATTTCTTTCAGATATCTCCATTATGAAGGAACAATATTAGCCTCAGCTGCATAGCAAC	612
DB	324	CATCTCTCGGATGTCACTGTGAATGAGGCGAGCAATGTAACTTGGTCTGCATGGCCAA	383
QY	613	TGGTAGCAGGCTACGGTTACTTGGAGACACATCTCTCCAAAGGGTTGGCTTTGT	672
DB	384	TGGGCGCCCTGAACCTGTATATCCTCGAGACACCTTACACCACTTGGAGAGAAATTTGA	443
QY	673	GAGTGAAGACCAATACTTTGGAAATTCAGGGCATCACCGGGAGCAGTCCAGGGACTAGA	732
DB	444	AGGAGAAGAGAATATCTGGAGATCTTAGGATCCTACCGGGAAACAGTCAGGCAAAATATGA	503
QY	733	GTGCAGTGCCTCCCAATGACGTGGCGCGCCCGTGTACGGAGAGTAAAGGTCAAGGTGAA	792
DB	504	GTGCAAGGCTGCCAAGCAGGTCTCTCTCGCGGATGTCAAACAAGTCAAGGTCACTGTGA	563
QY	793	CTATCCACCATACATTTTCAAGCAAGGTTACAGGTGTCCCGTGGGACAAAGGGGAC	852
DB	564	CTATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGACAAGCTTC	623
QY	853	ACTGAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTACAGGATGACAA	912
DB	624	CCTCAAATGTGAAGCTCAGCGGTGCTGACCTGACCTTTGAGTGGTACCGGGATGAC	683
QY	913	AAGACTGATTGAAGGAAGAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAACT	972
DB	684	CAG---GATAACAGTGCANAAGCGCTTGAGATTAAAGCACTGAGGGCCAGTCTCCCT	740
QY	973	CATCTTTCTTAATGTCTCTGAACATGACTATGGGAATCTACACTTGCCTGGCTCCAAACA	1032
DB	741	GACGGTGACCAACGCTCACTGAGGAACACTACGGCAACTATACCTGTGTGGCTGCCAACAA	800
QY	1033	GCTGGGCCACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGCTCAGCG	1085
DB	801	GCTCGGGGTCCCAATGCCAGCTAGTCTCTTTTTCAGACCCCGGGTCCGGTGAGAG	853

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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 30, 2005, 07:42:46 ; Search time 5171 Seconds
(without alignments)
3223.476 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKHNSISWAIPTGL.....RRAGCVWLLPLVLHLLKLF 344

Scoring table:
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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-DB=GenEmbl -QWTF=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALLIGN=200 -THR SCORES=ptc -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sv.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	1032	6	AR439648 Sequence
2	1806	100.0	1679	6	CQ768055 Sequence
3	1806	100.0	1679	6	AR528639 Sequence
4	1806	100.0	1679	6	AX358872 Sequence

5	1806	100.0	1679	6	AX362365 Sequence
6	1806	100.0	1679	6	AX403748 Sequence
7	1806	100.0	1679	6	AX454470 Sequence
8	1806	100.0	1679	6	AX464242 Sequence
9	1806	100.0	1679	6	AX490948 Sequence
10	1806	100.0	1679	9	AY358331 Homo sapi
11	1806	100.0	1693	6	AX439649 Sequence
12	1665.5	92.2	1839	6	AX665342 Sequence
13	1665.5	92.2	1839	9	AF126426 Homo sapi
14	1650	91.4	1068	6	AX665344 Sequence
15	1647.5	91.2	1615	10	BC023307 Mus muscu
16	1644	91.0	1104	6	AX665346 Sequence
17	1642	90.9	939	6	AX439650 Sequence
18	1639.5	90.8	2040	10	RNU16845
19	1638	90.7	1140	6	AX665348 Sequence
20	1616.5	89.5	1410	10	AF282980
21	1517	84.0	868	6	CQ729109 Sequence
22	1500.5	83.1	1325	9	BC050716 Homo sapi
23	1477.5	81.8	1257	5	GGCEPUI
24	1428	79.1	1058	5	AF292935
25	1427.5	79.0	1035	5	AB011810 Gallus ga
26	1393	77.1	1638	12	AF271233 Synthetic
27	1357.5	75.2	1013	5	AF292936
28	1307	72.4	6005	10	BC076581
29	1306.5	72.3	3216	5	GGCEPUS
30	1306	72.3	1533	5	FFNINH55A
31	1296.5	71.8	6380	9	MSM805672
32	1286.5	71.2	3069	10	RATCALMA
33	1276.5	70.7	1370	5	BC074283
34	1275.5	70.6	1556	5	AF292934
35	1271.5	70.4	2935	12	AF271618
36	1270.5	70.3	1108	9	BC074742
37	1268	70.2	1111	9	BC074773 Homo sapi
38	1268	70.2	1478	9	HUMOBICAM
39	1268	70.2	3110	6	AX665340 Sequence
40	1267	70.2	2593	4	BT0BCAM
41	1259	69.7	2179	10	RATCALMB
42	1259	69.7	2337	10	RATCALMC
43	993.5	55.0	2055	5	BC081685
44	951	52.7	756	12	AF271232
45	946	52.4	1107	5	GGLAMPG9
46	938.5	52.0	1158	5	GGLAMPGI9
47	938.5	52.0	2050	5	GGBI9SPRO
48	932.5	51.6	1640	9	BC033803
49	931.5	51.6	1017	9	HSU41901
50	931.5	51.6	1195	6	AR447794
51	930.5	51.5	1194	5	GGLAMPG11
52	926.5	51.3	1014	6	AR030577
53	926.5	51.3	1014	6	AR220260
54	926.5	51.3	1238	6	AR030575
55	926.5	51.3	1238	6	AR220258
56	926.5	51.3	1238	10	RNU31554
57	923.5	51.1	977	6	AR030574
58	923.5	51.1	977	6	AR220257
59	913	50.6	1276	10	AY326256
60	911	50.4	1410	5	BC074296
61	908	50.3	924	6	AR030579
62	907	50.2	945	6	AR030580
63	902	49.9	912	6	AR030578
64	893	49.4	1757	6	AX704805
65	886.5	49.1	861	6	AR030581
66	885.5	49.0	861	6	AR030582
67	868	48.1	1941	5	AF241638
68	859	47.6	503	5	CQ768057
69	842	46.6	1059	5	GGA132999
70	823	45.6	1196	6	AX662341
71	823	45.6	1327	6	AX704747
72	823	45.6	4834	6	AX358748
73	823	45.6	4834	6	AX362241
74	823	45.6	4834	6	AX403774
75	823	45.6	5582	9	MSM806161
76	822	45.4	1119	6	AX675563
77	820	45.4	2383	6	AX747470

78	820	45.4	2383	9	AK092307	AK092307 Homo sapi	151	297.5	16.5	84246	3	AC002512	AC002512 Drosophil
79	819	45.3	1165	6	AX662343	AX662343 Sequence	c 152	297.5	16.5	110000	3	AE001572_2	Continuation (3 of
80	815	45.1	1809	10	AB017139	AB017139 Rattus no	153	297.5	16.5	170801	3	AC095014	AC095014 Drosophil
81	815	45.1	2840	9	AX358132	AX358132 Homo sapi	154	297.5	16.5	298020	3	AE003674	AE003674 Drosophil
82	814	45.1	1179	10	MMU487032	AU487032 Mus muscu	c 155	293	16.2	157263	2	EX957285	EX957285 Danio rer
83	796.5	44.1	756	6	AR030589	AR030589 Sequence	156	290.5	16.1	8546	6	AX828406	AX828406 Sequence
84	795.5	44.0	756	6	AR030590	AR030590 Sequence	157	290.5	16.1	8546	6	HSA306906	AJ306906 Homo sapi
85	768.5	42.6	5605	9	BC036771	BC036771 Homo sapi	158	290.5	16.1	18207	6	AX828384	AX828384 Sequence
86	761	42.1	1017	6	AX644995	AX644995 Sequence	159	290.5	16.1	18207	6	AF156100	AF156100 Homo sapi
87	761	42.1	1018	6	AX644993	AX644993 Sequence	160	288.5	16.0	4073	6	AX269342	AX269342 Sequence
88	757	41.9	1136	6	AX644997	AX644997 Sequence	161	287.5	15.9	4398	5	D85084	D85084 Cynops pyrr
89	755.5	41.8	2070	5	BC080221	BC080221 Danio rer	162	284.5	15.8	1710	6	CQ588165	CQ588165 Sequence
90	755.5	41.8	2455	5	AF241637	AF241637 Danio rer	163	283.5	15.7	2583	10	MMNCAMR	Y00051 Mouse mrNA
91	742.5	41.1	1031	6	CQ728011	CQ728011 Sequence	164	282.5	15.6	2262	10	MMNCAMR	I15049 Mouse commo
92	721	39.9	1169	6	AX644999	AX644999 Sequence	165	282.5	15.6	2544	10	BC011310	BC011310 Mus muscu
c 93	704	39.0	203572	9	AC016769	AC016769 Homo sapi	166	279.5	15.5	2178	5	AB008162	AB008162 Xenopus l
c 94	670	37.1	197553	2	AC146103	AC146103 Pan trogl	167	279	15.4	237376	2	AC124949	AC124949 Rattus no
c 95	656.5	36.4	4323	10	AK122576	AK122576 Mus muscu	c 168	279	15.4	277228	2	AC106911	AC106911 Rattus no
96	652	36.1	5666	6	AX740565	AX740565 Sequence	169	278.5	15.4	1580	5	CR354352	CR354352 Gallus ga
97	632	35.0	537	6	AX593044	AX593044 Sequence	170	278.5	15.4	12699	5	D83390	D83390 Gallus gall
98	599	33.2	786	5	GCN13298	GCN13298 Gallus Ga	171	277.5	15.4	3170	10	RNNCAM14	X06564 Rat mrNA fo
99	578	32.0	452	6	AX079423	AX079423 Sequence	172	277.5	15.4	3720	5	XELNCAM	M25696 X.laevis ne
100	545	30.2	333	6	AX907426	AX907426 Sequence	173	277.5	15.4	4454	5	BC081181	BC081181 Xenopus l
101	545	30.2	333	6	BD042959	BD042959 Sequence	174	276.5	15.3	2256	5	BC057517	BC057517 Danio rer
102	509.5	28.2	531	6	CQ719449	CQ719449 Sequence	175	276	15.3	2799	9	HSNCAME	X16841 Human mrNA
103	490.5	27.2	585	6	AX079674	AX079674 Sequence	176	276	15.3	2960	6	AX658287	AX658287 Sequence
104	466.5	25.8	793	5	BX932289	BX932289 Gallus ga	177	276	15.3	2960	9	S71824	S71824 N-CAM=145 k
105	430	23.8	504	6	CQ715694	CQ715694 Sequence	178	276	15.3	3266	6	CQ728451	CQ728451 Sequence
106	429.5	23.8	20731	9	AP004721	AP004721 Homo sapi	179	276	15.3	3309	6	AX714869	AX714869 Sequence
107	429.5	23.8	43087	9	AP005155	AP005155 Homo sapi	180	276	15.3	3309	9	AX057509	AX057509 Homo sapi
108	424.5	23.5	168745	2	AC119552	AC119552 Rattus no	181	276	15.3	8513	6	AX207284	AX207284 Sequence
109	424.5	23.5	248329	2	AC109989	AC109989 Rattus no	182	275.5	15.3	3574	4	BTADCYC	X16451 Bovine mrNA
c 110	421	23.3	110000	2	AC102028_1	Continuation (2 of	183	275	15.2	2633	6	AR380405	AR380405 Sequence
c 111	400.5	22.2	408	6	AX684132	AX684132 Sequence	184	275	15.2	2633	9	HSU63041	US3041 Human neur
112	391.5	21.7	540	6	AX665354	AX665354 Sequence	185	274	15.2	5807	6	AR447664	AR447664 Sequence
113	391.5	21.7	116069	2	AP000784	AP000784 Homo sapi	186	273.5	15.1	2118	6	AR506699	AR506699 Sequence
c 114	391.5	21.7	123320	9	AP000863	AP000863 Homo sapi	187	273.5	15.1	2178	5	AB008163	AB008163 Xenopus l
115	391.5	21.7	176676	2	AC012234	AC012234 Homo sapi	188	273.5	15.1	7097	6	AX921114	AX921114 Sequence
116	391.5	21.7	177102	2	AP002808	AP002808 Homo sapi	c 189	273	15.1	184716	2	AC018368	AC018368 Homo sapi
117	382	21.2	642	6	CQ732119	CQ732119 Sequence	190	273	15.1	191071	9	AP004248	AP004248 Homo sapi
c 118	382	21.2	184012	10	AC116523	AC116523 Mus muscu	191	272.5	15.1	2879	5	BC075300	BC075300 Xenopus t
c 119	382	21.2	242565	2	AC094728	AC094728 Rattus no	192	272.5	15.1	3971	5	CHKONNE	D16541 Gallus gall
120	382	21.2	251570	2	AC094463	AC094463 Rattus no	193	272	15.1	131490	10	AC122207	AC122207 Mus muscu
121	378	20.9	371	6	CQ731074	CQ731074 Sequence	194	272	15.1	177251	10	AC124565	AC124565 Mus muscu
122	350.5	19.4	3847	3	BT010243	BT010243 Drosophil	195	271.5	15.0	4321	6	AX921112	AX921112 Sequence
123	349.5	19.4	3460	3	BT011190	BT011190 Drosophil	c 196	271.5	15.0	169582	2	AC102190	AC102190 Mus muscu
124	348	19.3	3590	3	BT003528	BT003528 Drosophil	197	271	15.0	4050	9	BC047244	BC047244 Homo sapi
125	344	19.0	352	6	AX886912	AX886912 Sequence	198	270.5	15.0	3814	5	XELNCAMA	M76710 Xenopus lae
126	344	19.0	352	6	BD026522	BD026522 Sequence	199	270	15.0	2190	6	CQ604731	CQ604731 Sequence
c 127	339	18.8	187203	2	AP000832	AP000832 Homo sapi	c 200	270	15.0	110000	2	AC102028_0	AC102028 Mus muscu
c 128	339	18.8	191204	9	AP000834	AP000834 Homo sapi	c 201	270	15.0	186110	2	AC102204	AC102204 Mus muscu
129	338.5	18.7	1242	6	CQ607488	CQ607488 Sequence	202	269.5	14.9	1912	3	SAREGALPT	X93601 S.americana
130	338.5	18.7	3106	3	AY060653	AY060653 Drosophil	c 203	269	14.9	142000	9	AC078813	AC078813 Homo sapi
131	336	18.6	292	6	CQ716587	CQ716587 Sequence	204	268.5	14.9	4491	6	CQ848038	CQ848038 Sequence
132	333	18.4	411	6	CQ731080	CQ731080 Sequence	205	268.5	14.9	4491	6	CQ848044	CQ848044 Sequence
133	333	18.4	948	6	CQ595959	CQ595959 Sequence	206	268.5	14.9	5510	6	AX409111	AX409111 Sequence
134	308.5	17.1	3927	3	DMU78177	U78177 Drosophila	207	268.5	14.9	5510	9	D86983	D86983 Human mrNA
135	306.5	17.0	2010	6	CQ586755	CQ586755 Sequence	208	268.5	14.9	6847	9	AF200348	AF200348 Homo sapi
136	306.5	17.0	4052	3	AY060363	AY060363 Drosophil	209	268.5	14.9	6939	6	AX780120	AX780120 Sequence
137	303.5	16.8	950	3	AY052162	AY052162 Drosophil	210	268.5	14.9	6939	6	AX780121	AX780121 Sequence
138	303.5	16.8	950	3	AY052163	AY052163 Drosophil	c 211	267	14.8	3060	6	CQ595958	CQ595958 Sequence
139	302.5	16.7	913	6	AR542162	AR542162 Sequence	212	267	14.8	64674	3	AC004247	AC004247 Drosophil
140	300.5	16.6	950	3	AY052156	AY052156 Drosophil	c 213	267	14.8	110526	2	AC019598	AC019598 Drosophil
141	300.5	16.6	950	3	AY052160	AY052160 Drosophil	c 214	267	14.8	174376	3	AC092230	AC092230 Drosophil
142	297.5	16.5	950	3	AY052157	AY052157 Drosophil	c 215	267	14.8	259718	4	AE003614	AE003614 Drosophil
143	297.5	16.5	950	3	AY052158	AY052158 Drosophil	216	266	14.7	268	4	AF271984	AF271984 Bos tauru
144	297.5	16.5	950	3	AY052159	AY052159 Drosophil	217	266	14.7	110000	2	AC110642_3	Continuation (4 of
145	297.5	16.5	950	3	AY052161	AY052161 Drosophil	218	265.5	14.7	6332	10	AK122223	AK122223 Mus muscu
146	297.5	16.5	1110	6	CQ575874	CQ575874 Sequence	219	265	14.7	8035	3	AF254867	AF254867 Drosophil
147	297.5	16.5	1563	3	CQ057874	AY051911 Drosophil	c 220	264	14.6	110000	2	AC110642_2	Continuation (3 of
148	297.5	16.5	2135	3	DROAMA	M23561 D.melanogas	221	263.5	14.6	6814	6	AR220825	AR220825 Sequence
c 149	297.5	16.5	3426	6	CQ575873	CQ575873 Sequence	222	263	14.6	11850	4	AY136513	AY136513 Canis fam
c 150	297.5	16.5	6228	2	AC020270	AC020270 Drosophil	223	262	14.5	3738	5	AY029401	AY029401 Danio rer

224	262	14.5	134184	2	ACL50028	Canis fam
225	261.5	14.5	1314	9	AF538973	Homo sapi
226	261.5	14.5	4619	5	GGF11	XI4877 Gallus gall
227	261.5	14.5	4991	5	GGCONTAC	Y00813 Chicken mRN
228	261.5	14.5	18848	4	OCY14852	YI4852 Oryctolagus
229	261	14.5	863	5	BX935847	BX935847 Gallus ga
230	261	14.5	4188	6	BD085986	BD085986 Method of
231	261	14.5	6440	3	AF040989	AF040989 Drosophil
232	261	14.5	10232	10	AF525411	AF525411 Rattus no
233	260.5	14.4	1956	3	AF134113	AF134113 Drosophil
234	260.5	14.4	2050	3	AY047524	AY047524 Drosophil
235	260.5	14.4	2113	6	CQ585189	CQ585189 Homo sapi
236	260	14.4	4290	9	BC014205	BC014205 Homo sapi
237	260	14.4	4355	6	CQ603804	CQ603804 Sequence
238	259.5	14.4	89623	6	CQ730839	CQ730839 Sequence
239	259	14.3	23887	9	HSTIITNN2	X90569 H. sapiens m
240	259	14.3	93801	6	BD186121	BD186121 Preventio
241	259	14.3	93805	6	CQ730837	CQ730837 Sequence
242	259	14.3	103053	6	CQ848088	CQ848088 Sequence
243	258.5	14.3	4272	6	CQ715893	CQ715893 Sequence
244	258.5	14.3	4833	9	AK125056	AK125056 Homo sapi
245	258	14.3	169206	10	ACL123550	ACL123550 Mus muscu
246	258	14.3	277603	2	AC079543	AC079543 Mus muscu
247	257	14.2	4221	5	BC045307	BC045307 Danio rer
248	256	14.2	2110	3	DR0LACH	LI3255 Fruitfly la
249	256	14.2	2131	6	CQ590793	CQ590793 Sequence
250	256	14.2	2157	3	AY051829	AY051829 Drosophil
251	255.5	14.1	2726	5	AY029402	AY029402 Danio rer
252	255.5	14.1	202505	2	AP000912	AP000912 Homo sapi
253	254.5	14.1	15597	3	AF074901	AF074901 Caenorhab
254	253.5	14.0	2116	6	AX058616	AX058616 Sequence
255	252.5	14.0	175963	2	ACL48913	ACL48913 Sus scrof
256	252	14.0	187746	2	AC087123	AC087123 Mus muscu
257	251.5	13.9	3485	10	AF016619	AF016619 Mus muscu
258	251.5	13.9	3488	10	AF001287	AF001287 Mus muscu
259	251.5	13.9	4496	6	CQ715482	CQ715482 Sequence
260	251.5	13.9	4821	10	AF001286	AF001286 Mus muscu
261	251	13.9	219713	2	ACL12456	ACL12456 Rattus no
262	251	13.9	234283	2	ACL114113	ACL114113 Rattus no
263	251	13.9	250355	2	AC127766	AC127766 Rattus no
264	251	13.9	263661	2	AC106603	AC106603 Rattus no
265	251	13.9	319104	2	ACL06602	ACL06602 Rattus no
266	250.5	13.9	2658	6	CQ583539	CQ583539 Sequence
267	250.5	13.9	4306	3	AF312580	AF312580 Drosophil
268	250.5	13.9	5514	3	BT015246	BT015246 Grasehopper
269	250	13.8	2007	3	SCALACH	LI3256 Grasehopper
270	250	13.8	2895	5	AY029403	AY029403 Danio rer
271	250	13.8	8907	9	AF478693	AF478693 Homo sapi
272	249.5	13.8	3588	6	CQ870412	CQ870412 Sequence
273	249.5	13.8	4306	9	AK124736	AK124736 Homo sapi
274	249.5	13.8	4479	9	HSTAG1	X68274 Homo sapien
275	249.5	13.8	4548	6	AR453309	AR453309 Sequence
276	249.5	13.8	4548	6	AX305052	AX305052 Sequence
277	249.5	13.8	4548	6	HSTAG1A	X67734 H. sapiens m
278	249.5	13.8	6137	6	CQ870414	CQ870414 Sequence
279	249.5	13.8	195993	2	ACL134953	ACL134953 Pan trogl
280	248.5	13.8	295	6	CQ732164	CQ732164 Sequence
281	248.5	13.8	1880	6	AX714170	AX714170 Sequence
282	248.5	13.8	1880	9	AK056336	AK056336 Homo sapi
283	248	13.7	1404	6	CQ605679	CQ605679 Sequence
284	248	13.7	2229	6	CQ729908	CQ729908 Sequence
285	248	13.7	74368	9	AL391239	AL391239 Human DNA
286	248	13.7	131457	9	AL356600	AL356600 Human DNA
287	248	13.7	153852	2	AC009694	AC009694 Homo sapi
288	248	13.7	214942	10	ACL125214	ACL125214 Mus muscu
289	248	13.7	315761	2	ALI58079	ALI58079 Homo sapi
290	247	13.7	172146	2	ACL130272	ACL130272 Papio anu
291	246.5	13.6	2988	9	BC036569	BC036569 Homo sapi
292	246.5	13.6	3314	6	AX556980	AX556980 Sequence
293	246.5	13.6	3314	6	HSU07819	HSU07819 Human conta
294	246.5	13.6	3319	6	CQ727274	CQ727274 Sequence
295	246.5	13.6	3335	9	AX556981	AX556981 Sequence
296	246.5	13.6	3335	9	HSU07820	HSU07820 Human conta

297	246.5	13.6	3360	6	AR001474	AR001474 Sequence
298	246.5	13.6	3360	6	CQ776853	CQ776853 Sequence
299	246.5	13.6	3360	6	I74665	I74665 Sequence 5
300	246.5	13.6	3360	6	I93559	I93559 Sequence 5
301	246.5	13.6	3360	6	AX331543	AX331543 Sequence
302	246.5	13.6	3360	6	AX331937	AX331937 Sequence
303	246.5	13.6	3360	6	AX556979	AX556979 Sequence
304	246.5	13.6	3360	9	HSCNCTNA	221488 H. sapiens c
305	246.5	13.6	3412	10	AY495696	AY495696 Rattus no
306	246.5	13.6	4249	10	AY495695	AY495695 Rattus no
307	246	13.6	3366	9	AK123606	AK123606 Homo sapi
308	246	13.6	4015	6	CQ726266	CQ726266 Sequence
309	246	13.6	4015	9	AB018349	AB018349 Homo sapi
310	246	13.6	168861	2	ACL130786	ACL130786 Papio anu
311	245	13.6	5095	5	BC072368	BC072368 Xenopus l
312	245	13.6	212752	9	AC063977	AC063977 Homo sapi
313	244.5	13.5	830	5	BX933439	BX933439 Gallus ga
314	244.5	13.5	163120	5	EX296535	EX296535 Zebrafish
315	244.5	13.5	180842	2	CR536619	CR536619 Danio rer
316	243.5	13.5	2962	9	AY358125	AY358125 Homo sapi
317	243.5	13.5	3214	10	RATP3A	D38492 Rat mRNA fo
318	243.5	13.5	3362	10	AY371925	AY371925 Mus muscu
319	243.5	13.5	3619	9	BC052946	BC052946 Homo sapi
320	243.5	13.5	3648	9	AY369208	AY369208 Homo sapi
321	243.5	13.5	3967	5	GDAXONIN	X63101 G.domesticu
322	242.5	13.4	3355	10	AY371924	AY371924 Rattus no
323	242.5	13.4	3897	10	BC066864	BC066864 Mus muscu
324	241.5	13.4	3412	4	BOVF3F11C	D32135 Bovine mRNA
325	241.5	13.4	3843	6	CQ777685	CQ777685 Sequence
326	241.5	13.4	3843	10	MMF3	X14943 Mouse mRNA
327	241.5	13.4	3870	6	AX714318	AX714318 Sequence
328	241.5	13.4	3870	9	AK056557	AK056557 Homo sapi
329	241.5	13.4	4723	9	HSU75330	U75330 Human neutra
330	241	13.3	229330	2	AC137057	AC137057 Rattus no
331	241	13.3	238070	2	AC134313	AC134313 Rattus no
332	241	13.3	242260	2	AC094567	AC094567 Rattus no
333	241	13.3	255120	2	ACL127219	ACL127219 Rattus no
334	240	13.2	12667	10	MUSPERPA	M77174 Mouse parle
335	239	13.2	1174	5	BC078550	BC078550 Xenopus l
336	239	13.2	2884	5	CR386716	CR386716 Gallus ga
337	238.5	13.2	2766	6	AX114541	AX114541 Sequence
338	238.5	13.2	2771	6	AX114540	AX114540 Sequence
339	238.5	13.2	2771	6	AX114542	AX114542 Sequence
340	238.5	13.2	3060	6	AX114543	AX114543 Sequence
341	238.5	13.2	3065	6	AX114539	AX114539 Sequence
342	238.5	13.2	3065	6	AX114544	AX114544 Sequence
343	237.5	13.2	5975	10	AK173030	AK173030 Mus muscu
344	237	13.1	219	6	AR030583	AR030583 Sequence
345	237	13.1	219	6	AR030584	AR030584 Sequence
346	236.5	13.1	2611	3	HMU92814	U92814 Hirudo medi
347	236	13.1	2451	6	CQ850834	CQ850834 Sequence
348	236	13.1	2451	9	AK128020	AK128020 Homo sapi
349	235.5	13.0	3373	5	AF461120	AF461120 Danio rer
350	235.5	13.0	4086	6	CQ850958	CQ850958 Sequence
351	235.5	13.0	4086	9	AK128160	AK128160 Homo sapi
352	235.5	13.0	4233	5	GGA309935	AXJ309935 Gallus ga
353	235.5	13.0	7872	9	AY273815	AY273815 Homo sapi
354	234.5	13.0	1198	5	BX935151	BX935151 Gallus ga
355	234.5	13.0	4053	3	AF103899	AF103899 Manduca s
356	234.5	13.0	5040	10	RATTAG1	M31725 Rat axonal
357	234.5	13.0	5626	3	AF103900	AF103900 Manduca s
358	234.5	13.0	39130	3	CBRG42E21	AC084594 Caenorhab
359	234	13.0	2420	6	AX746808	AX746808 Sequence
360	234	13.0	2420	9	AK091149	AK091149 Homo sapi
361	233.5	12.9	1427	6	AX454490	AX454490 Sequence
362	233.5	12.9	1427	6	AX490968	AX490968 Sequence
363	233.5	12.9	3682	9	AB013803	AB013803 Homo sapi
364	233.5	12.9	3904	6	CQ875308	CQ875308 Sequence
365	233.5	12.9	3904	6	CO6013802	CO6013802 Homo sapi
366	233.5	12.9	8410	6	CO603803	CO603803 Sequence
367	233.5	12.9	16652	2	AC014298	AC014298 Drosophil
368	233.5	12.9	169534	3	AE008350	AE008350 Drosophil
369	233.5	12.9	302225	3	AE003458	AE003458 Drosophil

370	233	12.9	3413	10	D87248	D87248 Rattus norv	443	224.5	12.4	7642	9	AF002246	Homo sapi
371	233	12.9	4956	5	BC044084	BC044084 Xenopus 1	444	224.5	12.4	7647	6	AR454602	Sequence
372	232.5	12.9	1073	5	DRU63292	U63292 Danio rerio	445	224	12.4	2436	9	BSM805023	Sequence
373	232.5	12.9	2611	10	AF115400	AF115400 Mus muscu	446	224	12.4	2500	6	CQ783752	Sequence
374	232.5	12.9	36859	3	U800022	U80022 Caenorhabdi	447	224	12.4	2500	6	BD127814	Primer fo
c 375	232.5	12.9	126899	3	AY130758	AY130758 Caenorhab	448	224	12.4	2500	9	AK074921	Homo sapi
376	232	12.8	7876	6	AX592082	AX592082 Sequence	449	224	12.4	3662	6	BD172466	Secreted
377	232	12.8	8270	6	AX592092	AX592092 Sequence	450	224	12.4	3662	6	BD172785	Secreted
378	232	12.8	152686	2	AC018913	AC018913 Homo sapi	451	224	12.4	3662	6	BD173104	Secreted
379	231.5	12.8	3218	5	D86505	D86505 Xenopus lae	452	224	12.4	3662	6	BD173423	Secreted
380	231.5	12.8	3821	10	MUSURAM	L02844 Mus musculu	453	224	12.4	3662	6	BD175457	Secretory
381	231.5	12.8	173270	9	AC024886	AC024886 Homo sapi	454	224	12.4	3662	6	AR410836	Sequence
382	231	12.8	3087	10	AB032602	AB032602 Mus muscu	455	224	12.4	3662	6	AR439200	Sequence
383	231	12.8	3346	6	C0728965	C0728965 Sequence	456	224	12.4	3662	6	AR473220	Sequence
384	231	12.8	3442	6	BD190857	BD190857 Secreted	457	224	12.4	3662	6	AR527206	Sequence
385	231	12.8	3530	9	AB003592	AB003592 Homo sapi	458	224	12.4	3662	6	AR566239	Sequence
386	231	12.8	4189	10	AF317839	AF317839 Mus muscu	459	224	12.4	3662	6	AX098383	Sequence
387	230.5	12.8	1766	6	CQ731700	CQ731700 Sequence	460	224	12.4	3662	6	AX697698	Sequence
388	230.5	12.8	2855	10	RNU334985	U34985 Rattus norv	461	224	12.4	3662	6	BD075606	Secretory
389	230.5	12.8	2869	6	A72401	A72401 Sequence 2	462	224	12.4	3662	9	AY358295	Sequence
390	230.5	12.8	2869	6	AR043363	AR043363 Sequence	463	224	12.4	3810	10	AF531873	Mus muscu
391	230.5	12.8	2869	6	I60497	I60497 Sequence 2	464	224	12.4	3864	9	AY505340	Homo sapi
392	230.5	12.8	2869	6	AR217165	AR217165 Sequence	465	224	12.4	4053	6	BD172468	Secreted
393	230.5	12.8	4988	5	BC066766	BC066766 Danio rer	466	224	12.4	4053	6	BD172787	Secreted
394	230.5	12.8	5868	10	BC066106	BC066106 Mus muscu	467	224	12.4	4053	6	BD173106	Secreted
395	230.5	12.8	8455	6	C0870409	C0870409 Sequence	468	224	12.4	4053	6	BD173425	Secreted
396	230.5	12.8	10976	6	C0869763	C0869763 Sequence	469	224	12.4	4053	6	BD175459	Secretory
397	230	12.7	2610	6	AR043379	AR043379 Sequence	470	224	12.4	4053	6	AR410838	Sequence
398	230	12.7	2610	6	C0847968	C0847968 Sequence	471	224	12.4	4053	6	AR439202	Sequence
399	230	12.7	2610	6	I60505	I60505 Sequence 17	472	224	12.4	4053	6	AR473222	Sequence
400	230	12.7	2610	6	AR217181	AR217181 Sequence	473	224	12.4	4053	6	AR527208	Sequence
401	230	12.7	2659	10	AK129481	AK129481 Mus muscu	474	224	12.4	4053	6	AR528627	Sequence
402	230	12.7	2666	9	AF006464	AF006464 Homo sapi	475	224	12.4	4053	6	AR566241	Sequence
403	230	12.7	2692	9	AY358128	AY358128 Homo sapi	476	224	12.4	4053	6	AX056647	Sequence
404	230	12.7	1793	9	HSEHSP	X62515 H. sapiens m	477	224	12.4	4053	6	AX098387	Sequence
405	229.5	12.7	2004	6	AX834890	AX834890 Sequence	478	224	12.4	4053	6	AX464218	Sequence
406	229.5	12.7	2004	6	AK097578	AK097578 Homo sapi	479	224	12.4	4053	6	AX697702	Sequence
407	229	12.7	5396	5	AF388036	AF388036 Xenopus 1	480	224	12.4	4053	6	BD075608	Secretory
408	228.5	12.7	3707	10	BC065142	BC065142 Mus muscu	481	224	12.4	4053	9	AY358288	Homo sapi
409	228.5	12.7	3893	10	AY053341	AY053341 Mus muscu	482	224	12.4	4256	10	BC076578	Mus muscu
410	228.5	12.7	3980	5	AF064799	AF064799 Danio rer	483	223	12.3	1254	10	AB183401	Mus muscu
411	228	12.6	3613	10	BC076594	BC076594 Mus muscu	484	223	12.3	1254	10	AY351388	Mus muscu
412	227.5	12.6	1954	10	AB114443	AB114443 Rattus no	485	223	12.3	1674	9	BC047021	Homo sapi
413	227.5	12.6	3341	10	D87212	D87212 Rattus norv	486	223	12.3	184716	2	AC1018368	Homo sapi
414	227.5	12.6	3788	5	CHKKGG	M62437 Chicken KLG	c 487	223	12.3	213331	2	AC125960	Rattus no
c 415	227.5	12.6	21829	10	AL645854	AL645854 Mouse DNA	488	222.5	12.3	3795	10	MUSCD22A	Mus musculu
416	227	12.6	4009	6	AX405987	AX405987 Sequence	489	222.5	12.3	95745	9	AL359510	Human DNA
417	227	12.6	4036	9	AB037776	AB037776 Homo sapi	490	222	12.3	4783	6	E34509	Novel rpoA.
418	227	12.6	4230	10	BC040281	BC040281 Mus muscu	491	222	12.3	4783	6	E34511	Novel rpoA.
419	227	12.6	4542	6	C0718773	C0718773 Sequence	492	222	12.3	4783	6	E34513	Novel utill
420	227	12.6	13149	6	C0728817	C0728817 Sequence	493	222	12.3	4783	6	E34515	Human LIG-1
421	227	12.6	186110	2	AC102204	AC102204 Mus muscu	c 494	222	12.3	7171	6	CQ604730	Sequence
422	226.5	12.5	1801	10	BC078966	BC078966 Rattus no	495	222	12.3	10002	2	AC020372	Drosophil
423	226.5	12.5	3870	10	BC036291	BC036291 Mus muscu	c 496	222	12.3	149801	2	CR382301	Danio rer
424	226	12.5	5171	5	BC060500	BC060500 Xenopus 1	497	222	12.3	156022	2	BX324195	Danio rer
425	226	12.5	46638	3	CBU33058	CBU33058 Caenorhabdi	498	222	12.3	157314	2	CR352289	Danio rer
426	226	12.5	46996	3	U88310	U88310 Caenorhabdi	499	222	12.3	168601	3	AC007471	Drosophil
427	226	12.5	65649	3	AF003131	AF003131 Caenorhab	c 500	222	12.3	180916	2	CR381704	Danio rer
428	226	12.5	294136	2	AC006901	AC006901 Caenorhab	501	222	12.3	201070	5	EX004830	Zebrafish
429	226	12.5	299719	2	AC006858	AC006858 Caenorhab	502	222	12.3	271696	3	AB003835	Drosophil
430	225.5	12.5	3328	10	NMU37708	U37708 Mus musculu	503	221.5	12.3	1112	9	AB094146	Homo sapi
431	225.5	12.5	3352	10	NMU37709	U37709 Mus musculu	504	221.5	12.3	1112	10	AB092414	Mus muscu
432	225	12.5	2607	6	AX179390	AX179390 Sequence	505	221.5	12.3	5314	5	BC074401	Xenopus 1
433	225	12.5	2607	6	AX259864	AX259864 Sequence	506	221	12.2	1308	3	AF456362	Caenorhab
434	225	12.5	5586	6	CQ729937	CQ729937 Sequence	507	221	12.2	4525	9	BSM805354	Homo sapi
435	225	12.5	14327	9	HOMHSPGB	M85289 Human hepar	508	221	12.2	5374	9	AF289030	Homo sapi
c 436	225	12.5	39158	3	CBRG19K24	AC087734 Caenorhab	509	221	12.2	5387	6	CQ731799	Sequence
437	224.5	12.4	2404	6	C0728038	C0728038 Sequence	510	221	12.2	6110	9	AF023449	Homo sapi
438	224.5	12.4	2611	10	AF115401	AF115401 Mus muscu	511	221	12.2	6413	9	AF023450	Homo sapi
439	224.5	12.4	3960	6	CQ849821	CQ849821 Sequence	512	221	12.2	6435	9	AF461119	Xenopus 1
440	224.5	12.4	3960	6	AK126878	AK126878 Homo sapi	513	221	12.2	6649	9	AF217525	Homo sapi
441	224.5	12.4	7642	6	CQ776627	CQ776627 Sequence	514	220.5	12.2	1011	10	AB183402	Mus muscu
442	224.5	12.4	7642	6	AX818174	AX818174 Sequence	515	220.5	12.2	1287	10	AB183400	Mus muscu

516	220.5	12.2	1329	6	BD261770	BD261770 12 human	589	218	12.1	6656	10	AF334385
517	220.5	12.2	1329	9	CR457157	CR457157 Homo sapi	590	218	12.1	6829	10	AY005483
518	220.5	12.2	1338	10	AB183399	AB183399 Mus muscu	591	218	12.1	146352	2	CR548641
519	220.5	12.2	1413	6	BD140567	BD140567 Polypepti	592	218	12.1	186279	5	BX950870
520	220.5	12.2	1413	6	AR429086	AR429086 Sequence	593	218	12.1	191779	2	CR376789
521	220.5	12.2	1413	6	AR534977	AR534977 Sequence	594	217	12.0	3429	4	SSC459296
522	220.5	12.2	1413	6	AR375966	AR375966 Sequence	595	217	12.0	4410	3	AF118274
523	220.5	12.2	1413	9	AY358334	AY358334 Homo sapi	596	217	12.0	41345	3	CEFI15G9
524	220.5	12.2	1448	9	BC035930	BC035930 Homo sapi	597	216.5	12.0	3057	6	CQ842487
525	220.5	12.2	1450	10	AB064265	AB064265 Mus muscu	598	216.5	12.0	3057	9	AK125460
526	220.5	12.2	1508	6	BD261716	BD261716 12 human	599	216.5	12.0	4054	3	MSU07119
527	220.5	12.2	1520	6	BD261709	BD261709 12 human	600	216.5	12.0	4430	10	BC062892
528	220.5	12.2	1548	6	AX136299	AX136299 Sequence	601	216	12.0	260998	2	AC099089
529	220.5	12.2	1548	6	BD123602	BD123602 Secretary	602	215.5	11.9	2957	6	CQ591957
530	220.5	12.2	1548	9	AR075502	AR075502 Homo sapi	603	215.5	11.9	3264	3	AY119465
531	220.5	12.2	1598	6	BD247472	BD247472 Molecules	604	215.5	11.9	3397	6	AX780431
532	220.5	12.2	1598	6	AR278813	AR278813 Sequence	605	215.5	11.9	3397	9	AF312678
533	220.5	12.2	1817	10	AF539424	AF539424 Mus muscu	606	215.5	11.9	3498	10	RNU81035
534	220.5	12.2	1862	6	AX399846	AX399846 Sequence	607	215.5	11.9	3853	3	DRONRGAA
535	220.5	12.2	1935	6	BD247473	BD247473 Molecules	608	215.5	11.9	4041	6	CQ573942
536	220.5	12.2	1935	6	AR278814	AR278814 Sequence	609	215.5	11.9	4044	9	BC002377
537	220.5	12.2	1958	10	BC057125	BC057125 Mus muscu	610	215.5	11.9	4044	9	BC014626
538	220.5	12.2	2024	10	AB052293	AB052293 Mus muscu	611	215.5	11.9	4433	3	AY058284
539	220.5	12.2	2940	6	CQ870000	CQ870000 Sequence	612	215.5	11.9	5026	6	CQ591956
540	220.5	12.2	4444	10	AF434663	AF434663 Mus muscu	613	215.5	11.9	8574	3	DMNRG2
541	220	12.2	4717	6	AX463544	CQ716675 Sequence	614	215.5	11.9	8883	10	AY273816
542	220	12.2	4717	6	AX463544	AX463544 Sequence	615	215.5	11.9	20510	6	CQ573941
543	220	12.2	4759	6	AX463530	AX463530 Sequence	616	215.5	11.9	62442	2	AC018325
544	220	12.2	5287	9	AB050468	AB050468 Homo sapi	617	215.5	11.9	71320	2	AC020124
545	220	12.2	5719	6	CQ869705	CQ869705 Sequence	618	215.5	11.9	166512	3	AC099010
546	219.5	12.2	991	5	AF364047	AF364047 Gallus ga	619	215.5	11.9	174287	3	AC007977
547	219.5	12.2	1247	5	BC078527	BC078527 Xenopus l	620	215.5	11.9	174367	3	AC0023696
548	219.5	12.2	1258	9	AF0005070	AF0005070 Homo sapi	621	215.5	11.9	185405	3	AC023743
549	219.5	12.2	2259	6	BD204924	BD204924 Novel mol	622	215.5	11.9	270766	3	AE003615
550	219.5	12.2	3512	9	AF132811	AF132811 Homo sapi	623	215.5	11.9	29686	3	AE003444
551	219.5	12.2	3534	9	AF027658	AF027658 Homo sapi	624	215	11.9	1332	3	AF456363
552	219.5	12.2	4002	9	BC075829	BC075829 Homo sapi	625	215	11.9	3213	6	CQ847970
553	219.5	12.2	4277	6	AX457372	AX457372 Sequence	626	215	11.9	4236	9	HSU33635
554	219.5	12.2	4277	6	AX454572	AX454572 Sequence	627	215	11.9	5067	5	AF304131
555	219.5	12.2	4277	6	AX491050	AX491050 Sequence	628	214.5	11.9	4956	2	AF041082
556	219.5	12.2	4277	6	AX696989	AX696989 Sequence	629	214	11.8	77635	2	DMBR40010
557	219.5	12.2	4277	9	AX358328	AX358328 Homo sapi	630	213.5	11.8	1121	6	CQ727036
558	219.5	12.2	4279	6	BD204923	BD204923 Novel mol	631	213.5	11.8	1242	9	AY046418
559	219.5	12.2	6789	9	HSU0711	Z95705 Human DNA s	632	213.5	11.8	1614	6	BD177640
560	219	12.1	756	6	CQ729341	CQ729341 Sequence	633	213.5	11.8	1614	6	E37854
561	219	12.1	2638	6	AX833755	AX833755 Sequence	634	213.5	11.8	1614	6	AX003003
562	219	12.1	2638	9	AK095729	AK095729 Homo sapi	635	213.5	11.8	1680	9	BC033819
563	219	12.1	3210	5	AB015205	AB015205 Xenopus l	636	213.5	11.8	1685	6	BD172296
564	219	12.1	3690	9	AF549455	AF549455 Homo sapi	637	213.5	11.8	1685	6	BD172615
565	219	12.1	4129	6	CQ849703	CQ849703 Sequence	638	213.5	11.8	1685	6	BD172934
566	219	12.1	4129	9	AK126745	AK126745 Homo sapi	639	213.5	11.8	1685	6	BD173253
567	219	12.1	4762	9	AF381545	AF381545 Homo sapi	640	213.5	11.8	1685	6	BD175287
568	219	12.1	4805	9	AF730707	AF730707 Homo sapi	641	213.5	11.8	1685	6	AR410665
569	219	12.1	4822	6	E12950	E12950 cDNA GA3-43	642	213.5	11.8	1685	6	AR439029
570	219	12.1	4822	10	D78572	D78572 Mus musculus	643	213.5	11.8	1685	6	AR473049
571	219	12.1	4832	10	CQ869702	CQ869702 Sequence	644	213.5	11.8	1685	6	AR527035
572	219	12.1	5035	9	AY090737	AY090737 Homo sapi	645	213.5	11.8	1685	6	AR528625
573	219	12.1	12255	5	AY584653	AY584653 Gallus ga	646	213.5	11.8	1685	6	AR566068
574	218.5	12.1	1425	6	CQ725721	CQ725721 Sequence	647	213.5	11.8	1685	6	AX454458
575	218.5	12.1	4015	9	BC030141	BC030141 Homo sapi	648	213.5	11.8	1685	6	AX464214
576	218.5	12.1	4020	6	CQ805098	CQ805098 Sequence	649	213.5	11.8	1685	6	AX490936
577	218.5	12.1	6922	10	NMU17793	Y17793 Mus musculus	650	213.5	11.8	1685	6	AX697492
578	218.5	12.1	152686	2	AC018913	AC018913 Homo sapi	651	213.5	11.8	1685	6	BD075436
579	218	12.1	1689	9	AB056375	AB056375 Macaca fa	652	213.5	11.8	1685	9	AX358332
580	218	12.1	1884	6	CQ734341	CQ734341 Sequence	653	213.5	11.8	1718	6	BD247477
581	218	12.1	2350	6	CQ878954	CQ878954 Sequence	654	213.5	11.8	1718	6	AR278800
582	218	12.1	3958	9	AF531872	AF531872 Homo sapi	655	213.5	11.8	2496	6	BD191411
583	218	12.1	4191	6	CQ789354	CQ789354 Sequence	656	213.5	11.8	3557	9	AF363367
584	218	12.1	4191	9	AF531868	AF531868 Homo sapi	657	213.5	11.8	4155	6	AX704746
585	218	12.1	4191	9	HSU40271	U40271 Homo sapien	658	213.5	11.8	4594	9	AB040929
586	218	12.1	4193	6	CQ715771	CQ715771 Sequence	659	213.5	11.8	5384	5	AF337036
587	218	12.1	4238	9	BC071557	BC071557 Homo sapi	660	213	11.8	177	6	AR030585
588	218	12.1	6267	10	AF315558	AF315558 Mus muscu	661	213	11.8	851	5	BX932255

AF334385	Rattus no
AY005483	Mus muscu
CR548641	Danio rer
BX950870	Zebrafish
CR376789	Danio rer
AX459296	Sub scrof
AY118274	Drosophil
Z47068	Caenorhabd
CQ842487	Sequence
AK125460	Homo sapi
U50719	Manduca sex
BC062892	Mus muscu
AC099089	Rattus no
CQ591957	Sequence
AY119465	Drosophil
AX780431	Sequence
AF312678	Homo sapi
U81035	Rattus norv
M28231	Drosophila
CQ573942	Sequence
BC002377	Homo sapi
BC014626	Homo sapi
AY058284	Drosophil
CQ591956	Sequence
AF050085	Drosophil
AY273816	Rattus no
CQ573941	Sequence
AC018325	Drosophil
AC020124	Drosophil
AC099010	Drosophil
AC007977	Drosophil
AC0023696	Drosophil
AC023743	Drosophil
AE003615	Drosophil
AE003444	Drosophil
AF456363	Caenorhab
CQ847970	Sequence
HSU33635	Human col
AF304131	Danio rer
AF041082	Rattus no
AL122024	Drosophil
CQ727036	Sequence
AY046418	Homo sapi
BD177640	MBGP1 pol
E37854	MBGP1 poly
AX003003	Sequence
BC033819	Homo sapi
BD172296	Secreted
BD172615	Secreted
BD172934	Secreted
BD173253	Secreted
BD175287	Secretory
AR410665	Sequence
AR439029	Sequence
AR473049	Sequence
AR527035	Sequence
AR528625	Sequence
AR566068	Sequence
AX454458	Sequence
AX464214	Sequence
AX490936	Sequence
AX697492	Sequence
BD075436	Secretory
AX358332	Homo sapi
BD247477	Molecules
AR278800	Sequence
BD191411	Secreted
AF363367	Homo sapi
AX704746	Sequence
AB040929	Homo sapi
AF337036	Danio rer
AR030585	Sequence
BX932255	Gallus ga

662	213	11.8	1605	6	CQ59856	Sequence
663	213	11.8	1892	5	AB117614	Xenopus 1
664	213	11.8	2043	6	C0717926	Sequence
665	213	11.8	4381	10	AK173340	Mus muscu
666	213	11.8	4479	5	AF538326	
667	212.5	11.8	2650	10	AF102134	Mus muscu
668	212.5	11.8	2732	10	NMBTG2A	
669	212.5	11.8	4071	9	AF531869	Homo sapi
670	212.5	11.8	4631	9	HSU72391	Human neoge
671	212.5	11.8	5021	6	C0729613	Sequence
672	212	11.7	177	6	AR030586	Sequence
673	212	11.7	3752	10	AY061639	Rattus no
674	212	11.7	4609	10	RU53371	Rattus norv
675	211.5	11.7	2818	3	DROFAS2A	
676	211.5	11.7	2901	3	BT014661	Drosophil
677	211.5	11.7	3070	3	DROFAS2B	
678	211.5	11.7	3132	10	MNNSK22	
679	211.5	11.7	3257	6	AX587800	
680	211.5	11.7	3414	6	CQ579258	
681	211.5	11.7	3798	10	AF388037	Mus muscu
682	211.5	11.7	4376	10	BC078631	
683	211.5	11.7	4460	2	AC020249	Drosophil
684	211.5	11.7	5297	6	AX587800	
685	211.5	11.7	5297	6	AX771417	
686	211.5	11.7	5297	9	HSU61262	
687	211.5	11.7	5506	6	AR447897	
688	211.5	11.7	6168	3	DMSEGO007	
689	211.5	11.7	165928	3	AC023725	
690	211.5	11.7	172784	3	AC105352	
691	211.5	11.7	295177	3	AE003430	Drosophil
692	211	11.7	1273	6	AR278799	Sequence
693	211	11.7	2377	10	AF195662	Mus muscu
694	211	11.7	3366	10	AY059393	
695	211	11.7	5563	9	AF068603	Homo sapi
696	211	11.7	5719	9	AF069601	Homo sapi
697	211	11.7	20435	9	HSAGJ2535	
698	210.5	11.7	1837	6	CQ869997	
699	210.5	11.7	3231	6	CQ724644	Sequence
700	210.5	11.7	5913	6	CQ869760	
701	210	11.6	577	6	AR496051	Sequence
702	210	11.6	577	6	AR511333	Sequence
703	210	11.6	4078	6	AR270557	Sequence
704	210	11.6	5193	4	AF509585	Sus scrof
705	210	11.6	5193	4	AF698036	Sequence
706	210	11.6	5193	6	AX698038	Sequence
707	210	11.6	5745	9	AX339601	Homo sapi
708	210	11.6	5770	9	AF069602	Homo sapi
709	210	11.6	5896	9	BC064695	Homo sapi
710	210	11.6	5926	6	AR482482	Sequence
711	210	11.6	5926	6	AX329738	Sequence
712	210	11.6	5926	6	AX330278	Sequence
713	210	11.6	5926	6	AX333040	Sequence
714	210	11.6	5926	6	AX337264	Sequence
715	210	11.6	5926	6	AX375038	Sequence
716	210	11.6	5926	6	AX410725	Sequence
717	210	11.6	5926	6	HSU48959	
718	210	11.6	5992	10	BC058610	Mus muscu
719	209.5	11.6	7644	6	CQ727360	Sequence
720	209.5	11.6	17193	6	CQ583538	Sequence
721	209.5	11.6	58651	2	AC017558	Drosophil
722	209.5	11.6	69992	3	AC005421	Drosophil
723	209.5	11.6	189315	3	AC008319	Drosophil
724	209.5	11.6	306696	3	AE003586	Drosophil
725	209	11.6	1248	6	CQ725953	Sequence
726	209	11.6	1450	6	AX287596	Sequence
727	209	11.6	1489	9	AK172829	Homo sapi
728	209	11.6	1565	9	AF279689	Homo sapi
729	209	11.6	3080	6	AX287610	Sequence
730	209	11.6	3080	9	HSAG277437	
731	209	11.6	3112	6	AX287608	Sequence
732	209	11.6	3145	6	CQ870633	Sequence
733	209	11.6	3305	9	BC036769	Homo sapi
734	209	11.6	3402	6	AR252460	Sequence

735	209	11.6	3402	6	AX080803	Sequence
736	209	11.6	3402	6	AX191426	Sequence
737	209	11.6	3402	6	AX403231	Sequence
738	209	11.6	3402	9	AY358303	Homo sapi
739	208.5	11.5	2811	10	AF487347	
740	208.5	11.5	3448	10	MUSNGP	
741	208.5	11.5	3678	3	BT014656	Drosophil
742	208.5	11.5	4956	6	BD085989	Method of
743	208.5	11.5	4956	9	AF040990	Homo sapi
744	208.5	11.5	5667	6	CQ606753	Sequence
745	208	11.5	6592	6	CQ598305	Sequence
746	208	11.5	152024	2	CR407703	Danio rer
747	207.5	11.5	2220	6	AX748214	Sequence
748	207.5	11.5	2220	9	AK093583	Homo sapi
749	207.5	11.5	188751	10	AC122038	Mus muscu
750	207.5	11.5	247498	10	AC135238	Mus muscu
751	207	11.5	2735	6	CQ728959	Sequence
752	207	11.5	2846	6	AX834922	Sequence
753	207	11.5	2846	9	AK097633	Homo sapi
754	207	11.5	5175	6	CQ585188	Sequence
755	207	11.5	36654	2	AC017551	
756	207	11.5	17736	3	AC005714	Drosophil
757	207	11.5	151467	3	AC008348	Drosophil
758	207	11.5	307323	3	AE003457	Drosophil
759	206.5	11.4	980	9	BC013797	Homo sapi
760	206	11.4	3762	3	AF456361	Caenorhab
761	205.5	11.4	708	5	CR385737	
762	205.5	11.4	1542	6	BD193028	207 human
763	205.5	11.4	1542	6	CQ822024	Sequence
764	205.5	11.4	2067	10	AY210400	
765	205.5	11.4	2539	6	CQ782770	Sequence
766	205.5	11.4	2539	6	BD127305	Primer fo
767	205.5	11.4	2539	9	AK074825	Homo sapi
768	205.5	11.4	4128	10	RNU11031	
769	205.5	11.4	4465	10	MMU543322	Mus muscu
770	205.5	11.4	5071	10	AK129207	Mus muscu
771	205.5	11.4	53424	3	AB055861	Procambur
772	205	11.4	1299	6	CQ728323	Sequence
773	205	11.4	1820	6	BD247476	Molecules
774	205	11.4	1820	6	AR278798	Sequence
775	205	11.4	2540	9	AF062733	Homo sapi
776	204.5	11.3	2096	6	CQ579750	Sequence
777	204.5	11.3	2111	5	AF035677	Gallus ga
778	204.5	11.3	4641	10	RNU68726	
779	204.5	11.3	6860	5	AF304130	Danio rer
780	204.5	11.3	83495	3	AC087076	Caenorhab
781	204	11.3	1038	5	BC083011	Xenopus 1
782	204	11.3	4517	10	MMDCCTSG	
783	204	11.3	4784	5	GDU07644	Gallus gall
784	204	11.3	5211	6	CQ870291	Sequence
785	204	11.3	5892	6	CQ588164	Sequence
786	204	11.3	20686	2	AC017508	Drosophil
787	204	11.3	149752	3	AC004616	Homo sapi
788	204	11.3	174920	3	AC010701	Drosophil
789	204	11.3	294272	3	AE003595	Drosophil
790	203.5	11.3	4435	5	AF388035	Xenopus 1
791	203.5	11.3	5824	6	AR338581	Sequence
792	203.5	11.3	6811	9	AF334384	Homo sapi
793	203.5	11.3	6834	9	AB032958	Homo sapi
794	203.5	11.3	6899	9	AF491813	Homo sapi
795	203	11.2	2749	5	DRES74916	Danio rer
796	203	11.2	2774	5	BC053245	Danio rer
797	203	11.2	4248	6	AX054979	Sequence
798	203	11.2	4775	3	CEU70618	
799	203	11.2	6021	10	AY237726	Mus muscu
800	203	11.2	18524	6	CQ730656	Sequence
801	202.5	11.2	2697	6	CQ728585	Sequence
802	202.5	11.2	3801	9	AF531870	Homo sapi
803	202.5	11.2	4340	3	AV118645	Drosophil
804	202.5	11.2	8487	6	CQ717135	Sequence
805	202.5	11.2	9645	6	CQ875263	Sequence
806	202.5	11.2	9645	9	AF245505	Homo sapi
807	202.5	11.2	35347	3	CET0989	

AX080803	Sequence
AX191426	Sequence
AX403231	Sequence
AY358303	Homo sapi
AF487347	Mus muscu
L01991	Mus musculu
BT014656	Drosophil
BD085989	Method of
AF040990	Homo sapi
CQ606753	Sequence
CQ598305	Sequence
CR407703	Danio rer
AX748214	Sequence
AK093583	Homo sapi
AC122038	Mus muscu
AC135238	Mus muscu
CQ728959	Sequence
AX834922	Sequence
AK097633	Homo sapi
CQ585188	Sequence
AC017551	Drosophil
AC005714	Drosophil
AC008348	Drosophil
AE003457	Drosophil
BC013797	Homo sapi
AF456361	Caenorhab
CR385737	Gallus ga
BD193028	207 human
CQ822024	Sequence
AY210400	Mus muscu
CQ782770	Sequence
BD127305	Primer fo
AK074825	Homo sapi
U11031	Rattus norv
AJ543322	Mus muscu
AK129207	Mus muscu
AB055861	Procambur
CQ728323	Sequence
BD247476	Molecules
AR278798	Sequence
AF062733	Homo sapi
CQ579750	Sequence
AF035677	Gallus ga
U68726	Rattus norv
AF304130	Danio rer
AC087076	Caenorhab
BC083011	Xenopus 1
X85788	M.musculus
U07644	Gallus gall
CQ870291	Sequence
CQ588164	Sequence
AC017508	Drosophil
AC004616	Homo sapi
AC010701	Drosophil
AE003595	Drosophil
AF388035	Xenopus 1
AR338581	Sequence
AF334384	Homo sapi
AB032958	Homo sapi
AF491813	Homo sapi
AF574916	Danio rer
BC053245	Danio rer
AX054979	Sequence
U70618	Caenorhabdi
AY237726	Mus muscu
CQ730656	Sequence
CQ728585	Sequence
AF531870	Homo sapi
AV118645	Drosophil
CQ717135	Sequence
CQ875263	Sequence
AF245505	Homo sapi
Z47070	Caenorhabdi

808	202	11.2	2472	6	CQ592467	CQ592467 Sequence	881	197	10.9	5292	10	AB0933285	AB0933285 Mus muscu
809	202	11.2	2844	5	AY143173	AY143173 Gallus ga	882	197	10.9	43940	3	AY686597	AY686597 Drosophil
810	202	11.2	2847	10	BC052773	BC052773 Mus muscu	883	196.5	10.9	1559	3	CR354016	CR354016 Gallus ga
811	202	11.2	3822	3	AF041053	AF041053 Caenorhab	884	196.5	10.9	3284	6	AX443486	AX443486 Sequence
812	202	11.2	5604	5	AF394058	AF394058 Danio rer	885	196.5	10.9	3651	10	RNU81036	U81036 Rattus norv
813	202	11.2	5680	5	AY082380	AY082380 Danio rer	886	196.5	10.9	4041	5	CGNEUFASC	X65224 G.gallus mr
814	202	11.2	6300	5	AY029280	AY029280 Danio rer	887	196.5	10.9	5822	10	RATANKBIND	L11002 Rat ankyrin
815	201.5	11.2	1161	6	AX645013	AX645013 Sequence	888	196.5	10.9	6218	9	AB002341	AB002341 Homo sapi
816	201.5	11.2	1307	6	AX512897	AX512897 Sequence	889	196.5	10.9	6219	6	CQ716062	CQ716062 Sequence
817	201.5	11.2	1514	6	AX645011	AX645011 Sequence	890	196.5	10.9	6254	6	BD190781	BD190781 Secreted
818	201.5	11.2	2176	9	AF363368	AF363368 Homo sapi	891	196.5	10.9	6254	6	AX099489	AX099489 Sequence
819	201.5	11.2	2859	6	CQ576375	CQ576375 Sequence	892	196.5	10.9	6384	6	AR448063	AR448063 Sequence
820	201.5	11.2	10242	6	CQ600663	CQ600663 Sequence	c 893	196.5	10.9	6384	6	AR531706	AR531706 Sequence
821	201.5	11.2	12601	10	AF215896	AF215896 Mus muscu	c 894	196.5	10.9	168144	2	CR792456	CR792456 Danio rer
822	201.5	11.2	12603	6	CQ589875	CQ589875 Mus muscu	895	196	10.9	1064	6	CQ870296	CQ870296 Sequence
823	201.5	11.2	13041	3	DME487018	DME487018 Sequence	896	196	10.9	2351	10	RN0536020	Y536020 Rattus no
824	201	11.1	3400	5	FSCTRKA	L11311 Torpedo cal	897	196	10.9	7631	5	GGFMYLCK	X52876 G.gallus mr
825	201	11.1	3405	5	GA535114	AY535114 Gallus ga	898	196	10.9	96468	2	AC006902	AC006902 Caenorhab
826	201	11.1	4521	9	AK024462	AK024462 Homo sapi	899	195.5	10.8	479	6	AX665358	AX665358 Sequence
827	201	11.1	5130	9	AF230073	AF230073 Homo sapi	900	195.5	10.8	2898	6	CQ587259	CQ587259 Sequence
828	201	11.1	252070	2	AC098426	AC098426 Rattus no	901	195	10.8	2313	9	AK097802	AK097802 Homo sapi
829	200.5	11.1	1103	6	CQ728252	CQ728252 Sequence	902	195	10.8	3384	6	AX714308	AX714308 Sequence
830	200.5	11.1	4119	5	AY376856	AY376856 Danio rer	903	195	10.8	3384	6	AK056544	AK056544 Homo sapi
831	200.5	11.1	5414	10	MNMOGEN	Y09535 M.musculus	904	195	10.8	4381	6	CQ869962	CQ869962 Sequence
c 832	200.5	11.1	177476	9	AC010680	AC010680 Homo sapi	905	195	10.8	4569	9	AY509035	AY509035 Homo sapi
833	200.5	11.1	294540	9	HSAT277892	AY277892 Homo sapi	906	195	10.8	5865	3	DMU71001	U71001 Drosophila
834	200	11.1	1967	6	AR156834	AR156834 Sequence	907	195	10.8	6279	6	CQ590850	CQ590850 Sequence
835	200	11.1	1967	6	BD269852	BD269852 The poly	908	195	10.8	6318	3	DMU71002	U71002 Drosophila
836	200	11.1	2193	10	MUSPGCBMA	J04055 Mouse basem	909	195	10.8	37091	6	CQ590849	CQ590849 Sequence
837	200	11.1	2274	10	MMU293947	AY293947 Mus muscu	c 910	195	10.8	52726	2	AC017352	AC017352 Drosophil
838	200	11.1	2277	6	AX287593	AX287593 Sequence	911	195	10.8	189557	3	AC007356	AC007356 Drosophil
839	200	11.1	2339	10	BC058745	BC058745 Mus muscu	912	195	10.8	221235	3	AC096965	AC096965 Rattus no
840	200	11.1	2359	10	AF321300	AF321300 Mus muscu	c 913	195	10.8	251435	2	AC128510	AC128510 Rattus no
841	199.5	11.0	2173	9	BC069457	BC069457 Homo sapi	c 914	195	10.8	264547	2	AC094432	AC094432 Rattus no
842	199.5	11.0	3727	6	CQ726408	CQ726408 Sequence	915	195	10.8	294169	3	AE003821	AE003821 Drosophil
843	199.5	11.0	4924	10	RN0568725	U68725 Rattus norv	916	194.5	10.8	3211	3	BT001692	BT001692 Drosophil
844	199.5	11.0	5443	10	BC054540	BC054540 Mus muscu	917	194.5	10.8	173690	2	AC011307	AC011307 Homo sapi
845	199.5	11.0	7855	9	AK122586	AK122586 Homo sapi	918	194.5	10.8	178137	9	AC011302	AC011302 Homo sapi
846	199	11.0	2943	10	AY167411	AY167411 Rattus no	919	194	10.7	3783	6	AR177819	AR177819 Sequence
847	199	11.0	3726	9	AF190637	AF190637 Homo sapi	920	194	10.7	3783	10	MMNCAM1	X12875 Mouse mRNA
848	199	11.0	4285	6	AR140634	AR140634 Sequence	921	194	10.7	5038	10	BC056988	BC056988 Mus muscu
849	199	11.0	4285	9	AF035835	AF035835 Homo sapi	c 922	194	10.7	216540	5	BX322647	BX322647 Zebrafish
850	199	11.0	4287	6	CQ721176	CQ721176 Sequence	923	193.5	10.7	826	6	CQ780202	CQ780202 Sequence
851	199	11.0	4871	5	AF337035	AF337035 Danio rer	924	193.5	10.7	826	6	CQ781611	CQ781611 Sequence
c 852	198.5	11.0	4285	6	CQ607487	CQ607487 Sequence	925	193.5	10.7	826	6	BD124911	BD124911 Primer fo
853	198.5	11.0	6645	10	AK131182	AK131182 Mus muscu	926	193.5	10.7	826	6	BD126320	BD126320 Primer fo
854	198.5	11.0	6729	9	AF304304	AF304304 Homo sapi	927	193.5	10.7	2499	6	CQ583689	CQ583689 Sequence
c 855	198.5	11.0	48870	2	AC017807	AC017807 Drosophil	928	193.5	10.7	4486	10	MMU543321	MMU543321 Mus muscu
c 856	198.5	11.0	155666	3	AC007854	AC007854 Drosophil	929	193.5	10.7	4944	10	BC055053	BC055053 Mus muscu
c 857	198.5	11.0	168471	3	AC006170	AC006170 Drosophil	930	193.5	10.7	5608	10	AK122252	AK122252 Mus muscu
c 858	198.5	11.0	231562	3	AE003767	AE003767 Drosophil	931	193.5	10.7	5925	6	AX921879	AX921879 Sequence
859	198	11.0	3233	6	CQ721186	CQ721186 Sequence	932	193	10.7	2687	3	DME312133	DME312133 Drosophil
860	198	11.0	3260	9	HSRNCAD22	X59350 H.sapiens m	933	193	10.7	3858	5	BC057728	BC057728 Xenopus l
861	198	11.0	4844	6	CQ728171	CQ728171 Sequence	934	193	10.7	4579	3	DME312134	DME312134 Drosophil
c 862	198	11.0	199446	10	AC125069	AC125069 Mus muscu	c 935	193	10.7	4846	5	XLU10986	XLU10986 Xenopus lae
c 863	198	11.0	202887	10	AL928789	AL928789 Mouse DNA	936	193	10.7	4901	9	HSB803665	HSB803665 Homo sapi
864	198	11.0	255090	2	AC033798	AC033798 Mus muscu	937	193	10.7	5099	3	DME312135	DME312135 Drosophil
865	197.5	10.9	1416	5	BX932504	BX932504 Gallus ga	938	193	10.7	5194	3	BT010247	BT010247 Drosophil
866	197.5	10.9	1861	10	AF061260	AF061260 Mus muscu	939	193	10.7	7606	3	DROLARM	M27700 D.melanogas
867	197.5	10.9	2256	9	HUMDDC	M32292 Human color	940	193	10.7	7928	6	AX039412	AX039412 Sequence
868	197.5	10.9	3525	6	CQ715490	CQ715490 Sequence	941	192.5	10.7	2481	6	AR237560	AR237560 Sequence
869	197.5	10.9	4305	6	CQ613728	CQ613728 Sequence	942	192.5	10.7	2715	6	AR237555	AR237555 Sequence
870	197.5	10.9	4344	6	AC054981	AC054981 Sequence	943	192.5	10.7	2724	6	AR237562	AR237562 Sequence
871	197.5	10.9	4608	6	AR153583	AR153583 Sequence	944	192.5	10.7	2958	6	AR237557	AR237557 Sequence
872	197.5	10.9	4608	9	HSDDCC	X76132 H.sapiens D	945	192.5	10.7	2976	6	AR237558	AR237558 Sequence
873	197.5	10.9	4715	3	AY121698	AY121698 Drosophil	946	192.5	10.7	3192	6	BD270852	BD270852 Pollistat
874	197.5	10.9	4726	3	AF210316	AF210316 Drosophil	947	192.5	10.7	3192	6	AR200355	AR200355 Sequence
875	197.5	10.9	4955	9	AB018239	AB018239 Homo sapi	948	192.5	10.7	3210	6	AR237553	AR237553 Sequence
876	197.5	10.9	5013	6	CQ870298	CQ870298 Homo sapi	949	192.5	10.7	3219	6	AR237561	AR237561 Sequence
877	197.5	10.9	5019	6	CQ870300	CQ870300 Sequence	950	192.5	10.7	3453	6	AR237556	AR237556 Sequence
878	197	10.9	2462	6	AX746553	AX746553 Sequence	951	192.5	10.7	3874	6	AR237568	AR237568 Sequence
879	197	10.9	2462	9	AK090639	AK090639 Homo sapi	952	192.5	10.7	3943	5	CHKBRVO	L08960 Chicken cel
880	197	10.9	3894	6	BD085988	BD085988 Method of	953	192.5	10.7	3943	5	GGNRACAM	X58482 Chicken mRN

AB0933285	Mus muscu
AY686597	Drosophil
CR354016	Gallus ga
AX443486	Sequence
U81036	Rattus norv
X65224	G.gallus mr
L11002	Rat ankyrin
AB002341	Homo sapi
CQ716062	Sequence
BD190781	Secreted
AX099489	Sequence
AR448063	Sequence
AR531706	Sequence
CR792456	Danio rer
CQ870296	Sequence
Y536020	Rattus no
X52876	G.gallus mr
AC006902	Caenorhab
AX665358	Sequence
CQ587259	Sequence
AK097802	Homo sapi
AX714308	Sequence
AK056544	Homo sapi
CQ869962	Sequence
AY509035	Homo sapi
DMU71001	Drosophila
CQ590850	Sequence
U71002	Drosophila
CQ590849	Sequence
AC017352	Drosophil
AC007356	Drosophil
AC096965	Rattus no
AC128510	Rattus no
AC094432	Rattus no
AE003821	Drosophil
BT001692	Drosophil
AC011307	Homo sapi
AC011302	Homo sapi
AR177819	Sequence
X12875	Mouse mRNA
BC056988	Mus muscu
BX322647	Zebrafish
CQ780202	Sequence
CQ781611	Sequence
BD124911	Primer fo
BD126320	Primer fo
CQ583689	Sequence
AJ543321	Mus muscu
BC055053	Mus muscu
AK122252	Mus muscu
AX921879	Sequence
AJ312133	Drosophil
BC057728	Xenopus l
AJ312134	Drosophil
U10986	Xenopus lae
AL823257	Homo sapi
AJ312135	Drosophil
BT010247	Drosophil
M27700	D.melanogas
AX039412	Sequence
AR237560	Sequence
AR237555	Sequence
AR237562	Sequence
AR237557	Sequence
AR237558	Sequence
BD270852	Pollistat
AR200355	Sequence
AR237553	Sequence
AR237561	Sequence
AR237556	Sequence
AR237568	Sequence
L08960	Chicken cel
X58482	Chicken mRN

954	192.5	10.7	3943	6	AR177825	AR177825 Sequence	c1027	188	10.4	143593	5	BX248311	BX248311 Zebrafish
955	192.5	10.7	4437	30	CQ777490	CQ777490 Sequence	1028	188	10.4	181728	3	AC008003	AC008003 Drosophila
956	192.5	10.7	4437	10	MM1L	X934310 M. musculus	c1029	188	10.4	185967	2	AB040499	AB040499 Danio rerio
957	192	10.6	1463	9	AX098838	AX098838 Homo sapi	1030	188	10.4	290034	3	AE003577	AE003577 Drosophila
958	192	10.6	2094	6	AR508344	AR508344 Sequence	1031	187.5	10.4	770	3	CR386810	CR386810 Gallus ga
959	192	10.6	2143	9	BC031063	BC031063 Homo sapi	1032	187.5	10.4	3311	9	AY302131	AY302131 Homo sapi
960	192	10.6	2256	6	AX747900	AX747900 Sequence	1033	187.5	10.4	3914	10	AF090866	AF090866 Mus muscu
961	192	10.6	2256	9	AX093069	AX093069 Homo sapi	1034	187.5	10.4	3991	5	GGNGCAM	GGNGCAM Chicken mRN
962	192	10.6	3450	3	AY095040	AY095040 Drosophila	1035	187.5	10.4	3991	6	AR177805	AR177805 Sequence
963	192	10.6	3531	6	CQ735712	CQ735712 Sequence	1036	187	10.4	1627	6	AX805542	AX805542 Sequence
964	192	10.6	3738	6	CQ715811	CQ715811 Sequence	1037	187	10.4	1746	6	CQ728058	CQ728058 Sequence
965	192	10.6	3864	6	CQ715175	CQ715175 Sequence	1038	187	10.4	1825	10	AF487345	AF487345 Mus muscu
966	192	10.6	3900	9	HSC7NRCAM	AJ001057 Homo sapi	1039	187	10.4	2155	6	AX805540	AX805540 Sequence
967	192	10.6	3997	6	AB7637	AB7637 Sequence 1	1040	187	10.4	2337	9	AF480410	AF480410 Homo sapi
968	192	10.6	4134	9	H8U55258	U52528 Human hBRV	1041	187	10.4	2476	6	AX376518	AX376518 Sequence
969	192	10.6	4279	6	CQ572460	CQ572460 Sequence	1042	187	10.4	2476	9	AY358743	AY358743 Homo sapi
970	192	10.6	4300	3	AY229991	AY229991 Drosophila	1043	187	10.4	3354	5	BC044264	BC044264 Xenopus 1
971	192	10.6	4573	10	AF004840	AF004840 Rattus no	1044	187	10.4	3562	6	AX179302	AX179302 Sequence
972	192	10.6	5103	6	AX399250	AX399250 Sequence	1045	187	10.4	3808	9	BD185197	BD185197 Homo sapi
973	192	10.6	5598	9	AB046788	AB046788 Homo sapi	1046	187	10.4	3808	9	AB058770	AB058770 Homo sapi
974	192	10.6	6240	9	HSM806153	BX538010 Homo sapi	1047	187	10.4	4346	10	BC055333	BC055333 Mus muscu
975	191.5	10.6	3650	10	AF182037	AF182037 Rattus no	1048	187	10.4	5037	5	AF180354	AF180354 Danio rerio
976	191.5	10.6	4171	10	BC060226	BC060226 Mus muscu	1049	187	10.4	5789	6	AX923367	AX923367 Sequence
977	191.5	10.6	61468	2	AC148988	AC148988 Xenopus t	1050	187	10.4	7100	3	AF205357	AF205357 Drosophila
978	191	10.6	1221	9	BC008124	BC008124 Homo sapi	1051	187	10.4	9530	5	AY578914	AY578914 Danio rerio
979	191	10.6	1806	6	AX662327	AX662327 Sequence	1052	186.5	10.3	972	6	CQ611625	CQ611625 Sequence
980	190.5	10.5	1788	6	AX287613	AX287613 Sequence	1053	186.5	10.3	4214	9	AF004841	AF004841 Homo sapi
981	190.5	10.5	1972	10	AY059394	AY059394 Mus muscu	1054	186.5	10.3	4705	5	DRU23839	DRU23839 Danio rerio
982	190.5	10.5	4044	10	RNU81037	U81037 Rattus norv	1055	186	10.3	1782	6	AX521482	AX521482 Sequence
983	190.5	10.5	7241	10	AY574276	AY574276 Rattus no	1056	186	10.3	2959	6	AX521478	AX521478 Sequence
984	190.5	10.5	7250	10	AY574273	AY574273 Rattus no	1057	186	10.3	2973	6	AX376516	AX376516 Sequence
985	190.5	10.5	7253	10	AY574274	AY574274 Rattus no	1058	186	10.3	2973	9	AY358742	AY358742 Homo sapi
986	190.5	10.5	7277	10	AY574275	AY574275 Rattus no	1059	186	10.3	3551	6	BC039269	BC039269 Sequence
987	190.5	10.5	7286	10	AY574272	AY574272 Rattus no	1060	186	10.3	4398	5	BC073282	BC073282 Xenopus 1
988	190.5	10.5	7556	10	AY574277	AY574277 Rattus no	c1061	186	10.3	4734	6	CQ592466	CQ592466 Sequence
989	190.5	10.5	15244	3	AB026845	AB026845 Drosophila	1062	186	10.3	5749	9	AK090455	AK090455 Homo sapi
990	190.5	10.5	15272	6	CQ575028	CQ575028 Sequence	1063	186	10.3	7792	3	BT003586	BT003586 Drosophila
991	190	10.5	2857	10	BC044882	BC044882 Mus muscu	1064	186	10.3	60978	2	AC017675	AC017675 Drosophila
992	190	10.5	5381	3	AF312579	AF312579 Drosophila	c1065	186	10.3	209071	3	AC005285	AC005285 Drosophila
993	190	10.5	6055	6	AR489887	AR489887 Sequence	1066	186	10.3	214621	3	AC093100	AC093100 Drosophila
994	190	10.5	6055	10	MUSRTKB	L07237 Mus musculu	c1067	186	10.3	280096	3	AE0031613	AE0031613 Drosophila
995	190	10.5	6275	10	D88689	D88689 Mus musculu	1068	185.5	10.3	1223	3	BD176670	BD176670 Soluble R
996	190	10.5	7630	6	CQ614817	CQ614817 Sequence	1069	185.5	10.3	1223	9	AB061668	AB061668 Homo sapi
997	190	10.5	90803	5	AL732421	AL732421 Zebrafish	1070	185.5	10.3	1268	9	AB036432	AB036432 Homo sapi
998	189.5	10.5	125293	2	CQ073582	CQ073582 Homo sapi	1071	185.5	10.3	1436	9	BC020669	BC020669 Homo sapi
999	189.5	10.5	1302	6	CQ591387	CQ591387 Sequence	1072	185.5	10.3	1451	9	AB061669	AB061669 Homo sapi
1000	189.5	10.5	1981	3	AY089628	AY089628 Drosophila	1073	185.5	10.3	2019	6	AX505112	AX505112 Sequence
1001	189.5	10.5	2525	3	APLCAMD12	M89648 Aplysia cal	1074	185.5	10.3	2031	6	A39900	A39900 Sequence 2
1002	189.5	10.5	2725	3	APLCAMD15	M89648 Aplysia cal	1075	185.5	10.3	2031	6	167748	167748 Sequence 2
1003	189.5	10.5	3028	3	DMTITIN1	AF045775 Drosophila	1076	185.5	10.3	2059	6	AX805534	AX805534 Sequence
1004	189.5	10.5	3284	3	AY102651	AY102651 Drosophila	1077	185.5	10.3	2097	6	AX3169	AX3169 Sequence 35
1005	189.5	10.5	3493	3	APLCAMD19	M89650 Aplysia cal	1078	185.5	10.3	2097	6	AR079553	AR079553 Sequence
1006	189.5	10.5	3843	5	GGNGCMVA	Z75013 G.gallus mR	1079	185.5	10.3	2109	6	CQ859390	CQ859390 Sequence
c1007	189.5	10.5	7412	6	CQ572459	CQ572459 Sequence	1080	185.5	10.3	2109	6	AX133977	AX133977 Sequence
1008	189.5	10.5	33855	2	AC014874	AC014874 Drosophila	1081	185.5	10.3	2109	6	AX468838	AX468838 Sequence
1009	189.5	10.5	151500	3	AC008355	AC008355 Drosophila	1082	185.5	10.3	2140	6	AX805538	AX805538 Sequence
1010	189.5	10.5	169511	3	AC007531	AC007531 Drosophila	1083	185.5	10.3	2167	6	AX805536	AX805536 Sequence
1011	189.5	10.5	29749	3	AE003606	AE003606 Drosophila	1084	185.5	10.3	2220	6	AR044683	AR044683 Sequence
1012	189	10.5	2250	3	AY724774	AY724774 Caenorhab	1085	185.5	10.3	2349	6	AR052808	AR052808 Sequence
1013	189	10.5	3801	5	CAU55211	U52211 Carassius a	1086	185.5	10.3	2349	6	AR288121	AR288121 Sequence
1014	188.5	10.4	1305	6	CQ608559	CQ608559 Sequence	1087	185.5	10.3	2349	6	AR567108	AR567108 Sequence
1015	188.5	10.4	3099	5	AY138255	AY138255 Danio rerio	1088	185.5	10.3	2434	6	AR052807	AR052807 Sequence
1016	188.5	10.4	6096	9	AF304305	AF304305 Homo sapi	1089	185.5	10.3	2434	6	AR288120	AR288120 Sequence
1017	188.5	10.4	98613	2	AC139630	AC139630 Takifugu	1090	185.5	10.3	2434	6	AR567107	AR567107 Sequence
1018	188	10.4	1218	6	CQ730900	CQ730900 Sequence	1091	185.5	10.3	2839	6	108156	108156 Sequence 2
1019	188	10.4	1263	10	AY017368	AY017368 Mus muscu	1092	185.5	10.3	2839	6	108166	108166 Sequence 8
1020	188	10.4	2228	10	BC023765	BC023765 Mus muscu	1093	185.5	10.3	2888	9	BC034671	BC034671 Homo sapi
1021	188	10.4	2384	10	AY243095	AY243095 Mus muscu	1094	185.5	10.3	2928	6	E01630	E01630 cDNA encodi
1022	188	10.4	3369	6	CQ598917	CQ598917 Sequence	1095	185.5	10.3	2928	6	E13123	E13123 Human gene
1023	188	10.4	4494	5	BC072835	BC072835 Xenopus 1	1096	185.5	10.3	2929	9	HUMCEA	HUMCEA Human carci
1024	188	10.4	5028	2	AC014370	AC014370 Drosophila	1097	185.5	10.3	2974	6	CQ833969	CQ833969 Sequence
1025	188	10.4	5093	10	RNNCAMLI	X59149 Rat mRNA fo	1098	185.5	10.3	2974	6	AX332574	AX332574 Sequence
c1026	188	10.4	5589	6	CQ580169	CQ580169 Sequence	1099	185.5	10.3	2974	6	AX409670	AX409670 Sequence

1100	185.5	10.3	2974	6	AX658324	Sequence	1173	182	10.1	3475	3	AF303661	AF303661	Halocynthia
1101	185.5	10.3	2974	6	AX677147	Sequence	1174	182	10.1	3906	5	AY056466	AY056466	Danio rer
1102	185.5	10.3	2974	6	AX805532	Sequence	1175	182	10.1	63209	3	CQ598304	CQ598304	Sequence
1103	185.5	10.3	2974	9	HUMCRAF	M29540 Human carci	1176	182	10.1	65758	2	AC019956	AC019956	Drosophila
1104	185.5	10.3	3036	6	CQ800159	Sequence	1177	182	10.1	172641	3	AC009739	AC009739	Drosophila
1105	185.5	10.3	3036	9	HUMANTCE	M17303 Human carci	1178	182	10.1	266426	3	AE003841	AE003841	Drosophila
1106	185.5	10.3	6215	6	AX556709	Sequence	1179	181.5	10.0	1364	3	MOTP4A	MOTP4A	M64346 Manduca sex
1107	185.5	10.3	10500	6	BS000599	Pan trogl	1180	181.5	10.0	3009	6	AX060540	AX060540	Sequence
1108	185.5	10.3	173078	9	AC146249	Pan trogl	1181	181.5	10.0	3146	10	AF026465	AF026465	Mus muscu
1109	185.5	10.2	1719	5	AX950396	Gallus ga	1182	181.5	10.0	3198	10	BC053057	BC053057	Mus muscu
1110	185	10.2	2092	9	HSCEAASP	X16455 Human mRNA	1183	181.5	10.0	3379	6	AX359721	AX359721	Sequence
1111	185	10.2	2106	6	AX133657	Sequence	1184	181.5	10.0	3430	6	AX359719	AX359719	Sequence
1112	185	10.2	2106	6	AX192349	Sequence	1185	181.5	10.0	4122	5	DRNADML1	DRNADML1	X89204 D. rerio mrn
1113	185	10.2	2370	10	AY249056	Rattus no	1186	181	10.0	4260	6	AX665356	AX665356	Sequence
1114	185	10.2	2370	10	AF480411	Mus muscu	1187	181	10.0	1764	6	CQ728797	CQ728797	Sequence
1115	185	10.2	3585	10	BC063072	BC063072 Mus muscu	1188	181	10.0	1859	6	AX179640	AX179640	Sequence
1116	185	10.2	4146	6	BD085987	BD085987 Method of	1189	181	10.0	1952	6	CQ095169	CQ095169	Sequence
1117	185	10.2	4992	6	CQ869959	Sequence	1190	181	10.0	1952	6	CQ133915	CQ133915	Sequence
1118	185	10.2	5259	10	AF060570	AF060570 Mus muscu	1191	181	10.0	1952	6	CQ172446	CQ172446	Sequence
1119	185	10.2	135055	2	AC010056	AC010056 Drosophila	1192	181	10.0	1952	6	CQ201614	CQ201614	Sequence
1120	185	10.2	135055	2	AC011909	AC011909 Drosophila	1193	181	10.0	1952	6	CQ217152	CQ217152	Sequence
1121	185	10.2	184266	2	BX571737	BX571737 Danio rer	1194	181	10.0	1952	6	CQ255729	CQ255729	Sequence
1122	184.5	10.2	198	6	AR030587	AR030587 Sequence	1195	181	10.0	1952	6	CQ292826	CQ292826	Sequence
1123	184.5	10.2	198	6	AR030588	AR030588 Sequence	1196	181	10.0	1952	6	CQ329804	CQ329804	Sequence
1124	184.5	10.2	1391	6	AX321600	AX321600 Sequence	1197	181	10.0	2944	6	AX747451	AX747451	Sequence
1125	184.5	10.2	1391	6	HUMRAGE	BM1211 Human recep	1198	181	10.0	2944	6	AK092284	AK092284	Homo sapi
1126	184.5	10.2	2139	5	CQ073724	CQ073724 Xenopus l	1199	181	10.0	3153	9	HSM804421	HSM804421	Sequence
1127	184.5	10.2	3015	9	CQ842363	Sequence	1200	181	10.0	3261	3	AF456360	AF456360	Caenorhab
1128	184.5	10.2	3015	9	AX123850	Homo sapi	1201	181	10.0	3570	9	HSM803401	HSM803401	Sequence
1129	184.5	10.2	9282	9	AX603755	Homo sapi	1202	181	10.0	4591	9	HSM803659	HSM803659	Sequence
1130	184	10.2	1524	6	CQ827992	Sequence	1203	181	10.0	4988	9	HSM806135	HSM806135	Sequence
1131	184	10.2	1818	9	AY017369	AY017369 Homo sapi	1204	181	10.0	5929	9	HSM804605	HSM804605	Sequence
1132	184	10.2	2013	10	RATWAGL	M14871 Rat myelin-fo	1205	181	10.0	11008	3	AF078161	AF078161	Manduca s
1133	184	10.2	2348	10	RATWAGB	X05301 Rat mRNA fo	1206	181	10.0	113063	2	AC010946	AC010946	Homo sapi
1134	184	10.2	2468	10	RATWAGB	M22357 Rat LB236/m	1207	181	10.0	122493	2	AC023270	AC023270	Homo sapi
1135	184	10.2	2475	6	AX700174	Sequence	1208	181	10.0	202505	2	AP000912	AP000912	Homo sapi
1136	184	10.2	2475	10	RATWAGA	M16800 Rat LB236/m	1209	180.5	10.0	2547	3	HVU59448	HVU59448	US9448 Hydra vulga
1137	184	10.2	2934	6	CQ828004	Sequence	1210	180.5	10.0	3729	10	AF168466	AF168466	Mus muscu
1138	184	10.2	4640	3	DNDTRK	X63453 D. melanogas	1211	180.5	10.0	3943	10	AF172256	AF172256	Mus muscu
1139	184	10.2	4645	6	CQ591393	Sequence	1212	180.5	10.0	4052	5	AX376855	AX376855	Danio rer
1140	184	10.2	4645	6	CQ847776	Sequence	1213	180.5	10.0	4239	6	E40576	E40576	Novel gene
1141	184	10.2	4775	3	EF015249	Sequence	1214	180.5	10.0	4239	6	E40577	E40577	Novel gene
1142	184	10.2	5505	5	AF487829	AF487829 Danio rer	1215	180.5	10.0	4603	10	AF191090	AF191090	Mus muscu
1143	184	10.2	7789	6	AX746187	Sequence	1216	180	10.0	1776	6	AX521472	AX521472	Sequence
1144	183.5	10.2	1357	3	MSU11879	U11879 Manduca sex	1217	180	10.0	2106	6	AX393888	AX393888	Sequence
1145	183.5	10.2	2728	6	CQ413817	Sequence	1218	180	10.0	2350	11	BV177759	BV177759	sgm96580
1146	183.5	10.2	3631	6	BD170702	BD170702 NF-kappa	1219	180	10.0	2656	6	BD157949	BD157949	Primer fo
1147	183.5	10.2	5303	9	AC071561	AC071561 Homo sapi	1220	180	10.0	2656	6	AX277406	AX277406	Sequence
1148	183.5	10.2	6999	6	CQ874027	Sequence	1221	180	10.0	2656	6	AX879647	AX879647	Sequence
1149	183.5	10.2	6999	9	AX310398	AX310398 Homo sapi	1222	180	10.0	2656	9	AK022708	AK022708	Homo sapi
1150	183	10.1	822	5	AX931320	Gallus ga	1223	180	10.0	6445	6	AX556703	AX556703	Sequence
1151	183	10.1	2748	6	CQ869976	CQ869976 Sequence	1224	179.5	9.9	921	5	CR352648	CR352648	Gallus ga
1152	183	10.1	6145	3	AF260530	AF260530 Drosophila	1225	179.5	9.9	1086	10	RN0401157	RN0401157	Rattus no
1153	183	10.1	79405	10	AL928721	AL928721 Mouse DNA	1226	179.5	9.9	1515	6	CQ603762	CQ603762	Sequence
1154	182.5	10.1	1565	5	AF364048	AF364048 Gallus ga	1227	179.5	9.9	2118	6	CQ859389	CQ859389	Sequence
1155	182.5	10.1	2118	6	CQ859385	Sequence	1228	179.5	9.9	2526	5	AY197498	AY197498	Danio rer
1156	182.5	10.1	2783	6	CQ580170	Sequence	1229	179.5	9.9	2532	5	AF389400	AF389400	Danio rer
1157	182.5	10.1	2931	10	MMU06483	U06483 Mus muscu	1230	179.5	9.9	2784	3	AK112938	AK112938	Ciona int
1158	182.5	10.1	3252	3	AF188751	AF188751 Caenorhab	1231	179.5	9.9	156150	2	BX322540	BX322540	Zebrafish
1159	182.5	10.1	4188	3	AX051656	AX051656 Drosophila	1232	179.5	9.9	174574	2	BX927363	BX927363	Danio rer
1160	182.5	10.1	4734	10	RATFLTI	D28498 Rattus norv	1233	179	9.9	900	6	A91702	A91702	Sequence 6
1161	182.5	10.1	4901	9	HSM807328	BM647184 Homo sapi	1234	179	9.9	900	6	BD023445	BD023445	Junction
1162	182.5	10.1	5201	3	AF275903	AF275903 Drosophila	1235	179	9.9	1374	6	A91700	A91700	Sequence 4
1163	182.5	10.1	5923	5	AX603753	AX603753 Danio rer	1236	179	9.9	1374	6	BD023443	BD023443	Junction
1164	182.5	10.1	6374	6	AX497861	AX497861 Sequence	1237	179	9.9	1851	10	BC021876	BC021876	Mus muscu
1165	182	10.1	1904	6	CQ721212	CQ721212 Sequence	1238	179	9.9	2029	10	MMU89915	MMU89915	Mus muscu
1166	182	10.1	1969	9	AX050301	AX050301 Homo sapi	1239	179	9.9	2429	10	MUSNAGX	MUSNAGX	Mouse myel
1167	182	10.1	2275	9	AX094545	AX094545 Homo sapi	1240	179	9.9	2700	6	AX497857	AX497857	Sequence
1168	182	10.1	2350	6	AX335887	AX335887 Sequence	1241	179	9.9	2967	9	BC042054	BC042054	Homo sapi
1169	182	10.1	2350	6	AX658213	AX658213 Sequence	1242	179	9.9	3022	9	BC067107	BC067107	Homo sapi
1170	182	10.1	2350	9	HUMWAG	M29273 Human myeli	1243	179	9.9	3887	9	BC070119	BC070119	Homo sapi
1171	182	10.1	2400	9	BC053347	BC053347 Homo sapi	1244	179	9.9	5494	6	CQ721268	CQ721268	Sequence
1172	182	10.1	3464	6	AX359697	AX359697 Sequence	1245	178.5	9.9	1401	9	AK000845	AK000845	Homo sapi

1246	178.5	9.9	2958	9	HSMB01204	AL117666 Homo sapi	1319	175	9.7	2224	5	CR848573	CR848573 Xenopus t
1247	178.5	9.9	3236	9	AK095256	AK095256 Homo sapi	1320	175	9.7	5754	9	HSMB05275	AL834247 Homo sapi
1248	178.5	9.9	3705	10	AF125521	AF125521 Rattus no	1321	175	9.7	117951	9	AL359821	AL359821 Human DNA
1249	178.5	9.9	3970	10	AF172255	AF172255 Rattus no	1322	174.5	9.7	4094	6	CQ714181	CQ714181 Sequence
1250	178.5	9.9	5820	10	AF161715	AF161715 Rattus no	1323	174	9.6	785	6	AR496309	AR496309 Sequence
1251	178.5	9.9	6847	6	CQ714785	CQ714785 Sequence	1324	174	9.6	785	6	AR511591	AR511591 Sequence
1252	178.5	9.9	140127	2	AC141742	AC141742 Apis mell	1325	174	9.6	868	5	EX933478	EX933478 Gallus ga
1253	178.5	9.9	1580	10	AF205078	AF205078 Mus muscu	1326	174	9.6	1034	5	CR387777	CR387777 Gallus ga
1254	178	9.9	2107	10	AV271309	AV271309 Rattus no	1327	174	9.6	1744	5	EX935017	EX935017 Gallus ga
1255	178	9.9	2684	10	BC076588	BC076588 Mus muscu	1328	174	9.6	2716	5	BC056023	BC056023 Xenopus l
1256	178	9.9	3581	10	AK173081	AK173081 Mus muscu	1329	174	9.6	3128	3	AF113638	AF113638 Drosophi
1257	177.5	9.8	1752	4	AB039957	AB039957 Bos tauru	1330	174	9.6	3550	6	AX133825	AX133825 Sequence
1258	177.5	9.8	2525	3	AY052120	AY052120 Drosophi	1331	174	9.6	3562	6	AX179300	AX179300 Sequence
1259	177.5	9.8	2763	5	PF06FR3	X75603 P.waltlii m	1332	174	9.6	3698	10	AY169782	AY169782 Mus muscu
1260	177.5	9.8	3749	10	AF525412	AF525412 Rattus no	1333	174	9.6	4023	9	AF129167	AF129167 Chloroce
1261	177.5	9.8	4980	3	AY060637	AY060637 Drosophi	1334	174	9.6	5831	3	AY047563	AY047563 Drosophi
1262	177.5	9.8	5164	6	CQ572346	CQ572346 Sequence	1335	174	9.6	14985	2	HSTITIN	EX9490 H.sapiens m
1263	177.5	9.8	7080	10	AY353236	AY353236 Mus muscu	1336	174	9.6	16799	9	AC020355	AC020355 Drosophi
1264	177.5	9.8	7158	6	CQ714120	CQ714120 Sequence	1337	174	9.6	23546	6	CQ573465	CQ573465 Sequence
1265	177.5	9.8	20448	6	CQ599466	CQ599466 Sequence	1338	174	9.6	23546	6	CQ847884	CQ847884 Sequence
1266	177.5	9.8	24971	6	CQ599465	CQ599465 Sequence	1339	174	9.6	68727	3	AC004516	AC004516 Drosophi
1267	177.5	9.8	27060	3	AB055927	AB055927 Procamb	1340	174	9.6	71023	2	AC004426	AC004426 Drosophi
1268	177.5	9.8	53757	2	AC017325	AC017325 Drosophi	1341	174	9.6	97698	2	AC019670	AC019670 Drosophi
1269	177.5	9.8	70398	3	DME271740	AY271740 Drosophi	1342	174	9.6	113320	2	AC010662	AC010662 Drosophi
1270	177.5	9.8	121584	2	AC008232	AC008232 Drosophi	1343	174	9.6	166417	10	AC127685	AC127685 Mus muscu
1271	177.5	9.8	144056	3	AC091222	AC091222 Drosophi	1344	174	9.6	193262	3	AC007579	AC007579 Drosophi
1272	177.5	9.8	194006	3	AC010063	AC010063 Drosophi	1345	174	9.6	260367	3	AE003808	AE003808 Drosophi
1273	177.5	9.8	315108	3	AB003473	AB003473 Drosophi	1346	173.5	9.6	1962	10	AK311121	AK311121 Mus muscu
1274	177	9.8	1129	5	AF337034	AF337034 Danio rer	1347	173.5	9.6	2550	6	AR008527	AR008527 Sequence
1275	177	9.8	2899	10	BC049361	BC049361 Mus muscu	1348	173.5	9.6	2550	6	AR014315	AR014315 Sequence
1276	177	9.8	2959	9	BC064925	BC064925 Homo sapi	1349	173.5	9.6	2550	6	AR068074	AR068074 Sequence
1277	177	9.8	3757	9	AF151909	AF151909 Homo sapi	1350	173.5	9.6	2550	6	186161	186161 Sequence 10
1278	177	9.8	3768	9	AB103655	AB102655 Pongo pyg	1351	173.5	9.6	2550	6	186871	186871 Sequence 10
1279	177	9.8	6726	9	AB037718	AB037718 Homo sapi	1352	173.5	9.6	2550	6	AX746327	AX746327 Sequence
1280	177	9.8	7710	6	AX056397	AX056397 Sequence	1353	173.5	9.6	2550	6	AX816907	AX816907 Sequence
1281	177	9.8	153114	2	BX927068	BX927068 Danio rer	1354	173.5	9.6	2550	6	BD064497	BD064497 ICAM-4 an
1282	177	9.8	158241	3	AC115483	AC115483 Drosophi	1355	173.5	9.6	2565	6	AX365516	AX365516 Sequence
1283	177	9.8	161682	3	AC092326	AC092326 Drosophi	1356	173.5	9.6	2598	9	AK000681	AK000681 Homo sapi
1284	177	9.8	161902	2	C8626902	C8626902 Danio rer	1357	173.5	9.6	2764	6	CQ767791	CQ767791 Sequence
1285	177	9.8	187746	2	AC089123	AC089123 Mus muscu	1358	173.5	9.6	2764	6	AX376050	AX376050 Sequence
1286	177	9.8	193180	2	AC112588	AC112588 Rattus no	1359	173.5	9.6	2764	6	AY358337	AY358337 Homo sapi
1287	177	9.8	303885	3	DROSADH01	AE003407 Drosophi	1360	173.5	9.6	2988	6	AR008519	AR008519 Sequence
1288	177	9.8	304771	3	AB003641	AB003641 Drosophi	1361	173.5	9.6	2988	6	AR014307	AR014307 Sequence
1289	176.5	9.8	905	6	AX136566	AX136566 Sequence	1362	173.5	9.6	2988	6	AR068066	AR068066 Sequence
1290	176.5	9.8	905	6	BD123806	BD123806 Secretary	1363	173.5	9.6	2988	6	186153	186153 Sequence 1
1291	176.5	9.8	1409	9	AX025843	AX025843 Homo sapi	1364	173.5	9.6	2988	6	186863	186863 Sequence 1
1292	176.5	9.8	1655	9	BC013867	BC013867 Homo sapi	1365	173.5	9.6	2988	6	AX746318	AX746318 Sequence
1293	176.5	9.8	2178	6	AX224732	AX224732 Sequence	1366	173.5	9.6	2988	6	AX816898	AX816898 Sequence
1294	176.5	9.8	2667	9	BC013955	BC013955 Homo sapi	1367	173.5	9.6	2988	6	BD064489	BD064489 ICAM-4 an
1295	176.5	9.8	2920	6	AX833622	AX833622 Sequence	1368	173.5	9.6	3563	3	AY121627	AY121627 Drosophi
1296	176.5	9.8	3183	9	AF337818	AF337818 Homo sapi	1369	173.5	9.6	3660	5	CHKC04	CHKC04 Gallus gall
1297	176.5	9.8	3488	9	BC042432	BC042432 Homo sapi	1370	173.5	9.6	3983	6	CQ581133	CQ581133 Sequence
1298	176.5	9.8	4347	9	AB023209	AB023209 Homo sapi	1371	173	9.6	1367	3	AY515320	AY515320 Bombyx mo
1299	176.5	9.8	5482	10	NMEWRK2	X78568 M.musculus	1372	173	9.6	1369	3	AB115084	AB115084 Bombyx mo
1300	176.5	9.8	5773	9	AF464873	AF464873 Homo sapi	1373	173	9.6	1370	3	AY515322	AY515322 Bombyx mo
1301	176.5	9.8	7424	5	AF537107	AF537107 Gallus ga	1374	173	9.6	1372	3	AY515321	AY515321 Bombyx mo
1302	176	9.7	843	6	CQ605682	CQ605682 Sequence	1375	173	9.6	1440	5	EX934867	EX934867 Gallus ga
1303	176	9.7	1383	3	AY515323	AY515323 Bombyx ma	1376	173	9.6	1451	5	EX936257	EX936257 Gallus ga
1304	176	9.7	2646	6	AX786890	AX786890 Sequence	1377	173	9.6	2307	10	AF247659	AF247659 Mus muscu
1305	176	9.7	2729	9	AX833631	AX833631 Sequence	1378	173	9.6	3189	6	AR081017	AR081017 Sequence
1306	176	9.7	2729	9	AX095529	AX095529 Homo sapi	1379	173	9.6	3768	9	AB102653	AB102653 Homo sapi
1307	176	9.7	3488	9	BC042432	BC042432 Homo sapi	1380	173	9.6	3774	6	AR036493	AR036493 Sequence
1308	176	9.7	3768	9	AB102654	AB102654 Pan trogl	1381	173	9.6	3774	6	AR036493	AR036493 Sequence
1309	176	9.7	3903	6	AX779837	AX779837 Sequence	1382	173	9.6	3774	6	AR081016	AR081016 Sequence
1310	176	9.7	3903	6	AX779838	AX779838 Sequence	1383	173	9.6	3888	6	ARI77813	ARI77813 Sequence
1311	176	9.7	4443	6	CQ579749	CQ579749 Sequence	1384	173	9.6	3888	9	HUMLICAM	M74387 Human cell
1312	176	9.7	149432	3	AC090412	AC090412 Drosophi	1385	173	9.6	4522	6	CQ728130	CQ728130 Sequence
1313	176	9.7	154840	3	AC099018	AC099018 Drosophi	1386	173	9.6	4523	9	HUMIGL1A	M77640 Homo sapien
1314	176	9.7	157851	2	AC020509	AC020509 Drosophi	1387	173	9.6	255090	2	AC073798	AC073798 Mus muscu
1315	176	9.7	308823	3	AB003462	AB003462 Drosophi	1388	172.5	9.6	2019	10	BC025840	BC025840 Mus muscu
1316	175.5	9.7	224166	2	AC110955	AC110955 Rattus no	1389	172.5	9.6	2273	9	AB072038	AB072038 Homo sapi
1317	175	9.7	711	9	AF529206	AF529206 Homo sapi	1390	172.5	9.6	6164	3	HMU92813	HMU92813 Hirudo medi
1318	175	9.7	2190	9	AY328482	AY328482 Homo sapi	1391	172	9.5	839	5	CR523669	CR523669 Gallus ga

1392 172 9.5 862 6 I08155 Sequence 1
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ALIGNMENTS

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 DEFINITION Sequence 1 from patent US 6664383.
 ACCESSION AR439648
 VERSION AR439648.1 GI:42665572
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 1032)
 AUTHORS Fukushima,D., Shibayama,S. and Tada,H.
 TITLE Polypeptides, cDNA encoding the same and utilization thereof
 JOURNAL Patent: US 6664383-A 1 16-DEC-2003;
 FEATURES Location/Qualifiers
 source 1..1032
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 6.44e-158 Length: 1032
 Score: 1806.00 Matches: 344
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-10-017-084A-523 (1-344) x AR439648 (1-1032)
 Oy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyIleu 20
 Db 1 ATGAAACCATCCAGCCAAAATGCACAAATTCATCTCTTTGGGCAATCTTCACGGGGCTG 60

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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40
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Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 121 GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 180
Qy 61 AenArgValThrArgValAlaThrLeuAenArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 181 AACCGGGTCACCGGGTGCCCTGCGTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 240
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100
Db 241 AAGTGGTGCCTGGATCTCTCGGTGGTCTTCTTGAGCAACACCCAAACCGCAGTACAGCATC 300
Qy 101 GluIleGlnAenValAspValIleAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 301 GAGATCCAGAACGTCGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 360
Qy 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 361 AACCAACCCAAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG 420
Qy 141 IleSerSerAspIleSerIleAenGlnGlyAenAenIleSerLeuThrCysIleAlaThr 160
Db 421 ATTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCTTCACCTGATAGCAACT 480
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 481 GGTAGACCAGACGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 540
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 541 AGTGAAGACGAATACTTGGAAATTCAGGGGCATCACCCGGGAGCAGTCCAGGGGACTACGAG 600
Qy 201 CysSerAlaSerAenAspValAlaAlaProValValArgValValLysValThrValAen 220
Db 601 TGCAGTGGCTCCATGACGTGGCCGCCGCCGTGGTACGGAGAGTAAAGGTCCACGTGNAAC 660
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 661 TATCCACCATACTTTCAGAGCCAAAGGCTACAGGTGTCGCCGTGGGACAAAGGGGACA 720
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260
Db 721 CTGCAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATTCAGTGGTACAAAGGATGACAAA 780
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
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Qy 281 IlePhePheAenValSerGluHisAspTyrGlyAenTyrThrCysValAlaSerAenLys 300
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Db 901 CTGGGCCACACCAATGCCAGCATCATGTGTTTGGTCCAGCGCGCTCAGCGAGGTGAGC 960
Qy 321 AenGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
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Qy 341 LeuLeuLysPhe 344
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RESULT 2

CQ768055

LOCUS

DEFINITION

Sequence 522 from Patent EP1386931.

1679 bp

DNA

linear

PAT 04-MAR-2004

ACCESSION CQ768055

VERSION CQ768055.1

KEYWORDS GI:45108887

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Wood, W. I., Goddard, A., Gurney, A., Yuan, J., Baker, K. P. and Chen, J.

TITLE Human neurotrophin homologue

JOURNAL Patent: EP 1386931-A 522 04-FEB-2004;

Genentech, Inc. (US)

FEATURES Location/Qualifiers

source 1..1679

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 1..19e-157

Score: 1806.00

Length: 1679

Percent Similarity: 100.00%

Matches: 344

Best Local Similarity: 100.00%

Conservative: 0

Query Match: 100.00%

Mismatches: 0

Indels: 0

DB: 6

Gaps: 0

US-10-017-084A-523 (1-344) x CQ768055 (1-1679)

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Db 134 ATGAAACCATCCAGCCCAAAATGCAATTCATCTCTTGGGCAATCTTCCAGGGGCTG 193

Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProlys 40

Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGAGATGCCACCTTCCCCAAA 253

Qy 41 AlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

Db 254 GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313

Qy 61 AenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyrAlaGlyAsnAsp 80

Db 314 AACCGGTCCACCGGTGGCTGCTTCTGAGCAACACCCCAACCGCAGTACAGCATC 373

Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100

Db 374 AAGTGGTGGCTGGGATCTCTCGCGTGGTCTTCTGAGCAACACCCCAACCGCAGTACAGCATC 433

Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120

Db 434 GAGATCCAGAACGTCGATGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493

Qy 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140

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Qy 141 IleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIleAlaThr 160

Db 554 ATTTCTTTCAGATATCTCCATTAATGAGGGAACAATATTAGCTTCACCTGATAGCAACT 613

Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180

Db 614 GGTAGACACAGACCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTG 673

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Db 734 TGCAGTGCCTCCAAATGACGTGGCGCCGCCGTGGTACGGAGAGTAAAGGTACCGGTGAAC 793


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Db 794 TATCCACCATATTCAGAAAGCCAAAGGGTACAGGTGCCCGTGGGACAAAGGGGACA 853
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Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTTCAGCAGAAATTCAGTGTGACAGATGACAAA 913
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCAAAACTC 973
Qy 281 IlePhePheAenValSerGluHisAspTyrGlyAenTyrThrCysValAlaSerAenLys 300
Db 974 ATCTTTCTCAATGTCTCGAAACATGACTATGGGAACATACACTTGGGTGGCCTCCAACAAG 1033
Qy 301 LeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
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Qy 321 AenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTCAGGAGGGCAGGCTCGCTCTGGCTGCTCTTCTGTCTTGCACCTG 1153
Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 3
AR528639 AR528639 1679 bp DNA linear PAT 08-OCT-2004
LOCUS Sequence 375 from patent US 6725730.
DEFINITION AR528639
ACCESSION AR528639
VERSION AR528639.1 GI:53916717
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1679)
TITLE Bollinger,C.L., Jr.
JOURNAL Crane test weight assembly and method
FEATURES Patent: US 6725730-A 375 27-APR-2004;
Location/Qualifiers
1..1679
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AR528639 (1-1679)

Qy 1 MetLysThrIleGlnProLysMethIleAenSerIleSerTrpAlaIlePheThrGlyLeu 20
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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAGAGTGGCCGTGCGCAGCGGAGATGCCACCTTCCCCAA 253
Qy 41 AlaMetAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGCAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
Qy 61 AenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyrAlaGlyAenAsp 80
Db 314 AACCGGGTCACCGGGTGGCGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
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Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyrSerIle 100
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Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTTGGATGTGTATGACGAGGGGCCCTTACACCTCTCGTGCAGACAGAC 493
Qy 121 AenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTTAGGGTCCACTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTTCAAGATCTCCATTAATGAAGGGAACAATATTAGCTCCTCAGCTCATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACGAGACGCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673
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Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
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Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGGAAACAGACCTTTCTCTCAAAACTC 973
Qy 281 IlePhePheAenValSerGluHisAspTyrGlyAenTyrThrCysValAlaSerAenLys 300
Db 974 ATCTTTCTCAATGTCTCTGAACATGACTATGGGAACATACACTTGGGTGGCCTCCAACAAG 1033
Qy 301 LeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATTTGTGTCAGGGCGCGTTCAGCGAGGTGAGC 1093
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Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

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LOCUS Sequence 125 from Patent WO0193983.
DEFINITION AX358872
ACCESSION AX358872
VERSION AX358872.1 GI:18675337
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
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the same
JOURNAL Patent: WO 0193983-A 125 13-DEC-2001;
Genentech Inc. (US)
FEATURES Location/Qualifiers
source 1..1679
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AX358872 (1-1679)

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Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
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Db 254 GCTATGGACAAAGTGCCTGCGCAGCGGAGAGCGCCACCTCAGGTGCATATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTACCCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTCCCTGGATCTCTCGGTGTCTCTTGAGCAACACCCAAACGCACTACGATC 433
Qy 101 GluIleGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAAAGTGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGGCAAGTATCTCCCAAAATTTGTAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAenIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCTCACCCTGATAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
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Db 734 TGCAGTGCTCCAATGACGTGGCCGCGCTGGTACGGAGATTAAGGTCAACGCTGAAC 793
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Qy 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 5
AX362365 1679 bp DNA linear PAT 15-FEB-2002
LOCUS Sequence 125 from Patent WO0208288.
DEFINITION AX362365
ACCESSION AX362365
VERSION AX362365.1 GI:18694640
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

REFERENCE
1 Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P.,
Watanabe, C.K. and Wood, W.I.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same
Patent: WO 0208288-A 125 31-JAN-2002;
Genentech, Inc. (US)

JOURNAL Location/Qualifiers
FEATURES source 1..1679
/organism="Homo sapiens"
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ORIGIN
Alignment Scores:
Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
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DEFINITION Sequence 103 from Patent WO0077037.
ACCESSION AX403748
VERSION AX403748.1 GI:21437184
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ashkenazi, A., Baker, K., Botstein, D., Deanoyers, L., Eaton, D.B.,
Ferrara, N., Fong, S., Gao, W.Q., Gerber, H., Gerritsen, M.E.,
Goddard, A., Godowski, P., Guney, A., Kljavin, I.J., Mather, J.,
Napier, M., Pan, J., Paoni, N., Roy, M., Tumas, D., Watanabe, C.,
Williams, P.M., Wood, W.I. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0077037-A 103 21-DEC-2000;
Genentech Inc. (US)
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/mol_type="unassigned DNA"
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Alignment Scores:
Pred. No.: 1,19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-017-084a-523 (1-344) x AX403748 (1-1679)
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Db 734 TGCAGTGCCTCAATGACGTGGCGCGCCCGTGTGTACGAGAGTAAAGGTACCGGTGAAC 793
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Gao, W.O., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L.,
Sherwood, S., Smith, V., Stewart, T.A., Tumas, D., Watanabe, C.K.,
Wood, W.L. and Zhang, Z.
Secreted and transmembrane polypeptides and nucleic acids encoding
same

PATENT: WO 0140466-A 375 07-JUN-2001;

JOURNAL

Genentech Inc. (US)

source

1. 1679

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

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Pred. No.: 1.19e-157 Length: 1679

Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

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US-10-017-084A-523 (1-344) x AX464242 (1-1679)

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Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180

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AX490948

LOCUS

DEFINITION Sequence 55 from Patent WO200690.

ACCESSION AX490948

VERSION AX490948.1 GI:22323811

KEYWORDS

SOURCE

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,

Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.P., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.

and Ye, W.

Compositions and methods for the diagnosis and treatment of

disorders involving angiogenesis

Patent: WO 020690-A 55 03-JAN-2002;

Genentech, Inc. (US)

LOCATION/Qualifiers

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1. 1679

/organism="Homo sapiens"

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Pred. No.: 1.19e-157 Length: 1679

Score: 1806.00 Matches: 344

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-10-017-084A-523 (1-344) x AX490948 (1-1679)

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LOCUS Homo sapiens clone DNA43316 HNT (UNQ297) mRNA, complete cds.
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VERSION AY358331.1 GI:37181786
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1679)
AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,

Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
Heldens,S., Huang,A., Kim,H.S., Klimoweki,L., Jin,Y., Johnson,S.,
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Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
Stinson,J., Vagts,A., Vanden,R., Watanabe,C., Wleand,D., Woods,K.,
Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment
Genome Res. 13 (10), 2265-2270 (2003)
JOURNAL PUBMED 12975309
REFERENCE 2 (bases 1 to 1679)
AUTHORS Clark,H.F.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA
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Pred. No.: 1.19e-157 Length: 1679
Score: 1806.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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ACCESSION AR439649
VERSION AR439649.1 GI:42665573
KEYWORDS
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ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1693)
AUTHORS Fukushima,D., Shibayama,S. and Tada,H.
TITLE Polypeptides, cDNA encoding the same and utilization thereof
JOURNAL Patent: US 6664383-A 2 16-DEC-2003;
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Alignment Scores: 1.21e-157 Length: 1693
Pred. No.: 1806.00 Matches: 344
Score:
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-017-084a-523 (1-344) x AR439649 (1-1693)
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Db 130 ATGAAACCATCCAGCCAAAAATGCACAATTCATCTCTTGGGCAATCTTTCACGGGGCTG 189
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 190 GCTCCTCTGTGTCTCTTCCAAAGGAGTCCCGTGGCAGCGGAGATGCCACCTTCCCCAAA 249
Qy 41 AlaMetAspAsnValThrValArgGlnGlyCysLeuSerAlaThrLeuArgCysThrIleAsp 60
Db 250 GCTATGACCAACGTGACGGTCCGCGAGGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 309
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 310 AACCGGCTCACCCGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 369
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100
Db 370 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCCAACGCGAGTACGACATC 429
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 430 GAGATCCAGAAACGTGGATGTATGACGAGGGCCCTTACACCTGCTCGGTGCACACAGAC 489
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 490 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG 549
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 550 ATTTCTTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTCACCTGTCATGCAACT 609
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 610 GGTAGACCAAGCCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTTGGCTTTGTG 669
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 670 AGTCAAGACGAATACTTTGGAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 729
Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220
Db 730 TGCAGTGCCTCCAATGACGTGGCCGCGCTGGTACGGAGAGTAAAGGTCACCGTGAAC 789
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
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Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260
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Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 910 AGACTGATTGAAGGAAGAAAGGGGTGAAAGTGGAAAAACAGACCTTTCTCTCAAAACTC 969
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1030 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCGCGTCAGCGAGGTGAGC 1089
Qy 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValHisLeu 340
Db 1154 CTTCTCAAAATTT 1165
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Db	775	CACATCTCTCCCAACGGGTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC	834
Qy	191	IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro	210
Db	835	ATCACCGGGAAACAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCCC	894
Qy	211	ValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGly	230
Db	895	GTGGTACGGAGAGTAAGAGTCACCGTAACTATCCACCATACATTTTCAGAAGCAAGGGT	954
Qy	231	ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer	250
Db	955	ACAGGTGTCCCTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCTCA	1014
Qy	251	AlaGluPheGlnTrpTyrLysAspAspLysAraLeuIleGluGlyLysGlyValLys	270
Db	1015	GCAGAAATTCAGTGGTACAGGATGACAAAGAGACTGATTCAGAGAAAGAGGGGTGAA	1074
Qy	271	ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyr	290
Db	1075	GTGGAAACAGACCTTTCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTAT	1134
Qy	291	GlyAsnTyrThrCysValAlaAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu	310
Db	1135	GGAACTACACTTTGCGTGGCTCAACAAAGCTGGGCCACACCAATGCCACATCATGCTA	1194
Qy	311	PheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysVal	330
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RESULT 13			
AF126426			
LOCUS	AF126426	1839 bp	mRNA linear PRI 10-JUN-2002
DEFINITION	Homo sapiens neurotrophin (HNT) mRNA, complete cds.		
ACCESSION	AF126426		
VERSION	AF126426.1	GI:7158997	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.		
AUTHORS	Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.		
TITLE	Cloning and identification of human neurotrophin full length cDNA		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1839)		
AUTHORS	Li, G., Jin, J., Tan, X., Hu, S., Yuan, J. and Qiang, B.		
TITLE	Direct Submission		
JOURNAL	Submitted (05-FEB-1999) Biochemistry, Institute of Basic Medical Sciences, 5 Dong Dan San Tiao, Beijing 100005, PR China		
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	/db_xref="GI:7158998"		
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LSKLIFFNVSEHDYGNITCVASNKLGHTNASIMLFGPCAVSEVSNGTSSRAGCVWLLP
LLVLHLLKF"

ORIGIN		ALIGNMENT SCORES				IDENTITY			
		Pred. No.:	1.44e-144	Length:	1839				
		Score:	1665.50	Matches:	322				
		Percent Similarity:	97.31%	Conservative:	3				
		Best Local Similarity:	96.41%	Mismatches:	8				
		Query Match:	92.22%	Indels:	2				
		DB:	9	Gaps:	1				
US-10-017-084A-523 (1-344) x AF126426 (1-1839)									
Qy	11	SerIleSerTrpAlaIlePheThrGlyLeuAlaLeuCysLeuPheGlnGlyValPro	30						
Db	299	AGTGCCTCGTGTCTGTCCTTCAGCGCTGCTTCTCTTG---TACCC-ACAGGAGTGCC	354						
Qy	31	ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly	50						
Db	355	GTGCGCAGCGAGATGCCACCTTCCCAAAGCTATGGACAACGTGACGCTCCGCGCAGGG	414						
Qy	51	GlusSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpIleuAsn	70						
Db	415	GAGAGCGCACCTTCAGGTGCATATTGACAAACGGGTCAACCGGGTGGCTGGGTAAAC	474						
Qy	71	ArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu	90						
Db	475	CGCAGCACCATCTCTATGTCTGGGAATGACAAAGTGTGCTGGATCTTCGCGTGTCTCT	534						
Qy	91	LeuSerAsnThrGlnThrGlnTyrsertIleGluIleGlnAsnValAspValTrzAspGlu	110						
Db	535	CTGAGCAACACCAACACGAGTACAGCATCGAGATCCAGAACGTGGATGTGTATGACGAG	594						
Qy	111	GlyProTyThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu	130						
Db	595	GGCCCTTACACTGCTCGGTGGAGACAGACAAACCAACCTCTAGGGTCCACCTC	654						
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Qy	151	AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArg	170						
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Qy	171	HisIleSerProLysAlaValGlyPheValSerGluAspGluTyLeuGluIleGlnGly	190						
Db	775	CACATCTCTCCAAAGCCGTTGGCTTTGTGAGTGAAGACGAATACTTGGAAATTCAGGGC	834						
Qy	191	IleThrArgGluGlnSerGlyAspTyrgGluCysSerAlaSerAsnAspValAlaAlaPro	210						
Db	835	ATCACCCGGGAACAGTCAGGGGACTACGAGTGCAGTGCTCCAAATGACGTGGCGCGGCC	894						
Qy	211	ValValArgValLysValThrValAsnTyProProTyTrIleSerGluAlaLysGly	230						
Db	895	GTGGTACCAGAGATTAAGGTCAACCGTGAACATATCACCATTACATTTTCAGAAGCCCAAGGT	954						
Qy	231	ThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSer	250						
Db	955	ACAGGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCTCA	1011						
Qy	251	AlaGluPheGlnTrpTyryeAspAspLysArgLeuIleGluGlyLysGlyValLys	270						
Db	1015	GCAGAAATTCAGTGTGTACAGGATGACAAAAGACTGATTGAAGGAAAGAAAGGGGTGAAA	1071						
Qy	271	ValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyTr	290						
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Qy	291	GlyAsnTyThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeu	310						
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Alignment Scores:

Pred. No.: 5,73e-143 Length: 1615
Score: 1647.50 Matches: 314
Percent Similarity: 95.83% Conservative: 8
Best Local Similarity: 93.45% Mismatches: 11
Query Match: 91.22% Indels: 3
DB: 10 Gaps: 1

US-10-017-084A-523 (1-344) x BC023307 (1-1615)

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Db 68 CTGCCCCGAAGTGGCTCTGCTGCTCTCTCAGGCTGCTATTCTTGTACCCACAGGA 127
QY 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
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Db 128 GTGCCGGTGGTAGCGGAGATGCCACCTTTCCCAAGCTATGGACAACCGTGACGGTCAGG 187
QY 49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
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Db 188 CAGGGGGAGAGCGCCACCTCTAGGTGCACAAATTGACACCGAGTCACCCGGGTGGCTGG 247
QY 69 LeuAsnArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
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Db 248 CTAAACCGGAGTACCACTCTCTATGCTGGAATGACARGTGGTGCCTAGATCCTCGTGTG 307
QY 89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
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Db 308 GTCCCTCTGAGTAAACACCCAGACCCAGTACAGCATTTGAGATCCAGAAATGTGGATGTGTAC 367
QY 109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
   |||||
Db 368 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACACACCCCTAAGACCTCCAGGGTC 427
QY 129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
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Db 428 CACCTCATTTGTAACAGTATCTCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAAT 487
QY 149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
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Db 488 GAAGGGAACAACATCAGCTCTCTGATAGCACAGGTAGACCGGAGGCTTACAGTAACC 547
QY 169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
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Db 548 TGGAGACATATTTCTCCCAAGGCCGTTGGCTTTGTGAGTGAGATGAGTACCTGGAGATC 607
QY 189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
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Db 608 CAGGGCATCACTCGGGAAACAGTCAGGCGAGTACGAGTGCAGCGCCTCCAACCGCTGGCG 667
QY 209 AlaProValValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAla 228
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Db 668 GCACCAAGTGGTAGAGAGTGAAGTCAACGTTGAACTATCCACCATACATCTCAGAGCT 727
QY 229 LysGlyThrGlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaVal 248
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Db 728 AAGGGCACAGGTGTCCTCCGCGGAGAGAGGGGACTCTGCAGTGTGAAGCTTCCGCAATC 787
QY 249 ProSerAlaGluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysGly 268
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Db 788 CCTTCAGCAGAAATTTCAATGGTTCAAGGATGACAAAGAGCTGTCGGAAGAAAGAGGA 847
QY 269 ValLysValGluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHis 288
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Db 848 GTCAAAAGTGGAAACAGACTTTCTTTCAAAACTCACCTTTTCAACGCTCTCTGAACAT 907
QY 289 AspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIle 308
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Db 908 GACTATGGGAACCTACACATGTGTGGCTCCAAACAGCTGGGTACACCAACCGCCAGCATC 967
QY 309 MetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGly 328
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Db 968 ATGCTATTGGTCCCGGTGCTCTCAGTGAGGTCAACAATGGGACATCAAGGAGGCGAGGC 1027

QY 329 CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLysPhe 344

Db 1028 TGCATTGGCTCTCCCTCTTCTGGTCTTACACCTGCTCTCAAAATTT 1075

Search completed: October 30, 2005, 14:01:02
Job time : 5317 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - nucleic search, using frame plus.p2n model
Run on: October 30, 2005, 11:25:06 ; Search time 641 Seconds
(without alignments)
3176.897 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412
Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi
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-NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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2: Geneseqn1990s:
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4: Geneseqn2001as:
5: Geneseqn2001bs:
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10: Geneseqn2003cs:
11: Geneseqn2003ds:
12: Geneseqn2004as:
13: Geneseqn2004bs:
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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RESULT 1						
ID	AAZ47892	standard;	cDNA;	1032	BP.	
DE	Human	protein	encoding	cDNA	SEQ ID NO:2.	
PN	WO9958668	-A1.				
PD	18-NOV-1999.					
PA	(ONVOY)	ONO PHARM	CO LTD.			
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 2						
ID	AAZ34324	standard;	cDNA;	1679	BP.	
DE	Human	PRO337	nucleotide	sequence.		
PN	WO9946281	-A2.				
PD	16-SEP-1999.					
PA	(GETH)	GENENTECH	INC.			
Percent Similarity:	100.00%				Conservative:	0
Best Local Similarity:	100.00%				Mismatches:	0
Query Match:	100.00%				Indels:	0
RESULT 3						
ID	AAC78590	standard;	cDNA;	1679	BP.	
DE	Human	PRO337	nucleotide	sequence	SEQ ID NO:522.	
PN	WO200053756	-A2.				

PD	14-SEP-2000.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
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		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				
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ID	AAC97037	standard;	cDNA;	1679	BP.		
DE	Nucleotide	sequence	of	human	polypeptide	PRO337.	
PN	WO200077037	-A2.					
PD	21-DEC-2000.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				
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PN	WO200140466	-A2.					
PD	07-JUN-2001.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
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		Query Match:	100.00%				
RESULT 6							
ID	ABK33598	standard;	cDNA;	1679	BP.		
DE	cDNA	encoding	human	PRO	protein,	Seq ID No 125.	
PN	WO200208288	-A2.					
PD	31-JAN-2002.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				
RESULT 7							
ID	ABL8099	standard;	cDNA;	1679	BP.		
DE	Human	PRO337	cDNA	sequence	SEQ ID NO:55.		
PN	WO20020690	-A2.					
PD	03-JAN-2002.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				
RESULT 8							
ID	ABL95588	standard;	cDNA;	1679	BP.		
DE	Human	angiogenesis	related	cDNA	PRO337	SEQ ID NO: 55.	
PN	WO200208284	-A2.					
PD	31-JAN-2002.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				
RESULT 9							
ID	ACA63892	standard;	cDNA;	1679	BP.		
DE	Novel	human	secreted	and	transmembrane	protein	PRO337
PN	US2002192706	-A1.					
PD	19-DEC-2002.	PA	(GETH)	GENENTECH	INC.	Conservative:	0
		Percent Similarity:	100.00%			Mismatches:	0
		Best Local Similarity:	100.00%			Indels:	0
		Query Match:	100.00%				

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Query Match: 100.00% Indels: 0
RESULT 10
ID ACA03790 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 11
ID ACA04996 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 12
ID ACA72056 standard; cDNA; 1679 BP.
DE Human secreted and transmembrane PRO polypeptide #37 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 13
ID ABX89328 standard; cDNA; 1679 BP.
DE DNA encoding novel secreted and transmembrane protein PRO337.
PN US2003017563-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 14
ID ABX92696 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO337 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 15
ID ACD41982 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #188.
PN US2003036179-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 16
ID ACA60526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2002177165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 17
ID ACA04516 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 18
ID ACA66437 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 19
ID ACA68559 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 20
ID ACA04211 standard; cDNA; 1679 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 375.
PN US2003032155-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 21
ID ACA65657 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO337.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 22
ID ADA45894 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003023238-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 23
ID ADA76325 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073212-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 24
ID ABT44288 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 25
ID ADA18975 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003054517-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 26
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ID ADA61598 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049816-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 27
ID ADB19383 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003068796-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 28
ID ADB27924 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082704-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 29
ID ADA96403 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082711-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 30
ID ADB15967 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 31
ID ADA47753 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 32
ID ADA67548 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 33
ID ADB30555 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 34
ID ADA85851 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.

ID ADA97063 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 35
ID ADA97063 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 36
ID ADA79367 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 37
ID ADA87506 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 38
ID ADB16708 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 39
ID ADA91800 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 40
ID ADB14863 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 41
ID ADA25061 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 42
ID ADA47275 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.

PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 43
ID ADB18824 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 44
ID ADA94039 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003077722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 45
ID ADB15935 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 46
ID ADB13247 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 47
ID ACD98611 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 48
ID ACD30038 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 49
ID ADA12722 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 50
ID ADA74501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068798-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 51
ID ADB24734 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 52
ID ADA82258 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 53
ID ADA75221 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 54
ID ADA85299 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 55
ID ADA84747 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 56
ID ADB30003 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 57
ID ADA80531 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 58
ID ADA75773 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082703-A1.
PD 01-MAY-2003.

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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 59
ID ADA4698 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 60
ID ADB25294 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 61
ID ADA93470 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200307721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 62
ID ADB26820 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 63
ID ADB31107 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 64
ID ABT44571 standard; cDNA; 1679 BP.
DE Human PRO337 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 65
ID ADA61035 standard; cDNA; 1679 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 66
ID ADB24182 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 67
ID ADA96511 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 68
ID ADA81083 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 69
ID ADA95959 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 70
ID ADB26268 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 71
ID ADB21753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 72
ID ACD82238 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO 337 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 73
ID ACD29453 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #133.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 74
ID ADA7532 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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Query Match: 100.00% Indels: 0
RESULT 75
ID ADB18272 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US200307710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 76
ID ADA86955 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 77
ID ADA88058 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 78
ID ADA46446 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 79
ID ADB28476 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 80
ID ADB29028 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 81
ID ADA76980 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 82
ID ADA8610 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073213-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 83
ID ADA97615 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 84
ID ADB27372 standard; cDNA; 1679 BP.
DE CDNA encoding human PRO polypeptide #188.
PN US2003022239-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 85
ID ADB22305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087344-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 86
ID ACD30273 standard; cDNA; 1679 BP.
DE Human CDNA encoding PRO337.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 87
ID ABT43944 standard; cDNA; 1679 BP.
DE Human membrane bound receptor/protein PRO337 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 88
ID ADA66996 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003068793-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 89
ID ADB22857 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US200307711-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 90
ID ADB23630 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307712-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 91
ID ADA92352 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
```

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PN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 92
ID ADB15415 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 93
ID ADB83615 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 94
ID ADB80721 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200308068-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 95
ID ADB73262 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200309698-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 96
ID ADB38667 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 97
ID ADB78344 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 98
ID ADB38115 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 99
ID ADB6587 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082689-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 100
ID ADB84992 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 101
ID ADB89667 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 102
ID ADB90399 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 103
ID ADB39500 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 104
ID ADB78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 105
ID ADB74028 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003045462-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 106
ID ADB87164 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Mismatches: 0
Indels: 0
Query Match: 100.00%
RESULT 107
ID ADB84746 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003092890-A1.
PD 15-MAY-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 108
ID ADB47123 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 109
ID ADB83861 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 110
ID ADB86730 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 111
ID ADB73016 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 112
ID ADB76744 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide sequence #133.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 113
ID ADB77335 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 114
ID ADB34492 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 115
ID ADB35596 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 116
ID ADB33940 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 117
ID ADB35044 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 118
ID ADB36148 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide SEQ ID NO 375.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 119
ID ADB46543 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 120
ID ADC44170 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 121
ID ADC61930 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 122
ID ADC63894 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

RESULT 123
ID ADC66994 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0

Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 124	
ID ADC69118 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003064407-A1.	
PD 03-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 125	
ID ADC63178 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003068648-A1.	
PD 10-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 126	
ID ADC68243 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003069178-A1.	
PD 10-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 127	
ID ADC41563 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003072745-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 128	
ID ADC67618 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003073131-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 129	
ID ADC62554 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003073624-A1.	
PD 17-APR-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 130	
ID ADC36854 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #63.	
PN US2003088065-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 131	
ID ADC42187 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003104998-A1.	
PD 05-JUN-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 132	
ID ADC21844 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #63.	
PN US2003096969-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 133	
ID ADC50416 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003092106-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 134	
ID ADC71963 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003092107-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 135	
ID ADC59942 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003092105-A1.	
PD 15-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 136	
ID ADC49875 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088064-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 137	
ID ADC49074 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088070-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 138	
ID ADC49591 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088071-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 139	
ID ADC47452 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088072-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 140	
ID ADC47452 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003088072-A1.	
PD 08-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0

RESULT 140
ID ADC52949 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087365-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 141
ID ADC57303 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 142
ID ADC60494 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 143
ID ADC50969 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 144
ID ADC65496 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 145
ID ADC54594 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 146
ID ADC53555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 147
ID ADC59078 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 148

ID ADC55956 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087360-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 149
ID ADC58526 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID375.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 150
ID ADC47197 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105288-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 151
ID ADD03200 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 152
ID ADC90192 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 153
ID ADC69611 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 154
ID ADC48500 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 155
ID ADD10029 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 156
ID ADC78072 standard; cDNA; 1679 BP.


```
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 157
ID ADD04604 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 158
ID ADD06307 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 159
ID ADC80560 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 160
ID ADD11067 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 161
ID ADD10344 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 162
ID ADC47948 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 163
ID ADC77826 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 164
ID ADC80008 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 165
ID ADD11304 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 166
ID ADD09477 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 167
ID ADD50789 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 168
ID ADD41190 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 169
ID ADD52329 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 170
ID ADD51035 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 171
ID ADD53069 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 172
ID ADD53621 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203437-A1.
```

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PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 173
ID ADD37097 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 174
ID ADD51777 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 175
ID ADD02576 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 176
ID ADD50516 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096971-A1.
PD 23-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 177
ID ADD20210 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 178
ID ADD50270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 179
ID ADD50270 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 180
ID ADD51281 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 181
ID ADE49556 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 182
ID ADD92509 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 183
ID ADD91405 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 184
ID ADE04019 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 185
ID ADE32316 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 186
ID ADE22248 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 187
ID ADD79472 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 188
ID ADE35610 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
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Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 189	
ID ADE16724 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003203435-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 190	
ID ADD73339 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003203436-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 191	
ID ADE42008 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003194772-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 192	
ID ADE17825 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199023-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 193	
ID ADD91957 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199053-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 194	
ID ADE33420 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003194767-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 195	
ID ADE33972 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO3337 cDNA.	
PN US2003194791-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 196	
ID ADD80024 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003207417-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0

Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 197	
ID ADD93061 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003194768-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 198	
ID ADD72697 standard; cDNA; 1679 BP.	
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.	
PN US2003194781-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 199	
ID ADE19481 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199025-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 200	
ID ADE18929 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199026-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 201	
ID ADE43125 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199033-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 202	
ID ADD95914 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003199059-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 203	
ID ADE22800 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003199064-A1.	
PD 23-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 204	
ID ADD78918 standard; cDNA; 1679 BP.	
DE cDNA encoding human PRO polypeptide #188.	
PN US2003203429-A1.	
PD 30-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0

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Query Match: 100.00% Indels: 0
RESULT 205
ID ADE32868 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 206
ID ADE42560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 207
ID ADE17348 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 208
ID ADD80576 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 209
ID ADD89604 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 210
ID ADE40888 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 211
ID ADE04687 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 212
ID ADE92816 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 213
ID ADF47362 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 214
ID ADG21525 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 215
ID ADG23166 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 216
ID ADF97501 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 217
ID ADG80565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 218
ID ADG53119 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 219
ID ADG60439 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 220
ID ADG80013 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 221
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ID ADG63784 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 222
ID ADH55305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 223
ID ADH55857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 224
ID ADI61199 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 225
ID ADI64076 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 226
ID ADI65025 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 227
ID ADI63524 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 228
ID ADH81938 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 229
ID ADH81386 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 230
ID ACD24040 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 231
ID ACA66903 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #63.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 232
ID ACD42387 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 233
ID ACD42857 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 234
ID ACD68655 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 235
ID ACA67181 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 236
ID ADM82555 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 237
ID ADNI5954 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
```

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PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 238
ID ADN16583 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 239
ID ADN15402 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 240
ID ADN14850 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 241
ID ADC48828 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 242
ID ADC81112 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 243
ID ADE20999 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 244
ID ADE05843 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 245
ID ADD76560 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003100087-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 246
ID ADD75072 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 247
ID ADD75818 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 248
ID ADD85050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 249
ID ADD86876 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 250
ID ADE20753 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 251
ID ADE39050 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US200309362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 252
ID ADD87924 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 253
ID ADD86328 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003100440-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0
Indel: 0
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 254
ID ADE05597 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 255
ID ADD73582 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 256
ID ADE75776 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 257
ID ADE48856 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 258
ID ADD78422 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 259
ID ADE41305 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #28.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 260
ID ADE33352 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 261
ID ADE21245 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 262
ID ADD77360 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 263
ID ADE20507 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 264
ID ADD75572 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 265
ID ADD74088 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 266
ID ADD74334 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 267
ID ADD76064 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 268
ID ADD85556 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0

RESULT 269
ID ADE23904 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatch: 0


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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 270
ID ADE24547 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 271
ID ADD87372 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 272
ID ADE05105 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 273
ID ADD75318 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 274
ID ADD76862 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 275
ID ADD86630 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 276
ID ADE89238 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 277
ID ADE41198 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 278
ID ADD78098 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 279
ID ADE18377 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 280
ID ADE88686 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 281
ID ADE89957 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOM/) GAO W.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 282
ID ADD77606 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 283
```

ID ADD77852 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 284
ID ADD85310 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 285
ID ADD73842 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 286
ID ADD74580 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 287
ID ADD77108 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 288
ID ADD85802 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 289
ID ADE05351 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 290
ID ADD74826 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 291
ID ADF61597 standard; cDNA; 1679 BP.

DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 292
ID ADF40289 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 293
ID ADF46095 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 294
ID ADE94706 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 295
ID ADE91117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 296
ID ADE95258 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 297
ID ADE93368 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 298
ID ADF24481 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 299
ID ADF40913 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.

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PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 300
ID ADF23857 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 301
ID ADF33840 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 302
ID ADF34949 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 303
ID ADF27307 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 304
ID ADF27943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 305
ID ADE92264 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 306
ID ADE90565 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 307
ID ADF41537 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199435-A1.
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PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 308
ID ADF33216 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 309
ID ADF25582 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 310
ID ADF26683 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 311
ID ADF34472 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 312
ID ADF46709 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO3337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 313
ID ADE91712 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 314
ID ADG05638 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO3337 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 315
ID ADG27192 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
```

PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 316
ID ADG02291 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 317
ID ADG22077 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 318
ID ADG20147 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 319
ID ADF98053 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 320
ID ADG24270 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 321
ID ADF98624 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 322
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 323
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 324
ID ADG16761 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207359-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 325
ID ADG05220 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 326
ID ADG19487 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 327
ID ADG11255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 328
ID ADG13324 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 329
ID ADG08381 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 330
ID ADG15551 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 331
ID ADG12034 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 332
ID ADG03455 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 333
ID ADF99176 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 332	
ID ADP96949 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003207371-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 333	
ID ADG06134 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003207374-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 334	
ID ADG23718 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207389-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 335	
ID ADG04007 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003207423-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 336	
ID ADG24908 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207427-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 337	
ID ADF94591 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003096964-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 338	
ID ADG07205 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207350-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 339	
ID ADG07757 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207356-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 340	
ID ADG06687 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #83.	
PN US2003096966-A1.	
PD 22-MAY-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 341	
ID ADG55252 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003194778-A1.	
PD 16-OCT-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 342	
ID ADG60916 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207390-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 343	
ID ADG62020 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207428-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 344	
ID ADG82221 standard; cDNA; 1679 BP.	
DE Human PRO polynucleotide #188.	
PN US2003207358-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 345	
ID ADG57460 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207362-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 346	
ID ADG56908 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207364-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 347	
ID ADG55804 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207365-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0
RESULT 348	
ID ADG07757 standard; cDNA; 1679 BP.	
DE Novel human secreted and transmembrane protein PRO337 cDNA.	
PN US2003207356-A1.	
PD 06-NOV-2003.	
PA (GETH) GENENTECH INC.	
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 100.00%	Indels: 0

RESULT 348
ID ADG58564 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 349
ID ADG70930 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 350
ID ADH39031 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 351
ID ADG58012 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 352
ID ADG53596 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 353
ID ADG71482 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 354
ID ADG50695 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 355
ID ADG81669 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 356
ID ADH30631 standard; cDNA; 1679 BP.

DE Human PRO polynucleotide #188.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 357
ID ADG63633 standard; cDNA; 1679 BP.
DE Human secreted/transmembrane polypeptide PRO337 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 358
ID ADH11998 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 359
ID ADG50071 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 360
ID ADG51943 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 361
ID ADG52420 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 362
ID ADG54148 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 363
ID ADG49447 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
RESULT 364
ID ADG81117 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.

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PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 365
ID ADG56356 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 366
ID ADH12622 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 367
ID ADG48823 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 368
ID ADG61468 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 369
ID ADH28555 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 370
ID ADG54700 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 371
ID ADG59740 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 372
ID ADG51319 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
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PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 373
ID ADH43488 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 374
ID ADG59263 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 375
ID ADG34121 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 376
ID ADG62719 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 377
ID ADI81164 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 378
ID ADI33591 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 379
ID ADH69685 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 380
ID ADH25744 standard; cDNA; 1679 BP.
DE Human PRO337 encoding cDNA SEQ ID NO:522.
PN EP1386931-A1.
PD 04-FEB-2004.
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PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 381
ID ADG09907 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 382
ID ADI15378 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 383
ID ADG09255 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 384
ID ADI14710 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 385
ID ADI29846 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 386
ID ADI18305 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 387
ID ADM27243 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 388
ID ADJ63586 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 389
ID ADJ77481 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #188.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 390
ID ADKG2833 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #28.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 391
ID ADKG6601 standard; cDNA; 1679 BP.
DE Human PRO polynucleotide #63.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 392
ID ADJ65603 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 393
ID ADM27739 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 394
ID ADMI7521 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 395
ID ADL07355 standard; cDNA; 1679 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
RESULT 396
ID ADM42463 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004058424-A1.
PD 25-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 397
ID ADM28325 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 398
ID ADI95807 standard; cDNA; 1679 BP.
DE cDNA encoding human PRO polypeptide #188.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 399
ID ADI96359 standard; cDNA; 1679 BP.
DE Novel human secreted and transmembrane protein PRO337 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 400
ID AAZ47893 standard; cDNA; 1693 BP.
DE Human protein encoding cDNA SEQ ID NO:3.
PN WO958668-A1.
PD 18-NOV-1999.
PA (ONQY) ONO PHARM CO LTD.
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
RESULT 401
ID AAA88790 standard; cDNA; 1603 BP.
DE Human SECK cDNA Clone 11753149.0.6.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 402
ID ADD18288 standard; DNA; 1603 BP.
DE Human molecule (MOL) protein MOL10 DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 403
ID AAA88791 standard; cDNA; 2012 BP.
DE Human SECK cDNA Clone 11753149.0.37.
PN WO200061754-A2.
PD 19-OCT-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0
RESULT 404
ID ADD18290 standard; DNA; 2012 BP.
DE Human molecule (MOL) protein MOL11 DNA sequence.
PN WO2003003984-A2.
PD 16-JAN-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 99.71% Conservative: 0
Best Local Similarity: 99.71% Mismatches: 1
Query Match: 99.61% Indels: 0

Query Match: 99.61% Indels: 0
RESULT 405
ID ABK49272 standard; cDNA; 1873 BP.
DE Human Kruppel associated DNA binding protein 42 cDNA.
PN WO200183541-A1.
PD 08-NOV-2001.
PA (SHAN-) SHANGHAI BOWINDOW GENE DEV INC.
Percent Similarity: 89.32% Conservative: 0
Best Local Similarity: 89.32% Mismatches: 1
Query Match: 97.23% Indels: 41
RESULT 406
ID AAI59655 standard; cDNA; 1690 BP.
DE Human polynucleotide SEQ ID NO 3644.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 97.01% Indels: 3
RESULT 407
ID ADI21360 standard; cDNA; 1690 BP.
DE Novel human expressed sequence tag, EST #59.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 99.13% Conservative: 0
Best Local Similarity: 99.13% Mismatches: 1
Query Match: 97.01% Indels: 3
RESULT 408
ID ABT17393 standard; DNA; 1061 BP.
DE Human IG gene related nucleic acid SEQ ID NO 19.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 409
ID AAI57869 standard; cDNA; 1678 BP.
DE Human polynucleotide SEQ ID NO 72.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 410
ID ABT17390 standard; DNA; 1839 BP.
DE Human IG gene related nucleic acid SEQ ID NO 16.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 411
ID ABX76448 standard; DNA; 1839 BP.
DE Lung cancer-associated polynucleotide #312.
PN WO200286443-A2.
PD 31-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2
RESULT 412
ID ADG63208 standard; DNA; 1839 BP.
DE Human neurotrophin DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 97.31% Conservative: 3
Best Local Similarity: 96.41% Mismatches: 8
Query Match: 92.22% Indels: 2

RESULT 413
ID ADN39137 standard; cDNA; 1839 BP.
DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:455.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Percent Similarity: 97.31%
Best Local Similarity: 97.31%
Query Match: 96.41%
Indels: 2
Conservative: 3
Mismatches: 8
Indels: 2
RESULT 414
ID ADI21817 standard; cDNA; 2884 BP.
DE Novel human protein cDNA #76.
PN WO2003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 97.31%
Best Local Similarity: 96.41%
Query Match: 92.22%
Indels: 2
Conservative: 3
Mismatches: 8
Indels: 2
RESULT 415
ID ADQ22984 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5804.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 97.31%
Best Local Similarity: 97.31%
Query Match: 92.22%
Indels: 2
Conservative: 3
Mismatches: 8
Indels: 2
RESULT 416
ID ADQ24601 standard; DNA; 3987 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7421.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 97.31%
Best Local Similarity: 96.41%
Query Match: 92.22%
Indels: 2
Conservative: 3
Mismatches: 8
Indels: 2
RESULT 417
ID ADG63210 standard; DNA; 1068 BP.
DE Human neurotrophin DNA +33bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 94.20%
Best Local Similarity: 93.33%
Query Match: 91.36%
Indels: 13
Conservative: 3
Mismatches: 8
Indels: 13
RESULT 418
ID ABT17391 standard; DNA; 1094 BP.
DE Human IG gene related nucleic acid SEQ ID No 17.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 94.20%
Best Local Similarity: 93.33%
Query Match: 91.36%
Indels: 13
Conservative: 3
Mismatches: 8
Indels: 13
RESULT 419
ID ADI35771 standard; DNA; 2129 BP.
DE Human neurotrophin DNA.
PN US2003100485-A1.
PD 29-MAY-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 94.20%
Best Local Similarity: 93.33%
Query Match: 91.36%
Indels: 13
Conservative: 3
Mismatches: 8
Indels: 13
RESULT 420
ID ADG63212 standard; DNA; 1104 BP.
DE Human neurotrophin DNA +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 91.04%
Best Local Similarity: 90.20%
Query Match: 91.03%
Indels: 25
Conservative: 3
Mismatches: 8
Indels: 25
RESULT 421

ID ABT17392 standard; DNA; 1130 BP.
DE Human IG gene related nucleic acid SEQ ID No 18.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 91.04%
Best Local Similarity: 90.20%
Query Match: 91.03%
Indels: 25
Conservative: 3
Mismatches: 8
Indels: 25
RESULT 422
ID AAZ47894 standard; cDNA; 939 BP.
DE Human protein encoding cDNA SEQ ID NO:5.
PN WO9958668-A1.
PD 18-NOV-1999.
PA (ONCY) ONO PHARM CO LTD.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 90.92%
Indels: 0
Conservative: 0
Mismatches: 0
Indels: 0
RESULT 423
ID ADG63214 standard; DNA; 1140 BP.
DE Human neurotrophin DNA +108bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 88.08%
Best Local Similarity: 87.26%
Query Match: 90.70%
Indels: 37
Conservative: 3
Mismatches: 8
Indels: 37
RESULT 424
ID ADE07017 standard; DNA; 3298 BP.
DE Novel coding sequence (useful for identifying genetic disorders) #83.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 82.89%
Best Local Similarity: 71.39%
Query Match: 71.79%
Indels: 1
Conservative: 39
Mismatches: 57
Indels: 1
RESULT 425
ID AAQ51015 standard; cDNA; 3069 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN) LEE N M.
PA (LOHH) LOH H H.
PA (LIPP) LIPPMAN D.
Percent Similarity: 82.01%
Best Local Similarity: 71.39%
Query Match: 71.23%
Indels: 1
Conservative: 36
Mismatches: 60
Indels: 1
RESULT 426
ID ABT17408 standard; DNA; 1071 BP.
DE Human IG gene related nucleic acid SEQ ID No 34.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Indels: 3
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 427
ID ABT17407 standard; DNA; 1080 BP.
DE Human IG gene related nucleic acid SEQ ID No 33.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Indels: 3
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 428
ID ABT17409 standard; DNA; 1478 BP.
DE Human IG gene related nucleic acid SEQ ID No 35.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Indels: 3
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 429
ID ADG63212 standard; DNA; 1104 BP.
DE Human neurotrophin DNA +69bp isoform.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 91.04%
Best Local Similarity: 90.20%
Query Match: 91.03%
Indels: 25
Conservative: 3
Mismatches: 8
Indels: 25
RESULT 421

RESULT 429
ID ABT17406 standard; DNA; 3110 BP.
DE Human IG gene related nucleic acid SEQ ID No 32.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Indels: 3
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 430
ID ADG63206 standard; DNA; 3110 BP.
DE Opioid-binding protein/cell adhesion molecule-like DNA.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 83.28%
Best Local Similarity: 72.24%
Query Match: 70.21%
Indels: 3
Conservative: 37
Mismatches: 54
Indels: 3
RESULT 431
ID AAO51017 standard; cDNA; 2179 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Percent Similarity: 81.31%
Best Local Similarity: 71.22%
Query Match: 69.77%
Indels: 4
Conservative: 34
Mismatches: 59
Indels: 4
RESULT 432
ID AAO51016 standard; cDNA; 2337 BP.
DE Rat opioid receptor gene.
PN WO9321309-A1.
PD 28-OCT-1993.
PA (LEEN/) LEE N M.
PA (LOHH/) LOH H H.
PA (LIPP/) LIPPMAN D.
Percent Similarity: 81.31%
Best Local Similarity: 71.22%
Query Match: 69.77%
Indels: 4
Conservative: 34
Mismatches: 59
Indels: 4
RESULT 433
ID AAA44536 standard; cDNA; 832 BP.
DE Human secreted expressed sequence tag SEQ ID NO:1111.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 99.56%
Best Local Similarity: 99.11%
Query Match: 64.95%
Indels: 0
Conservative: 1
Mismatches: 1
Indels: 0
RESULT 434
ID ABT17404 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 30.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.63%
Indels: 5
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 435
ID AAL50356 standard; cDNA; 1411 BP.
DE Human limbic system associated membrane protein 36-85 coding sequence.
PN CN1345756-A.
PD 24-APR-2002.
PA (SHAN-) SHANGHAI BLOWNDOWN GENE DEV INC.
Percent Similarity: 72.62%
Best Local Similarity: 53.87%
Query Match: 51.63%
Indels: 7
Conservative: 63
Mismatches: 85
Indels: 7
RESULT 436
ID ABT17402 standard; DNA; 1017 BP.
DE Human IG gene related nucleic acid SEQ ID No 28.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.

Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Indels: 5
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 437
ID ABX63560 standard; cDNA; 1195 BP.
DE Human cDNA #560 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Indels: 5
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 438
ID ADL12674 standard; cDNA; 1195 BP.
DE Human steroid-induced C3A liver cell cDNA #403.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 73.85%
Best Local Similarity: 55.38%
Query Match: 51.58%
Indels: 5
Conservative: 60
Mismatches: 80
Indels: 5
RESULT 439
ID AAT42081 standard; cDNA to mRNA; 1014 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 73.54%
Best Local Similarity: 55.08%
Query Match: 51.30%
Indels: 5
Conservative: 60
Mismatches: 81
Indels: 5
RESULT 440
ID AAT42080 standard; cDNA to mRNA; 1238 BP.
DE Rat LAMP coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 73.54%
Best Local Similarity: 55.08%
Query Match: 51.30%
Indels: 5
Conservative: 60
Mismatches: 81
Indels: 5
RESULT 441
ID ABT17403 standard; DNA; 1075 BP.
DE Human IG gene related nucleic acid SEQ ID No 29.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 71.51%
Best Local Similarity: 53.71%
Query Match: 51.19%
Indels: 17
Conservative: 60
Mismatches: 79
Indels: 17
RESULT 442
ID AAT42079 standard; cDNA to mRNA; 977 BP.
DE Human LAMP residues 8-332 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 74.06%
Best Local Similarity: 55.31%
Query Match: 51.14%
Indels: 5
Conservative: 60
Mismatches: 78
Indels: 5
RESULT 443
ID AAT42116 standard; cDNA to mRNA; 1307 BP.
DE Rat LAMP clone 6c coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 68.97%
Best Local Similarity: 51.72%
Query Match: 50.55%
Indels: 28
Conservative: 60
Mismatches: 80
Indels: 28
RESULT 444
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 68.97%
Best Local Similarity: 51.72%
Query Match: 50.55%
Indels: 28
Conservative: 60
Mismatches: 80
Indels: 28
RESULT 445
ID AAT42084 standard; cDNA to mRNA; 924 BP.
DE Human LAMP residues 8-315 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 75.50%
Conservative: 58

Best Local Similarity: 56.29% Mismatches: 70
 Query Match: 50.28% Indels: 4
 RESULT 445
 ID AAT42085 standard; cDNA to mRNA; 945 BP.
 DE Rat LAMP residues 1-315 coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 75.50% Conservative: 58
 Best Local Similarity: 56.29% Mismatches: 70
 Query Match: 50.22% Indels: 4
 RESULT 446
 ID AAT42083 standard; cDNA to mRNA; 930 BP.
 DE Rat mature LAMP coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 74.12% Conservative: 59
 Best Local Similarity: 55.27% Mismatches: 77
 Query Match: 50.11% Indels: 4
 RESULT 447
 ID AAT42082 standard; cDNA to mRNA; 912 BP.
 DE Human mature LAMP coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 74.68% Conservative: 59
 Best Local Similarity: 55.52% Mismatches: 74
 Query Match: 49.94% Indels: 4
 RESULT 448
 ID ABZ76264 standard; cDNA; 1757 BP.
 DE Human GENSET cDNA clone name SLAMP.
 PN WO2003014151-A2.
 PD 20-FEB-2003.
 PA (GEST) GENSET SA.
 Percent Similarity: 72.14% Conservative: 61
 Best Local Similarity: 53.25% Mismatches: 76
 Query Match: 49.45% Indels: 14
 RESULT 449
 ID AAT42086 standard; cDNA to mRNA; 861 BP.
 DE Human LAMP residues 29-315 coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 76.21% Conservative: 57
 Best Local Similarity: 56.55% Mismatches: 66
 Query Match: 49.09% Indels: 3
 RESULT 450
 ID AAT42087 standard; cDNA to mRNA; 861 BP.
 DE Rat LAMP residues 29-315 coding sequence.
 PN WO9630052-A1.
 PD 03-OCT-1996.
 PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
 Percent Similarity: 76.21% Conservative: 57
 Best Local Similarity: 56.55% Mismatches: 66
 Query Match: 49.03% Indels: 3
 RESULT 451
 ID AAH34425 standard; cDNA; 1153 BP.
 DE Human colon cancer antigen encoding cDNA SEQ ID NO:1507.
 PN WO200122920-A2.
 PD 05-APR-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Percent Similarity: 68.68% Conservative: 60
 Best Local Similarity: 51.44% Mismatches: 81
 Query Match: 49.00% Indels: 29
 RESULT 452
 ID ADM47274 standard; DNA; 617 BP.
 DE Oestrogen regulated protein like NOVX 25b gene.
 PN WO2003083039-A2.
 PD 09-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Percent Similarity: 56.59% Conservative: 4
 Best Local Similarity: 55.39% Mismatches: 8

Query Match: 48.37% Indels: 138
 RESULT 453
 ID AAZ34325 standard; DNA; 503 BP.
 DE Human EST DNA42301.
 PN WO9946281-A2.
 PD 16-SEP-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 454
 ID AAC78591 standard; cDNA; 503 BP.
 DE Human EST DNA42301 nucleotide sequence SEQ ID NO:524.
 PN WO200053756-A2.
 PD 14-SEP-2000.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 455
 ID ACA63893 standard; cDNA; 503 BP.
 DE Novel human secreted and transmembrane protein DNA42301.
 PN US2002192706-A1.
 PD 19-DEC-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 456
 ID ACA72057 standard; DNA; 503 BP.
 DE Human PRO polypeptide associated oligonucleotide SEQ ID NO 524.
 PN US2002177553-A1.
 PD 28-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 457
 ID ABX92697 standard; cDNA; 503 BP.
 DE Human PRO337 EST polynucleotide sequence.
 PN US2002169284-A1.
 PD 14-NOV-2002.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 458
 ID ACA66438 standard; cDNA; 503 BP.
 DE Human secreted/transmembrane protein EST DNA42301.
 PN US2003004102-A1.
 PD 02-JAN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 459
 ID ADA25063 standard; cDNA; 503 BP.
 DE Novel human secreted and transmembrane protein EST DNA42301.
 PN US2003050241-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0
 RESULT 460
 ID ACD30039 standard; cDNA; 503 BP.
 DE Novel human secreted and transmembrane protein EST DNA42301.
 PN US2003050240-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 47.56% Indels: 0

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RESULT 461
ID ADA12724 standard; cDNA; 503 BP.
DE Human secreted/transmembrane polypeptide PRO337 EST.
PN US2003052216-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 462
ID ADC29454 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #134.
PN US2003049633-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 463
ID ADB74030 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003045462-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 464
ID ADB76746 standard; cDNA; 503 BP.
DE Human PRO polynucleotide sequence #134.
PN US2003083248-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 465
ID ADC44172 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003054986-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 466
ID ADC61932 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003049684-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 467
ID ADC63896 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003054405-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 468
ID ADC66996 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 469
ID ADC69120 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003060406-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 470
ID ADC63180 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003068648-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 471
ID ADC68245 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003069178-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 472
ID ADC41565 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003072745-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 473
ID ADC67620 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003073131-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 474
ID ADC62556 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003073624-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 475
ID ADC42189 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104998-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 476
ID ADE49558 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
RESULT 477
ID ADE35612 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003096744-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indels: 0
Query Match: 47.56%
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PN US2003203434-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 478
ID ADE16726 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203435-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 479
ID ADD73341 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203436-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 480
ID ADD72699 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 481
ID ADE17350 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 482
ID ADF47364 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195333-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 483
ID ADG53121 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216561-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 484
ID ADG60441 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003206915-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 485
ID ADI61201 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003077700-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 486
ID ACD42858 standard; cDNA; 503 BP.
DE Novel human secreted and transmembrane protein EST DNA42301.
PN US2003050239-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 487
ID ADE48858 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003104536-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 488
ID ADE89959 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003130181-A1.
PD 10-JUL-2003.
PA (ASHK/) ASHKENAZI A J.
PA (BAKE/) BAKER K P.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERR/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GIRM/) GIRMALDI J C.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (KUOS/) KUO S S.
PA (NAPI/) NAPIER M A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (SHEL/) SHELTON D L.
PA (STEW/) STEWART T A.
PA (TUNA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 489
ID ADF61599 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003195345-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
RESULT 490
ID ADF40291 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003198994-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Conservative: 0
Mismatch: 0
Indel: 0
Query Match: 47.56%
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Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 499			
ID	ADP33218 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003211091-A1.		
PD	13-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 500			
ID	ADP25584 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003211092-A1.		
PD	13-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 501			
ID	ADP26685 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003193674-A1.		
PD	23-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 502			
ID	ADP34474 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003194410-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 503			
ID	ADP46711 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003195344-A1.		
PD	16-OCT-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 504			
ID	ADG50697 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003207803-A1.		
PD	06-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 505			
ID	ADG50073 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003215905-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 506			
ID	ADG51945 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003215908-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 507			
ID	ADG51945 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003215908-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0
RESULT 508			
ID	ADG51945 standard; cDNA; 503 BP.		
DE	Human EST from secreted/transmembrane protein, PRO3337.		
FN	US2003215908-A1.		
PD	20-NOV-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	47.56%	Indels:	0

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Query Match: 47.56% Indels: 0
RESULT 507
ID ADG49449 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 508
ID ADG48825 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 509
ID ADG51321 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 510
ID ADG59265 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 511
ID ADG62721 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 512
ID ADH25746 standard; cDNA; 503 BP.
DE Human DNA2301 expressed sequence tag (EST) SEQ ID NO:524.
PN EP1386931-A1.
PD 04-FEB-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 513
ID ADH17523 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 514
ID ADL07357 standard; cDNA; 503 BP.
DE Human EST from secreted/transmembrane protein, PRO337.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 47.56%
Indels: 0
RESULT 515
ID ABT17405 standard; DNA; 898 BP.
DE Human IG gene related nucleic acid SEQ ID NO 31.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 74.65%
Best Local Similarity: 55.56%
Query Match: 47.12%
Indels: 2
RESULT 516
ID ABQ82337 standard; cDNA; 1196 BP.
DE Human NOV12a encoding cDNA SEQ ID NO:23.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 517
ID ADI28059 standard; cDNA; 1327 BP.
DE ECMCAD gene clone 7087904CB1.
PN WO200202634-A2.
PD 10-JAN-2002.
PA (INCI-) INCIYTE GENOMICS INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 518
ID AAC87055 standard; cDNA; 4834 BP.
DE Nucleotide sequence of human polypeptide PRO6004.
PN WO200077037-A2.
PD 21-DEC-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 519
ID ABK33536 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO protein, Seq ID No 1.
PN WO200208288-A2.
PD 31-JAN-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 520
ID ACA05014 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003032063-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 521
ID ACA60544 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US200217165-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 522
ID ACA4534 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 DNA.
PN US2003032062-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 523
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ID ACA68497 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088063-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 524
ID ACA65675 standard; cDNA; 4834 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO6004.
PN US2003032057-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 525
ID ABT44226 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
PN US2003050448-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 526
ID ADA47301 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003044844-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 527
ID ABT44509 standard; cDNA; 4834 BP.
DE Human PRO6004 cDNA.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 528
ID ACD82176 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO 6004 cDNA.
PN US2003044934-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 529
ID ACD30291 standard; cDNA; 4834 BP.
DE Human cDNA encoding Pro6004.
PN US2003044902-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 530
ID ABT43982 standard; cDNA; 4834 BP.
DE Human membrane bound receptor/protein PRO6004 cDNA sequence.
PN US2003065147-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 531
ID ADB83491 standard; cDNA; 4834 BP.

DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003073814-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 532
ID ADB80597 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088068-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 533
ID ADB73138 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096968-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 534
ID ADB78220 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092889-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 535
ID ADB84868 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003073817-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 536
ID ADB77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092886-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 537
ID ADB87040 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003088067-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 538
ID ADB84622 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003092890-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 539
ID ADB83737 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.

PN US2003069397-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 540
ID ADBY2892 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092887-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 541
ID ADC36730 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003088085-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 542
ID ADC21720 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096969-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 543
ID ADC49751 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088064-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 544
ID ADC48950 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088070-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 545
ID ADC49467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088071-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 546
ID ADC47328 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088072-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 547
ID ADC47073 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105288-A1.

PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 548
ID ADC77948 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 549
ID ADD06183 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 550
ID ADC77702 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 551
ID ADD50665 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 552
ID ADD50911 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 553
ID ADD50392 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096971-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 554
ID ADD50146 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096970-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 63
Mismatches: 105
Indels: 2
Query Match:
RESULT 555
ID ADD51157 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003105289-A1.
PD 05-JUN-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 556
ID ADG63810 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003170721-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 557
ID ACA6841 standard; cDNA; 4834 BP.
DE cDNA encoding human PRO polypeptide #1.
PN US2003036635-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 558
ID ACD42405 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003040014-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 559
ID ACD68593 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003045687-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 560
ID ADC48704 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 561
ID ADE20875 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 562
ID ADE05719 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 563
ID ADD74948 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 564
ID ADD75694 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 565
ID ADD84926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 566
ID ADD86752 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 567
ID ADE20629 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 568
ID ADE38926 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 569
ID ADE05473 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 570
ID ADD73458 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 571
ID ADD78298 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Conservative: 63
Mismatches: 105
Indels: 2

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Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 572
ID ADE21121 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 573
ID ADD7236 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 574
ID ADE20383 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 575
ID ADD7548 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 576
ID ADD73964 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 577
ID ADD74210 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 578
ID ADD75940 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 579
ID ADD85432 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100721-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 580
ID ADE04981 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100726-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 581
ID ADD75194 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100714-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 582
ID ADD76738 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100715-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 583
ID ADD86506 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100719-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 584
ID ADE41224 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003104558-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 585
ID ADD77974 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100731-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 586
ID ADD77482 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100729-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
RESULT 587
ID ADD77728 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100730-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18% Conservative: 63
Best Local Similarity: 47.85% Mismatches: 105
Query Match: 45.57% Indels: 2
```

RESULT 588
ID ADD85186 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100725-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 589
ID ADD73718 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100710-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 590
ID ADD74456 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100713-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 591
ID ADD76984 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100716-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 592
ID ADD85678 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003100720-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 593
ID ADE05227 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100723-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 594
ID ADD74702 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003100724-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 595
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 596
ID ADG05514 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2

ID ADG27068 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 597
ID ADG11131 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096967-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 598
ID ADG11910 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 599
ID ADP94467 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 600
ID ADG06563 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 601
ID ADH38907 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 602
ID ADG63658 standard; cDNA; 4834 BP.
DE Human secreted/transmembrane polypeptide PRO6004 cDNA.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 603
ID ADG33997 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004006206-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Conservative: 63
Mismatches: 105
Indels: 2
RESULT 604
ID ADI33467 standard; cDNA; 4834 BP.


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DE Human PRO polynucleotide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 605
ID ADH69561 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 606
ID ADI29722 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 607
ID ADM27119 standard; cDNA; 4834 BP.
DE Novel human secreted and transmembrane protein PRO6004 cDNA.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 608
ID ADK66477 standard; cDNA; 4834 BP.
DE Human PRO polynucleotide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 609
ID ADS82049 standard; DNA; 4891 BP.
DE Human cancer-associated protein coding sequence #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS ) LG LIFE SCI LTD.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 610
ID ABN85384 standard; DNA; 1119 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.51%
Indels: 2
RESULT 611
ID ADB62841 standard; cDNA; 2383 BP.
DE Human cDNA encoding clone OCBPF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 66.87%
Best Local Similarity: 47.85%
Query Match: 45.40%
Indels: 2
RESULT 612
ID ABQ82338 standard; cDNA; 1165 BP.
DE Human NOV6, KILON-like protein, coding sequence.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 67.18%
Best Local Similarity: 47.85%
Query Match: 45.57%
Indels: 2
RESULT 613
ID ABT17401 standard; DNA; 1809 BP.
DE Human IG gene related nucleic acid SEQ ID NO 27.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 67.06%
Best Local Similarity: 47.48%
Query Match: 45.13%
Indels: 10
RESULT 614
ID AAC78596 standard; cDNA; 2840 BP.
DE Human PRO4993 nucleotide sequence SEQ ID NO:611.
PN WO200053756-A2.
PD 14-SEP-2000.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 615
ID ACA63979 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2002192706-A1.
PD 19-DEC-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 616
ID ACA72143 standard; cDNA; 2840 BP.
DE Human secreted and transmembrane PRO polypeptide #39 cDNA.
PN US2002177553-A1.
PD 28-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 617
ID ABX92783 standard; cDNA; 2840 BP.
DE cDNA encoding human PRO4993 polypeptide.
PN US2002169284-A1.
PD 14-NOV-2002.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 618
ID ACA66524 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO4993.
PN US2003004102-A1.
PD 02-JAN-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 619
ID ADA25149 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
PN US2003050241-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
RESULT 620
ID ADC30125 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane protein PRO4993 cDNA.
```

PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 621
ID ADA12811 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane polypeptide cDNA #139.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 622
ID ADC29540 standard; cDNA; 2840 BP.
DE Novel human secreted and transmembrane polypeptide cDNA #139.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 623
ID ADB74117 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003045482-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 624
ID ADB76833 standard; cDNA; 2840 BP.
DE Human PRO polynucleotide sequence #139.
PN US2003083248-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 625
ID ADC44259 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054986-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 626
ID ADC62019 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003049684-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 627
ID ADC63983 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003054408-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 628
ID ADC67083 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003060406-A1.
PD 27-MAR-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 629
ID ADC69207 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003064407-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 630
ID ADC63267 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003068648-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 631
ID ADC68332 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003069178-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 632
ID ADC41652 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003072745-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 633
ID ADC67707 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073131-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 634
ID ADC62643 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003073624-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 635
ID ADC42276 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003104998-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 636
ID ADE49645 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003096744-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 637
 ID ADE35699 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203434-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 638
 ID ADE16813 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203435-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 639
 ID ADD73428 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203436-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 640
 ID ADD72786 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003194781-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 641
 ID ADE17437 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003203433-A1.
 PD 30-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 642
 ID ADF47451 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003195333-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 643
 ID ADG53208 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003216561-A1.
 PD 20-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 644
 ID ADG60528 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003206915-A1.
 PD 06-NOV-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63

Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 645
 ID ADI61288 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003077700-A1.
 PD 24-APR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 646
 ID ACD42944 standard; cDNA; 2840 BP.
 DE Novel human secreted and transmembrane protein PRO4993 cDNA.
 PN US2003050239-A1.
 PD 13-MAR-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 647
 ID ADE48945 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003104536-A1.
 PD 05-JUN-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 648
 ID ADE90046 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003130181-A1.
 PD 10-JUL-2003.
 PA (ASHK/) ASHENAZI A J.
 PA (BAKE/) BAKER K P.
 PA (BOTS/) BOTSTEIN D.
 PA (DESN/) DESNOYERS L.
 PA (EATO/) EATON D L.
 PA (FERR/) FERRARA N.
 PA (FILV/) FILVAROFF E.
 PA (FONG/) FONG S.
 PA (GAOW/) GAO W.
 PA (GERB/) GERBER H.
 PA (GERR/) GERRITSEN M E.
 PA (GODD/) GODDARD A.
 PA (GODO/) GODOWSKI P J.
 PA (GIRM/) GIRMALDI J C.
 PA (GURN/) GURNEY A L.
 PA (HILL/) HILLAN K J.
 PA (KLJA/) KLJAVIN I J.
 PA (KUOS/) KUO S S.
 PA (NAPI/) NAPIER M A.
 PA (PANJ/) PAN J.
 PA (PAON/) PAONI N F.
 PA (ROYM/) ROY M A.
 PA (SHEL/) SHELTON D L.
 PA (STEW/) STEWART T A.
 PA (TUNA/) TUNAS D.
 PA (WOOD/) WILLIAMS P M.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2
 RESULT 649
 ID ADF61686 standard; cDNA; 2840 BP.
 DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
 PN US2003195345-A1.
 PD 16-OCT-2003.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 66.87% Conservative: 63
 Best Local Similarity: 47.55% Mismatches: 106
 Query Match: 45.13% Indels: 2

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RESULT 650
ID ADF40378 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003198934-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 651
ID ADF46174 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195148-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 652
ID ADF24570 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003204055-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 653
ID ADF41002 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199021-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 654
ID ADF23946 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003203402-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 655
ID ADF33929 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194780-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 656
ID ADF27396 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199436-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 657
ID ADF28032 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 658
ID ADF41626 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 659
ID ADF33305 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 660
ID ADF25671 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 661
ID ADF26772 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 662
ID ADF34561 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 663
ID ADF46798 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 664
ID ADG50784 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003207803-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 665
ID ADG50160 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215905-A1.
PD 20-NOV-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 66.87%
Best Local Similarity: 47.55%
Query Match: 45.13%
Indels: 2
Conservative: 63
Mismatches: 106
Indels: 2
RESULT 666
ID ADG52032 standard; cDNA; 2840 BP.
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DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003215908-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 667
ID ADG49536 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216305-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 668
ID ADG48912 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2003216560-A1.
PD 20-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 669
ID ADG51408 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005312-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 670
ID ADG59352 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004005657-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 671
ID ADG62808 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004006219-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 672
ID ADM17610 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004048332-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 673
ID ADL07444 standard; cDNA; 2840 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO4993.
PN US2004063921-A1.
PD 01-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 66.87% Conservative: 63
Best Local Similarity: 47.55% Mismatches: 106
Query Match: 45.13% Indels: 2
RESULT 674
ID AAT42094 standard; cDNA to mRNA; 756 BP.
DE Human LAMP residues 46-294 coding sequence.
PN US2003215908-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 76.68% Conservative: 50
Best Local Similarity: 56.92% Mismatches: 58
Query Match: 44.10% Indels: 1
RESULT 675
ID AAT42095 standard; cDNA to mRNA; 756 BP.
DE Rat LAMP residues 46-294 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 76.68% Conservative: 50
Best Local Similarity: 56.92% Mismatches: 58
Query Match: 44.05% Indels: 1
RESULT 676
ID ADH71417 standard; DNA; 1030 BP.
DE Human gene of the invention NOV1lg SEQ ID NO:313.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.20% Conservative: 44
Best Local Similarity: 50.62% Mismatches: 104
Query Match: 42.25% Indels: 12
RESULT 677
ID ADH71411 standard; DNA; 1033 BP.
DE Human gene of the invention NOV1ln SEQ ID NO:307.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.20% Conservative: 44
Best Local Similarity: 50.62% Mismatches: 104
Query Match: 42.25% Indels: 12
RESULT 678
ID ADH71413 standard; DNA; 1035 BP.
DE Human gene of the invention NOV1lo SEQ ID NO:309.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.20% Conservative: 44
Best Local Similarity: 50.62% Mismatches: 104
Query Match: 42.25% Indels: 12
RESULT 679
ID ABS76364 standard; DNA; 1427 BP.
DE DNA encoding human immunoglobulin superfamily protein IGSPF-9.
PN WO200272794-A2.
PD 19-SEP-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 64.20% Conservative: 44
Best Local Similarity: 50.62% Mismatches: 104
Query Match: 42.25% Indels: 12
RESULT 680
ID AAD47371 standard; DNA; 2653 BP.
DE Human LP289 DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 64.20% Conservative: 44
Best Local Similarity: 50.62% Mismatches: 104
Query Match: 42.25% Indels: 12
RESULT 681
ID ADH71395 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lf SEQ ID NO:291.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.40% Conservative: 45
Best Local Similarity: 50.46% Mismatches: 103
Query Match: 42.19% Indels: 12
RESULT 682
ID ADH71389 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lc SEQ ID NO:285.
PN WO2003102155-A2.

```
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.40%
Best Local Similarity: 50.46%
Query Match: 42.19%
Indels: 12
RESULT 683
ID ADH71401 standard; DNA; 926 BP.
DE Human gene of the invention NOV111 SEQ ID NO:297.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 684
ID ADH71405 standard; DNA; 927 BP.
DE Human gene of the invention NOV11k SEQ ID NO:301.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 685
ID ADH71409 standard; DNA; 946 BP.
DE Human gene of the invention NOV11m SEQ ID NO:305.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 686
ID ADH71393 standard; DNA; 946 BP.
DE Human gene of the invention NOV11e SEQ ID NO:289.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 687
ID ADH71415 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lp SEQ ID NO:311.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 688
ID ADH71397 standard; DNA; 976 BP.
DE Human gene of the invention NOV1lg SEQ ID NO:293.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 689
ID ABS71699 standard; DNA; 1017 BP.
DE DNA encoding human NOV5b protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 690
ID ADL35978 standard; cDNA; 1017 BP.
DE Human NOVX cDNA #12.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 691
ID ABS71698 standard; DNA; 1018 BP.
DE DNA encoding human NOV5a protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 692
ID ADL35976 standard; cDNA; 1018 BP.
DE Human NOVX cDNA #11.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATI/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 693
ID ADH71399 standard; DNA; 1018 BP.
DE Human gene of the invention NOV1lh SEQ ID NO:295.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 694
ID ADH71387 standard; DNA; 1033 BP.
DE Human gene of the invention NOV1lb SEQ ID NO:283.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 695
ID ADH71385 standard; DNA; 1271 BP.
DE Human gene of the invention NOV1la SEQ ID NO:281.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 66.11%
Best Local Similarity: 52.49%
Query Match: 42.14%
Indels: 8
RESULT 696
ID ADH71421 standard; DNA; 1271 BP.
```

DE Human gene of the invention NOV11s SEQ ID NO:317.
PN WO2003102155-A2.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 63.89% Conservative: 43
Best Local Similarity: 50.62% Mismatches: 105
Query Match: 42.08% Indels: 12
RESULT 697
ID ABS71700 standard; DNA; 1136 BP.
DE DNA encoding human NOV5c protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 65.78% Conservative: 40
Best Local Similarity: 52.49% Mismatches: 95
Query Match: 41.92% Indels: 8
RESULT 698
ID ADH71403 standard; DNA; 1171 BP.
DE Human gene of the invention NOV11j SEQ ID NO:299.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 65.78% Conservative: 40
Best Local Similarity: 52.49% Mismatches: 95
Query Match: 41.92% Indels: 8
RESULT 699
ID ADH71419 standard; DNA; 1271 BP.
DE Human gene of the invention NOV11r SEQ ID NO:315.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 63.89% Conservative: 44
Best Local Similarity: 50.31% Mismatches: 105
Query Match: 41.92% Indels: 12
RESULT 700
ID ADP28685 standard; DNA; 834 BP.
DE Human secreted protein encoding sequence SEQ ID #683.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 68.33% Conservative: 40
Best Local Similarity: 54.09% Mismatches: 84
Query Match: 41.67% Indels: 5
RESULT 701
ID ABK35606 standard; DNA; 1011 BP.
DE Gene encoding novel human secreted or membrane-associated protein #25.
PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 65.12% Conservative: 44
Best Local Similarity: 50.50% Mismatches: 97
Query Match: 40.20% Indels: 8
RESULT 702
ID ABS71701 standard; DNA; 1169 BP.
DE DNA encoding human NOV5d protein.
PN WO200266643-A2.
PD 29-AUG-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.78% Conservative: 43
Best Local Similarity: 50.50% Mismatches: 98
Query Match: 39.92% Indels: 8
RESULT 703
ID ADH71407 standard; DNA; 1169 BP.
DE Human gene of the invention NOV11l SEQ ID NO:303.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 64.78% Conservative: 43
Best Local Similarity: 50.50% Mismatches: 98
Query Match: 39.92% Indels: 8
RESULT 704
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.

ID ABA06475 standard; cDNA; 2813 BP.
DE Human cDNA SEQ ID NO: 141.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 70.45% Conservative: 53
Best Local Similarity: 50.38% Mismatches: 77
Query Match: 39.89% Indels: 1
RESULT 705
ID ABV83812 standard; cDNA; 2813 BP.
DE Human polynucleotide SEQ ID NO 141.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 70.45% Conservative: 53
Best Local Similarity: 50.38% Mismatches: 77
Query Match: 39.89% Indels: 1
RESULT 706
ID AAD47374 standard; DNA; 2601 BP.
DE Human LP319b DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 65.12% Conservative: 44
Best Local Similarity: 50.50% Mismatches: 97
Query Match: 39.04% Indels: 9
RESULT 707
ID ACH15238 standard; cDNA; 437 BP.
DE Human adult brain cDNA #2450.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 99.25% Conservative: 0
Best Local Similarity: 99.25% Mismatches: 1
Query Match: 38.21% Indels: 0
RESULT 708
ID ADH71391 standard; DNA; 760 BP.
DE Human gene of the invention NOV11d SEQ ID NO:287.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 68.40% Conservative: 32
Best Local Similarity: 55.60% Mismatches: 74
Query Match: 38.07% Indels: 5
RESULT 709
ID ADL35982 standard; cDNA; 1168 BP.
DE Human NOVX cDNA #14.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOV S G.
PA (SPVT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PAITTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEGUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Percent Similarity: 64.24% Conservative: 43
Best Local Similarity: 50.00% Mismatches: 99
Query Match: 37.76% Indels: 10
RESULT 710
ID ABK35605 standard; DNA; 1056 BP.
DE Gene encoding novel human secreted or membrane-associated protein #24.

PN WO200204600-A2.
PD 17-JAN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 64.26%
Best Local Similarity: 51.89%
Query Match: 37.74%
Indels: 19
Conservative: 36
Mismatches: 86

RESULT 711
ID ADL35980 standard; cDNA; 1133 BP.
DE Human NOVX cDNA #13.
PN US2003207800-A1.
PD 06-NOV-2003.
PA (MALY/) MALYANKAR U M.
PA (SHEN/) SHENOY S G.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (GUOX/) GUO X.
PA (KEKU/) KEXUDA R.
PA (GANG/) GANGOLLI E A.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (LILL/) LI L.
PA (PADI/) PADIGARU M.
Percent Similarity: 64.78%
Best Local Similarity: 51.16%
Query Match: 37.71%
Indels: 11
Conservative: 41
Mismatches: 98

RESULT 712
ID AAS28811 standard; cDNA; 4656 BP.
DE Human immunoglobulin encoding cDNA SEQ ID NO 57.
PN WO20015315-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 69.81%
Best Local Similarity: 49.43%
Query Match: 37.35%
Indels: 3
Conservative: 54
Mismatches: 78

RESULT 713
ID ADB31536 standard; cDNA; 4656 BP.
DE Human cDNA encoding a novel protein SEQ ID NO 57.
PN US2003077606-A1.
PD 24-APR-2003.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 69.81%
Best Local Similarity: 49.43%
Query Match: 37.35%
Indels: 3
Conservative: 54
Mismatches: 78

RESULT 714
ID AAD47373 standard; DNA; 2597 BP.
DE Human LP319a DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 59.57%
Best Local Similarity: 45.90%
Query Match: 36.68%
Indels: 28
Conservative: 45
Mismatches: 106

RESULT 715
ID ABL99899 standard; cDNA; 5666 BP.
DE Human secretory polynucleotide (sptm) 154.
PN WO20020756-A2.
PD 14-MAR-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 63.61%
Best Local Similarity: 44.08%
Query Match: 36.10%
Indels: 14
Conservative: 66
Mismatches: 109

RESULT 716
ID AAC91321 standard; cDNA; 537 BP.
DE Human polynucleotide for diagnostics and therapeutics, SEQ ID NO: 21.
PN WO200073509-A2.
PD 07-DEC-2000.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 97.54%
Best Local Similarity: 97.54%
Query Match: 34.99%
Indels: 0
Conservative: 0
Mismatches: 3

RESULT 717
ID AAD47372 standard; DNA; 754 BP.
DE Human LP289 splice variant (LP343) DNA.
PN WO200274906-A2.
PD 26-SEP-2002.
PA (ELIL) LILLY & CO ELI.
Percent Similarity: 69.27%
Best Local Similarity: 55.96%
Query Match: 33.58%
Indels: 5
Conservative: 29
Mismatches: 62

RESULT 718
ID AAS78035 standard; cDNA; 484 BP.
DE DNA encoding novel human diagnostic protein #13839.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 90.30%
Best Local Similarity: 86.57%
Query Match: 33.22%
Indels: 0
Conservative: 5
Mismatches: 13

RESULT 719
ID ADP28686 standard; DNA; 666 BP.
DE Human secreted protein encoding sequence SEQ ID #684.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 67.70%
Best Local Similarity: 53.98%
Query Match: 33.19%
Indels: 5
Conservative: 31
Mismatches: 68

RESULT 720
ID ACH46276 standard; cDNA; 409 BP.
DE Human infant brain cDNA #339.
PN US2003073623-A1.
PD 17-APR-2003.
PA (DRNA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
Percent Similarity: 95.87%
Best Local Similarity: 94.21%
Query Match: 32.06%
Indels: 0
Conservative: 2
Mismatches: 5

RESULT 721
ID AAF93346 standard; cDNA; 452 BP.
DE Spinal cord tissue cDNA encoding SRT protein SEQ ID 167.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 32.00%
Indels: 0
Conservative: 0
Mismatches: 0

RESULT 722
ID AAS78034 standard; cDNA; 443 BP.
DE DNA encoding novel human diagnostic protein #13838.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 88.89%
Best Local Similarity: 88.89%
Query Match: 31.53%
Indels: 11
Conservative: 0
Mismatches: 3

RESULT 723
ID ADQ83739 standard; cDNA; 919 BP.
DE Human tumour-associated antigenic target (TAT) cDNA sequence #553.
PN WO2004060270-A2.
PD 22-JUL-2004.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
Percent Similarity: 64.96%
Best Local Similarity: 50.00%
Query Match: 30.79%
Indels: 8
Conservative: 35
Mismatches: 74

RESULT 724
ID AAC19214 standard; cDNA; 333 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 23289.
PN EP1033401-A2.
Indels: 0

PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 95.50%
Best Local Similarity: 94.59%
Query Match: 30.18%
Indels: 1
RESULT 725
ID AAS78003 standard; cDNA; 2883 BP.
DE DNA encoding novel human diagnostic protein #13807.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 56.58%
Best Local Similarity: 45.55%
Query Match: 29.10%
Indels: 50
RESULT 726
ID ADE08816 standard; DNA; 2883 BP.
DE Novel DNA-related contig nucleotide sequence #60.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 56.58%
Best Local Similarity: 45.55%
Query Match: 29.10%
Indels: 50
RESULT 727
ID AAF93597 standard; cDNA; 585 BP.
DE Unimolecular vein endothelial cell cDNA encoding SRT protein SEQ ID 418.
PN WO200107611-A2.
PD 01-FEB-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 71.58%
Best Local Similarity: 50.53%
Query Match: 27.16%
Indels: 4
RESULT 728
ID ABS52769 standard; cDNA; 408 BP.
DE Murine tuberosus sclerosis complex 8 (TSC8) DNA.
PN WO200246475-A2.
PD 13-JUN-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 75.00%
Best Local Similarity: 55.88%
Query Match: 22.18%
Indels: 1
RESULT 729
ID ADG63283 standard; DNA; 540 BP.
DE Human OBCAM gene exon 2.
PN WO2003002765-A2.
PD 09-JAN-2003.
PA (IMCR) IMPERIAL CANCER RES TECHNOLOGY LTD.
Percent Similarity: 78.38%
Best Local Similarity: 69.37%
Query Match: 21.68%
Indels: 13
RESULT 730
ID AAC02777 standard; cDNA; 352 BP.
DE Human secreted protein 5' EST, SEQ ID NO: 2775.
PN EP1033401-A2.
PD 06-SEP-2000.
PA (GEST) GENSET.
Percent Similarity: 82.80%
Best Local Similarity: 73.12%
Query Match: 19.05%
Indels: 1
RESULT 731
ID ABL25337 standard; DNA; 1242 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 27484.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.93%
Best Local Similarity: 27.99%
Query Match: 18.74%
Indels: 63
RESULT 732
ID ABL17651 standard; DNA; 948 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4426.
PN WO200171042-A2.
PD 27-SEP-2001.

PA (PEKE) PE CORP NY.
Percent Similarity: 50.17%
Best Local Similarity: 31.86%
Query Match: 18.44%
Indels: 22
RESULT 733
ID ABL11515 standard; cDNA; 2010 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 29027.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 47.64%
Best Local Similarity: 28.72%
Query Match: 16.97%
Indels: 30
RESULT 734
ID ABX71182 standard; cDNA; 913 BP.
DE Novel human cDNA sequence #407.
PN WO200281731-A2.
PD 17-OCT-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 66.13%
Best Local Similarity: 46.77%
Query Match: 16.75%
Indels: 1
RESULT 735
ID ABL04261 standard; cDNA; 1110 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7265.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 44.37%
Best Local Similarity: 29.69%
Query Match: 16.47%
Indels: 27
RESULT 736
ID ABL04260 standard; cDNA; 3426 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 7262.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 44.37%
Best Local Similarity: 29.69%
Query Match: 16.47%
Indels: 27
RESULT 737
ID ABX56303 standard; DNA; 8243 BP.
DE Human NOV25b CG93858-02 DNA SEQ ID 85.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.47%
Best Local Similarity: 30.14%
Query Match: 16.47%
Indels: 63
RESULT 738
ID ADK60477 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Indels: 63
RESULT 739
ID ADK60778 standard; DNA; 8546 BP.
DE Angiogenesis differentially expressed gene GS-N52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Indels: 63
RESULT 740
ID ADP73100 standard; DNA; 8546 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N52.

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PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 741
ID ADS09799 standard; DNA; 8546 BP.
DE Human therapeutic DNA - SEQ ID 36.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 742
ID ADO08272 standard; cDNA; 15659 BP.
DE Human NOVX polynucleotide #10.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERR/) ZERHUSEN B D.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 743
ID ACA10120 standard; cDNA; 15660 BP.
DE Human NOVX polynucleotide #10.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 744
ID ADH72105 standard; DNA; 15660 BP.
DE Human gene of the invention NOV43c SEQ ID NO:1001.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 42.12%
Best Local Similarity: 29.79%
Query Match: 16.09%
Conservative: 36
Mismatch: 106
Indels: 63
RESULT 745
ID ADK60455 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 746
ID ADK60756 standard; DNA; 18207 BP.
DE Angiogenesis differentially expressed gene GS-N29.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 747
ID ADP73078 standard; DNA; 18207 BP.
DE Angiogenesis inhibitor human DNA sequence, GS-N29.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Percent Similarity: 42.56%
Best Local Similarity: 31.14%
Query Match: 16.09%
Conservative: 33
Mismatch: 109
Indels: 57
RESULT 748
ID ADH72103 standard; DNA; 2136 BP.
DE Human gene of the invention NOV43b SEQ ID NO:999.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 749
ID ACA10119 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 750
ID ADH72101 standard; DNA; 2153 BP.
DE Human gene of the invention NOV43a SEQ ID NO:997.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatch: 111
Indels: 51
RESULT 751
ID ADO08270 standard; cDNA; 2153 BP.
DE Human NOVX polynucleotide #9.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEFLEY D M.
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PA (LILL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLER I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 752
ID AC003633 standard; cDNA; 2916 BP.
DE Novel human GPCR related protein NOV9b cDNA.
PN WO200299116-A2.
PD 12-DEC-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.97%
Best Local Similarity: 30.50%
Query Match: 15.97%
Conservative: 38
Mismatches: 117
Indels: 41
RESULT 753
ID AAS68120 standard; cDNA; 3910 BP.
DE DNA encoding novel human diagnostic protein #3924.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 754
ID AA172024 standard; cDNA; 4073 BP.
DE Human thrombospondin protein, BTL012, coding sequence.
PN WO200174852-A2.
PD 11-OCT-2001.
PA (FARB) BAYER CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 755
ID ADL93996 standard; cDNA; 5877 BP.
DE Human G-coupled protein receptor-related gene #44.
PN US2004006205-A1.
PD 08-JAN-2004.
PA (LILL/) LI L.
PA (GERL/) GERLACH V.
PA (LIUX/) LIU X.
PA (MILL/) MILLER C E.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (ZHON/) ZHONG H.
PA (SMIT/) SMITHSON G.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (VOSS/) VOSS E Z.
PA (VERN/) VERNET C A.
PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTAK K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 756
ID ADB16057 standard; DNA; 5935 BP.
DE G-coupled protein receptor related polypeptide DNA, SEQ ID No 87.
PN WO200283841-A2.
PD 24-OCT-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 757
ID ABX56304 standard; DNA; 6343 BP.
DE Human NOV25c CG56914-03 DNA SEQ ID 87.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 758
ID ADH72107 standard; DNA; 6343 BP.
DE Human gene of the invention NOV43d SEQ ID NO:1003.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 759
ID ABO86156 standard; DNA; 16908 BP.
DE Novel human gene. SEQ ID 27.
PN WO200250105-A1.
PD 27-JUN-2002.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
PA (GLAX) GLAXO GROUP LTD.
Percent Similarity: 43.36%
Best Local Similarity: 31.12%
Query Match: 15.97%
Conservative: 35
Mismatches: 111
Indels: 51
RESULT 760
ID ADQ22570 standard; DNA; 18248 BP.
DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 5390.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 43.77%
Best Local Similarity: 30.25%
Query Match: 15.92%
Conservative: 38
Mismatches: 117
Indels: 41
RESULT 761
ID ADM93822 standard; DNA; 2916 BP.
DE DNA encoding human NOV protein #21.
PN US2004009480-A1.
PD 15-JAN-2004.
PA (ANDE/) ANDERSON D W.
PA (BAUM/) BAUMGARTNER J C.
PA (BOLD/) BOLDOG F L.
PA (CASM/) CASMAN S J.
PA (EDIN/) EDINGER S R.
PA (GANG/) GANGOLLI E A.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUOX/) GUO X S.
PA (HJAL/) HJALT T.
PA (KEKU/) KEKUDA R.
PA (LILL/) LI L.
PA (MACD/) MACDOUGALL J R.

PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATI/) PATTURAJAN M.
PA (PENA/) PENA C E A.
PA (RAST/) RASTELLI L.
PA (SHIM/) SHIMKETS R A.
PA (STON/) STONE D J.
PA (SPYT/) SPYTEK K A.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Percent Similarity: 43.01%
Best Local Similarity: 30.07%
Query Match: 15.86%
Indels: 49
RESULT 762
ID ABL12455 standard; cDNA; 1710 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 31847.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 43.10%
Best Local Similarity: 26.15%
Query Match: 15.75%
Indels: 39
RESULT 763
ID ADB53259 standard; DNA; 3170 BP.
DE Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3801.
PN WO2003065993-A2.
PD 14-AUG-2003.
PA (GENE-) GENE LOGIC INC.
Percent Similarity: 42.52%
Best Local Similarity: 25.51%
Query Match: 15.37%
Indels: 37
RESULT 764
ID ADI24496 standard; cDNA; 2960 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:46.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
Indels: 28
RESULT 765
ID ADA53985 standard; cDNA; 3309 BP.
DE Human coding sequence, SEQ ID 1553.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
Indels: 28
RESULT 766
ID AAH98595 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 452.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
Indels: 28
RESULT 767
ID AAH98610 standard; cDNA; 4710 BP.
DE Human EST-derived coding sequence SEQ ID NO: 467.
PN WO200154477-A2.
PD 02-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
Indels: 28
RESULT 768
ID AAD14203 standard; DNA; 8513 BP.
DE MESVR/EGFP/IRESNCAPro(ori) vector.

PN WO200155371-A1.
PD 02-AUG-2001.
PA (SCRI) SCRIPPS RES INST.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.28%
Indels: 28
RESULT 769
ID ADD25618 standard; DNA; 2633 BP.
DE Binding domain-immunoglobulin fusion protein-associated DNA #93.
PN US2003118592-A1.
PD 26-JUN-2003.
PA (GENE-) GENE CRAFT INC.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.23%
Indels: 28
RESULT 770
ID ADI31624 standard; cDNA; 2633 BP.
DE Human cDNA #950.
PN US6607879-B1.
PD 19-AUG-2003.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.23%
Indels: 28
RESULT 771
ID ADL12516 standard; cDNA; 5807 BP.
DE Human steroid-induced C3A liver cell cDNA #245.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 43.31%
Best Local Similarity: 25.70%
Query Match: 15.17%
Indels: 28
RESULT 772
ID AAD56185 standard; DNA; 6801 BP.
DE Human LRRCAPS DNA #2.
PN WO2003035831-A2.
PD 01-MAY-2003.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 39.58%
Best Local Similarity: 29.17%
Query Match: 15.17%
Indels: 56
RESULT 773
ID ADH48823 standard; DNA; 7097 BP.
DE NOV45B coding sequence, SEQ ID 107.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.99%
Best Local Similarity: 29.00%
Query Match: 15.14%
Indels: 28
RESULT 774
ID ADH48921 standard; DNA; 4321 BP.
DE NOV45A coding sequence, SEQ ID 105.
PN WO200268652-A2.
PD 06-SEP-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 41.74%
Best Local Similarity: 28.97%
Query Match: 15.03%
Indels: 36
RESULT 775
ID AAL62047 standard; cDNA; 3360 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-35 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 41.84%
Best Local Similarity: 24.83%
Query Match: 15.01%
Indels: 38
RESULT 776
ID ABL23499 standard; DNA; 2190 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21970.
PN WO200171042-A2.

PA (PILA/) PILARSKY C. 38.70% Conservative: 32
Percent Similarity: 28.79% Mismatches: 147
Best Local Similarity: 14.87% Indels: 51
Query Match: 14.87%
RESULT 792
ID ADR66267 standard; DNA; 6847 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 121 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 38.70% Conservative: 32
Best Local Similarity: 28.79% Mismatches: 147
Query Match: 14.87% Indels: 51
RESULT 793
ID ADR66768 standard; DNA; 6847 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 61 #4.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 38.70% Conservative: 32
Best Local Similarity: 28.79% Mismatches: 147
Query Match: 14.87% Indels: 51
RESULT 794
ID ADF81722 standard; DNA; 6939 BP.
DE Leukaemia-related DNA sequence #2278.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 38.70% Conservative: 32
Best Local Similarity: 28.79% Mismatches: 147
Query Match: 14.87% Indels: 51
RESULT 795
ID ADF81721 standard; DNA; 6939 BP.
DE Leukaemia-related DNA sequence #2277.
PN WO2003039443-A2.
PD 15-MAY-2003.
PA (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.
PA (HAFE/) HAFERLACH T.
PA (SCHO/) SCHOCH C.
PA (KERN/) KERN W.
Percent Similarity: 38.70% Conservative: 32
Best Local Similarity: 28.79% Mismatches: 147
Query Match: 14.87% Indels: 51
RESULT 796
ID ABL17650 standard; DNA; 3060 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 4423.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 44.74% Conservative: 54
Best Local Similarity: 28.53% Mismatches: 124
Query Match: 14.78% Indels: 62
RESULT 797
ID ABS70409 standard; cDNA; 6814 BP.
DE Human bone remodelling gene #66.
PN US6426186-B1.
PD 30-JUL-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.39% Conservative: 32
Best Local Similarity: 28.48% Mismatches: 148

Query Match: 14.59% Indels: 51
RESULT 798
ID ABX63089 standard; cDNA; 4978 BP.
DE Human CDNA #89 differentially expressed in activated vascular tissue.
PN US2002137081-A1.
PD 26-SEP-2002.
PA (BAND/) BANDMAN O.
Percent Similarity: 43.15% Conservative: 50
Best Local Similarity: 26.03% Mismatches: 133
Query Match: 14.56% Indels: 33
RESULT 799
ID AAX55767 standard; cDNA; 4188 BP.
DE Drosophila Robo 1 polypeptide encoding CDNA.
PN WO9925833-A1.
PD 27-MAY-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 42.16% Conservative: 49
Best Local Similarity: 26.14% Mismatches: 127
Query Match: 14.45% Indels: 50
RESULT 800
ID AAX57250 standard; cDNA; 4188 BP.
DE Drosophila sp. ROBO1 CDNA.
PN WO9920764-A1.
PD 29-APR-1999.
PA (REGC) UNIV CALIFORNIA.
Percent Similarity: 42.16% Conservative: 49
Best Local Similarity: 26.14% Mismatches: 127
Query Match: 14.45% Indels: 50
RESULT 801
ID ABL10471 standard; cDNA; 2113 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25895.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.34% Conservative: 58
Best Local Similarity: 26.18% Mismatches: 134
Query Match: 14.42% Indels: 73
RESULT 802
ID ABL22881 standard; DNA; 4355 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20116.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.16% Conservative: 49
Best Local Similarity: 26.14% Mismatches: 127
Query Match: 14.40% Indels: 50
RESULT 803
ID ABX13540 standard; DNA; 93801 BP.
DE Human RGS11 DNA.
PN WO2002103355-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Percent Similarity: 42.96% Conservative: 37
Best Local Similarity: 29.60% Mismatches: 132
Query Match: 14.34% Indels: 26
RESULT 804
ID ADQ89963 standard; DNA; 103052 BP.
DE Antagonist of cell cycle progression nucleotide sequence #197.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Percent Similarity: 42.96% Conservative: 37
Best Local Similarity: 29.60% Mismatches: 132
Query Match: 14.34% Indels: 26
RESULT 805
ID ADM74170 standard; DNA; 1140 BP.
DE Human NOV3A gene sequence SeqID9.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.38% Conservative: 52
Best Local Similarity: 27.38% Mismatches: 123
Query Match: 14.31% Indels: 61

RESULT 806
ID AA206640 standard; cDNA; 1335 BP.
DE Beta-secretase polynucleotide.
PN US5942400-A.
PD 24-AUG-1999.
PA (ELAN-) ELAN PHARM INC.
Percent Similarity: 42.39%
Best Local Similarity: 26.63%
Query Match: 14.17%
Conservative: 58
Mismatch: 137
Indels: 76
RESULT 807
ID AAC65809 standard; cDNA; 1335 BP.
DE Beta-secretase cDNA.
PN US6221645-B1.
PD 24-APR-2001.
PA (ELAN-) ELAN PHARM INC.
Percent Similarity: 42.39%
Best Local Similarity: 26.63%
Query Match: 14.17%
Conservative: 58
Mismatch: 137
Indels: 76
RESULT 808
ID ABL14207 standard; cDNA; 2131 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 37103.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 39.78%
Best Local Similarity: 24.93%
Query Match: 14.17%
Conservative: 53
Mismatch: 131
Indels: 84
RESULT 809
ID ADM74176 standard; DNA; 918 BP.
DE Human NOV3D gene sequence SeqID15.
PN WO2004015079-A2.
PD 19-FEB-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.38%
Best Local Similarity: 27.08%
Query Match: 14.04%
Conservative: 53
Mismatch: 123
Indels: 61
RESULT 810
ID ABL17377 standard; DNA; 1216 BP.
DE Human IG gene related nucleic acid SEQ ID No 3.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.60%
Best Local Similarity: 26.83%
Query Match: 14.04%
Conservative: 55
Mismatch: 124
Indels: 61
RESULT 811
ID ABL17376 standard; DNA; 1242 BP.
DE Human IG gene related nucleic acid SEQ ID No 2.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.60%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 812
ID AD119787 standard; DNA; 2113 BP.
DE Human NOV12 DNA.
PN US2004002134-A1.
PD 01-JAN-2004.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 813
ID AAF27862 standard; cDNA; 2116 BP.
DE Human NOV12 cDNA.
PN WO200075321-A2.
PD 14-DEC-2000.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 814
ID ABL54191 standard; cDNA; 2196 BP.

ID ABL17375 standard; DNA; 2116 BP.
DE Human IG gene related nucleic acid SEQ ID No 1.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 815
ID ACD40265 standard; DNA; 2116 BP.
DE Human breast tumour associated protein 47-like polypeptide NOV12 DNA.
PN US2003027158-A1.
PD 06-FEB-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 816
ID ADM56388 standard; cDNA; 2116 BP.
DE Human CDNA encoding cell adhesion molecule NOV12.
PN US2003082554-A1.
PD 01-MAY-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 817
ID ADF66750 standard; cDNA; 2116 BP.
DE CDNA encoding novel human protein NOV12.
PN US2003199103-A1.
PD 23-OCT-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 818
ID ADO60260 standard; DNA; 2116 BP.
DE Human NOV12 DNA.
PN US2003134430-A1.
PD 17-JUL-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 819
ID ABK94901 standard; cDNA; 2422 BP.
DE Human novel polynucleotide #12.
PN WO200244340-A2.
PD 06-JUN-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.06%
Best Local Similarity: 26.91%
Query Match: 14.04%
Conservative: 57
Mismatch: 137
Indels: 65
RESULT 820
ID AAS86623 standard; cDNA; 16421 BP.
DE DNA encoding novel human diagnostic protein #22427.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.86%
Best Local Similarity: 26.19%
Query Match: 14.04%
Conservative: 42
Mismatch: 115
Indels: 29
RESULT 821
ID ADO47373 standard; DNA; 1761 BP.
DE Human neurotrophin-like protein-related DNA SeqID8.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 43.97%
Best Local Similarity: 27.36%
Query Match: 14.01%
Conservative: 51
Mismatch: 132
Indels: 40
RESULT 822
ID ABL54191 standard; cDNA; 2196 BP.

DE Neurotrophin-like protein splice variant coding sequence.
PN WO200151715-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 43.97% Conservative: 51
Best Local Similarity: 27.36% Mismatches: 132
Query Match: 14.01% Indels: 40
RESULT 823
ID ADO47371 standard; DNA; 2196 BP.
DE Human neurotrophin-like protein-related gene SeqID6.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 43.97% Conservative: 51
Best Local Similarity: 27.36% Mismatches: 132
Query Match: 14.01% Indels: 40
RESULT 824
ID ABL09371 standard; cDNA; 2658 BP.
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 22595.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PERE-) PE CORP NY.
Percent Similarity: 42.56% Conservative: 54
Best Local Similarity: 26.49% Mismatches: 122
Query Match: 13.87% Indels: 71
RESULT 825
ID ABL54189 standard; cDNA; 1124 BP.
DE Neurotrophin-like protein partial coding sequence.
PN WO200151715-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 826
ID ADO47367 standard; DNA; 1124 BP.
DE Human neurotrophin-like protein-related gene SeqID2.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 827
ID ADO47370 standard; cDNA; 1377 BP.
DE Human neurotrophin-like protein-related cDNA SeqID5.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 828
ID ABL54190 standard; cDNA; 1699 BP.
DE Neurotrophin-like protein coding sequence.
PN WO200151715-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 829
ID ADO47368 standard; cDNA; 1699 BP.
DE Human neurotrophin-like protein-related cDNA SeqID3.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 830
ID ADS09923 standard; DNA; 1699 BP.
DE Human therapeutic DNA - SEQ ID 160.

PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 831
ID ADO47384 standard; DNA; 2868 BP.
DE Human neurotrophin-like protein-related DNA SeqID12.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 832
ID AAL62046 standard; cDNA; 3257 BP.
DE Human cell adhesion and extracellular matrix protein (CADECM)-34 cDNA.
PN WO2003047526-A2.
PD 12-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 833
ID ADO47382 standard; DNA; 3312 BP.
DE Human neurotrophin-like protein-related gene SeqID17.
PN WO2004039942-A2.
PD 13-MAY-2004.
PA (NUVE-) NUVELO.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 834
ID ADS09924 standard; DNA; 3312 BP.
DE Human therapeutic DNA - SEQ ID 161.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 835
ID ADS10423 standard; DNA; 3386 BP.
DE Human therapeutic DNA - SEQ ID 660.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 836
ID AAS76287 standard; cDNA; 3868 BP.
DE DNA encoding novel human diagnostic protein #12091.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 837
ID ADH72133 standard; DNA; 4141 BP.
DE Human gene of the invention NOV46f SEQ ID NO:1029.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 44.89% Conservative: 47
Best Local Similarity: 27.74% Mismatches: 123
Query Match: 13.84% Indels: 28
RESULT 838
ID ABX70427 standard; DNA; 4169 BP.
DE DNA encoding human GPCR related protein NOV13a.
PN WO200279398-A2.

PD 10-OCT-2002.
 PA (CURA-) CURAGEN CORP. Conservative: 47
 Percent Similarity: 44.89% Mismatches: 123
 Best Local Similarity: 27.74% Indels: 28
 Query Match: 13.84%
 RESULT 839
 ID ADH72137 standard; DNA; 4169 BP.
 DE Human gene of the invention NOV46h SEQ ID NO:1033.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP. Conservative: 47
 Percent Similarity: 44.89% Mismatches: 123
 Best Local Similarity: 27.74% Indels: 28
 Query Match: 13.84%
 RESULT 840
 ID ADL24006 standard; cDNA; 4169 BP.
 DE Human NOVX cDNA #26.
 PN US2004002120-A1.
 PD 01-JAN-2004.
 PA (KEKU/) KEKUDA R. Conservative: 47
 (TCHE/) TCHERNEV V T. Mismatches: 123
 (LIUX/) LIU X. Indels: 28
 (SPYT/) SPYTEK K A.
 PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (GORM/) GORMAN L.
 PA (MALT/) MALYANKAR U M.
 PA (BOLD/) BOLDOG F L.
 PA (GUOX/) GUO X.
 PA (SHEN/) SHENOY S G.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUPIER R J.
 PA (MILL/) MILLER C E.
 PA (CASM/) CASMAN S J.
 PA (PENA/) PENNA C E A.
 PA (GANG/) GANGOLLI E A.
 PA (GUSE/) GUSEV V V.
 PA (SMIT/) SMITHSON G.
 PA (ZERR/) ZERRHUSEN B D.
 PA (GERL/) GERLACH V.
 PA (POCH/) POCHART P F.
 PA (FERN/) FERNANDES E R.
 PA (SHIM/) SHIMKETS R A.
 PA (RAST/) RASTELLI L.
 PA (SPAD/) SPADERNA S K.
 PA (LARO/) LAROCHELLE W J.
 PA (ZHON/) ZHONG M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (VOSS/) VOSS E Z.
 PA (HERR/) HERRMANN J L.
 Percent Similarity: 44.89%
 Best Local Similarity: 27.74%
 Query Match: 13.84%
 RESULT 841
 ID ABD33040 standard; cDNA; 3588 BP.
 DE Human cancer-associated cDNA HR22-025.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 842
 ID AAI64283 standard; DNA; 4548 BP.
 DE Human transient axonal glycoprotein (tag-1) DNA.
 PN WO200188546-A2.
 PD 22-NOV-2001.
 PA (UNMI) UNIV MICHIGAN. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 843
 ID ABD33041 standard; cDNA; 6137 BP.
 DE Human cancer-associated cDNA HR22-025.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 846
 ID ADQ23368 standard; DNA; 7625 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 847
 ID ADQ24513 standard; DNA; 7625 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (VERN/) VERNET C A M.
 PA (LILL/) LI L.
 PA (GORM/) GORMAN L.
 PA (MALT/) MALYANKAR U M.
 PA (BOLD/) BOLDOG F L.
 PA (GUOX/) GUO X.
 PA (SHEN/) SHENOY S G.
 PA (PADI/) PADIGARU M.
 PA (TAUP/) TAUPIER R J.
 PA (MILL/) MILLER C E.
 PA (CASM/) CASMAN S J.
 PA (PENA/) PENNA C E A.
 PA (GANG/) GANGOLLI E A.
 PA (GUSE/) GUSEV V V.
 PA (SMIT/) SMITHSON G.
 PA (ZERR/) ZERRHUSEN B D.
 PA (GERL/) GERLACH V.
 PA (POCH/) POCHART P F.
 PA (FERN/) FERNANDES E R.
 PA (SHIM/) SHIMKETS R A.
 PA (RAST/) RASTELLI L.
 PA (SPAD/) SPADERNA S K.
 PA (LARO/) LAROCHELLE W J.
 PA (ZHON/) ZHONG M.
 PA (KHRA/) KHRAMTSOV N V.
 PA (VOSS/) VOSS E Z.
 PA (HERR/) HERRMANN J L.
 Percent Similarity: 44.89%
 Best Local Similarity: 27.74%
 Query Match: 13.84%
 RESULT 843
 ID ABD33040 standard; cDNA; 3588 BP.
 DE Human cancer-associated cDNA HR22-025.1.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 844
 ID AAI64283 standard; DNA; 4548 BP.
 DE Human transient axonal glycoprotein (tag-1) DNA.
 PN WO200188546-A2.
 PD 22-NOV-2001.
 PA (UNMI) UNIV MICHIGAN. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 845
 ID ABD33041 standard; cDNA; 6137 BP.
 DE Human cancer-associated cDNA HR22-025.2.
 PN WO2004074320-A2.
 PD 02-SEP-2004.
 PA (SAGR-) SAGRES DISCOVERY INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 846
 ID ADQ23368 standard; DNA; 7625 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6188.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC. Conservative: 40
 Percent Similarity: 40.70% Mismatches: 110
 Best Local Similarity: 26.67% Indels: 59
 Query Match: 13.82%
 RESULT 847
 ID ADQ24513 standard; DNA; 7625 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 7333.
 PN WO2004048938-A2.
 PD 10-JUN-2004.

PA (PROT-) PROTEIN DESIGN LABS INC.
Percent Similarity: 40.70%
Best Local Similarity: 26.67%
Query Match: 13.82%
Conservative: 40
Mismatches: 110
Indels: 59
RESULT 848
ID ADO28580 standard; cDNA; 7650 BP.
DE Human axonin-1 precursor (AXO1) encoding cDNA SEQ ID NO:9.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 40.70%
Best Local Similarity: 26.67%
Query Match: 13.82%
Conservative: 40
Mismatches: 110
Indels: 59
RESULT 849
ID ADA53286 standard; cDNA; 1880 BP.
DE Human coding sequence, SEQ ID 854.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 44.31%
Best Local Similarity: 26.46%
Query Match: 13.78%
Conservative: 58
Mismatches: 126
Indels: 55
RESULT 850
ID ABL24131 standard; DNA; 1404 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 23866.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 42.08%
Best Local Similarity: 27.41%
Query Match: 13.73%
Conservative: 38
Mismatches: 72
Indels: 78
RESULT 851
ID ABK94709 standard; DNA; 3314 BP.
DE Neurodegenerative disease associated polynucleotide #18.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 852
ID ABK94710 standard; DNA; 3335 BP.
DE Neurodegenerative disease associated polynucleotide #19.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 853
ID AAQ74440 standard; cDNA; 3360 BP.
DE Human contactin cDNA (EMBL Accession #Z21488).
PN EP618293-A1.
PD 05-OCT-1994.
PA (BECT) BECTON DICKINSON CO.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 854
ID ABL64109 standard; DNA; 3360 BP.
DE Breast cancer related gene sequence SEQ ID NO:2446.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 855
ID ABL63715 standard; DNA; 3360 BP.
DE Breast cancer related gene sequence SEQ ID NO:2052.
PN WO200194629-A2.
PD 13-DEC-2001.
PA (AVAL-) AVALON PHARM.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 856
ID ABK94708 standard; DNA; 3360 BP.
DE Neurodegenerative disease associated polynucleotide #17.
PN WO200240996-A2.
PD 23-MAY-2002.
PA (MITO-) MITOKOR.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 857
ID ADE71112 standard; DNA; 3360 BP.
DE Contactin gene, SEQ ID 66.
PN WO2003070889-A2.
PD 28-AUG-2003.
PA (IDEC-) IDEC PHARM CORP.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 858
ID ADJ75287 standard; DNA; 3360 BP.
DE Marker gene SEQ ID NO:539.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 859
ID AAT07313 standard; cDNA; 3395 BP.
DE Human contactin coding sequence.
PN WO9535373-A2.
PD 28-DEC-1995.
PA (LJOL-) LA JOLLA CANCER RES FOUND.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 860
ID ADO28658 standard; cDNA; 3427 BP.
DE Human CONT encoding cDNA SEQ ID NO:87.
PN WO200404178-A2.
PD 27-MAY-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 41.85%
Best Local Similarity: 24.60%
Query Match: 13.65%
Conservative: 54
Mismatches: 133
Indels: 49
RESULT 861
ID ADR66243 standard; DNA; 4015 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 97 #2.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 39.04%
Best Local Similarity: 27.03%
Query Match: 13.62%
Conservative: 40
Mismatches: 146
Indels: 57
RESULT 862
ID ADR66585 standard; DNA; 4015 BP.
DE Human prostatic carcinoma derived DNA SEQ ID 97 #3.
PN WO2004076614-A2.
PD 10-SEP-2004.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (ROSE/) ROSENTHAL A.
PA (HERM/) HERMANN K.
PA (PILA/) PILARSKY C.
Percent Similarity: 39.04%
Conservative: 40

Best Local Similarity: 27.03% Mismatches: 146
Query Match: 13.62% Indels: 57
RESULT 863
ID AAS67246 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #3050.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 864
ID AAS71723 standard; cDNA; 2678 BP.
DE DNA encoding novel human diagnostic protein #7527.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 865
ID AAS64445 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #249.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 866
ID AAS64798 standard; cDNA; 3131 BP.
DE DNA encoding novel human diagnostic protein #602.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 45.21% Conservative: 60
Best Local Similarity: 27.25% Mismatches: 99
Query Match: 13.43% Indels: 87
RESULT 867
ID ABK90037 standard; cDNA; 7764 BP.
DE Human OCP cDNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 868
ID ABK90051 standard; cDNA; 7770 BP.
DE Coding sequence of human OCP protein.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 869
ID ADL02243 standard; cDNA; 7770 BP.
DE Human OCP cDNA #5.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.47% Conservative: 46
Best Local Similarity: 26.98% Mismatches: 129
Query Match: 13.40% Indels: 74
RESULT 870
ID AAT15929 standard; cDNA; 2178 BP.
DE Neural cell adhesion molecule splice variant cDNA.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Percent Similarity: 41.98% Conservative: 57
Best Local Similarity: 24.38% Mismatches: 157

Query Match: 13.37% Indels: 31
RESULT 871
ID AAT15928 standard; cDNA; 2450 BP.
DE Neural cell adhesion molecule full-length DNA.
PN WO9604396-A1.
PD 15-FEB-1996.
PA (SYST-) SYSTEMIX INC.
Percent Similarity: 41.98% Conservative: 57
Best Local Similarity: 24.38% Mismatches: 157
Query Match: 13.37% Indels: 31
RESULT 872
ID ADJ76119 standard; DNA; 3843 BP.
DE Marker gene SEQ ID NO:1371.
PN EPI394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Percent Similarity: 41.85% Conservative: 55
Best Local Similarity: 24.28% Mismatches: 133
Query Match: 13.37% Indels: 49
RESULT 873
ID ADA53434 standard; cDNA; 3870 BP.
DE Human coding sequence, SEQ ID 1002.
PN EPI293569-A2.
PD 19-MAR-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 44.33% Conservative: 48
Best Local Similarity: 27.84% Mismatches: 109
Query Match: 13.37% Indels: 53
RESULT 874
ID ADI24497 standard; cDNA; 4723 BP.
DE Human modifier of Chk1 (MCHK) encoding cDNA SEQ ID NO:47.
PN WO2004004785-A1.
PD 15-JAN-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 41.67% Conservative: 55
Best Local Similarity: 24.69% Mismatches: 158
Query Match: 13.37% Indels: 31
RESULT 875
ID AB211468 standard; cDNA; 6599 BP.
DE Human polynucleotide SEQ ID NO 350.
PN WO200270539-A2.
PD 12-SEP-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 42.60% Conservative: 44
Best Local Similarity: 26.71% Mismatches: 131
Query Match: 13.34% Indels: 28
RESULT 876
ID ADM43986 standard; cDNA; 6599 BP.
DE Novel human arginine-rich protein cDNA #350.
PN US2004053250-A1.
PD 18-MAR-2004.
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
Percent Similarity: 42.60% Conservative: 44
Best Local Similarity: 26.71% Mismatches: 131
Query Match: 13.34% Indels: 28
RESULT 877
ID AAD04326 standard; DNA; 2766 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_2 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 878
ID AAD04325 standard; DNA; 2771 BP.
DE Human cell adhesion molecule homologue (CAM-H) DNA #2.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.

Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 879
ID AAD04327 standard; DNA; 2771 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_c_1 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 880
ID AAD04328 standard; DNA; 3060 BP.
DE Human nuclear cell adhesion molecule homologue, NCAM_d_2 DNA.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 881
ID AAD04324 standard; DNA; 3065 BP.
DE Human cell adhesion molecule homologue (CAM-H) DNA #1.
PN WO200129215-A2.
PD 26-APR-2001.
PA (COMP-) COMPUGEN LTD.
Percent Similarity: 41.28% Conservative: 52
Best Local Similarity: 25.38% Mismatches: 109
Query Match: 13.21% Indels: 83
RESULT 882
ID ADJ56383 standard; cDNA; 6829 BP.
DE C.elegans cDNA differentially expressed in MYCN activated cells SeqID189.
PN US2003119009-A1.
PD 26-JUN-2003.
PA (STUA/) STUART S G.
PA (NUCH/) NUCHTERN J G.
PA (PLOW/) PLOW S E.
PA (SHOH/) SHOHEI J M.
Percent Similarity: 38.39% Conservative: 32
Best Local Similarity: 28.48% Mismatches: 148
Query Match: 13.18% Indels: 52
RESULT 883
ID ABS54189 standard; cDNA; 8180 BP.
DE Human osteoclast protein (OCP) cDNA 5+3 corrected.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 884
ID ADL02228 standard; cDNA; 8180 BP.
DE Human OCP cDNA #3.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 885
ID ABK90038 standard; cDNA; 8262 BP.
DE Human 5+3 corrected OCP cDNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75

RESULT 886
ID AAI72586 standard; cDNA; 8262 BP.
DE Human OCP cDNA.
PN US2002022026-A1.
PD 21-FEB-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 887
ID ABS54187 standard; cDNA; 8262 BP.
DE Human osteoclast protein (OCP) cDNA.
PN US2002086825-A1.
PD 04-JUL-2002.
PA (EINA/) EINAT P.
PA (SEGE/) SEGEV O.
PA (SKAL/) SKALITER R.
PA (FEIN/) FEINSTEIN E.
PA (FAER/) FAERMAN A.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 888
ID ADL02226 standard; cDNA; 8262 BP.
DE Human OCP cDNA #2.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64% Conservative: 47
Best Local Similarity: 26.90% Mismatches: 128
Query Match: 13.15% Indels: 75
RESULT 889
ID AAT42088 standard; cDNA to mRNA; 219 BP.
DE Human LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 77.78% Conservative: 14
Best Local Similarity: 58.33% Mismatches: 16
Query Match: 13.12% Indels: 0
RESULT 890
ID AAT42089 standard; cDNA to mRNA; 219 BP.
DE Rat LAMP residues 46-118 coding sequence.
PN WO9630052-A1.
PD 03-OCT-1996.
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.
Percent Similarity: 77.78% Conservative: 14
Best Local Similarity: 58.33% Mismatches: 16
Query Match: 13.12% Indels: 0
RESULT 891
ID ADRO7797 standard; cDNA; 2451 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1303.
PN EP1447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 40.83% Conservative: 34
Best Local Similarity: 29.07% Mismatches: 133
Query Match: 13.07% Indels: 39
RESULT 892
ID ADH71831 standard; DNA; 2902 BP.
DE Human gene of the invention NOV29af SEQ ID NO:727.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.59% Conservative: 46
Best Local Similarity: 27.06% Mismatches: 127
Query Match: 13.04% Indels: 75
RESULT 893
ID ADH71817 standard; DNA; 2902 BP.

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DE Human gene of the invention NOV29y SEQ ID NO:713.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.59%
Best Local Similarity: 27.06%
Query Match: 13.04%
Conservative: 46
Mismatches: 127
Indels: 75
RESULT 894
ID ABK90046 standard; DNA; 3518 BP.
DE Middle fragment (B) comprising central region of human OCP DNA.
PN WO200246364-A2.
PD 13-JUN-2002.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 895
ID ADL02247 standard; cDNA; 3518 BP.
DE Human OCP cDNA #7.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 896
ID ADRO7921 standard; cDNA; 4086 BP.
DE Full length human cDNA useful for treating neurological disease Seq 1427.
PN EPI447413-A2.
PD 18-AUG-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 897
ID ADL02251 standard; cDNA; 7872 BP.
DE Human OCP cDNA #10.
PN US2004053301-A1.
PD 18-MAR-2004.
PA (QUAR-) QUARK BIOTECH INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 898
ID ADS09892 standard; DNA; 7996 BP.
DE Human therapeutic DNA - SEQ ID 129.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 899
ID ADS09893 standard; DNA; 8782 BP.
DE Human therapeutic DNA - SEQ ID 130.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Percent Similarity: 40.64%
Best Local Similarity: 26.90%
Query Match: 13.04%
Conservative: 47
Mismatches: 128
Indels: 75
RESULT 900
ID ADB62179 standard; cDNA; 2420 BP.
DE Human cDNA encoding clone CTONG20036990.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Percent Similarity: 43.35%
Best Local Similarity: 26.62%
Query Match: 12.98%
Conservative: 44
Mismatches: 103
Indels: 46
RESULT 901
ID ABL88109 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 902
ID ABL95598 standard; cDNA; 1427 BP.
DE Human anglogenesis related cDNA PRO7261 SEQ ID NO: 75.
PN WO200208284-A2.
PD 31-JAN-2002.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 903
ID ADD10364 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 904
ID ADD11324 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 905
ID ADD37117 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 906
ID ADE41325 standard; cDNA; 1427 BP.
DE Human secreted/transmembrane PRO polypeptide cDNA #38.
PN US2003100497-A1.
PD 29-MAY-2003.
PA (GETH-) GENENTECH INC.
Percent Similarity: 39.45%
Best Local Similarity: 24.91%
Query Match: 12.93%
Conservative: 42
Mismatches: 132
Indels: 43
RESULT 907
ID ADH43508 standard; cDNA; 1427 BP.
DE Human PRO polynucleotide #38.
PN US2003224984-A1.
PD 04-DEC-2003.
PA (GETH-) GENENTECH INC.
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Percent Similarity: 39.45% Conservative: 42
Best Local Similarity: 24.91% Mismatches: 132
Query Match: 12.93% Indels: 43
RESULT 908
ID ADK82853 standard; cDNA; 1427 BP.
DE Human PRO polynucleotide #38.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 39.45% Conservative: 42
Best Local Similarity: 24.91% Mismatches: 132
Query Match: 12.93% Indels: 43
RESULT 909
ID ADR67151 standard; DNA; 3904 BP.
DE Human bladder cancer associated nucleotide sequence.
PN WO2004076613-A2.
PD 10-SEP-2004.
PA (HERR/) HERR A.
PA (HINZ/) HINZMANN B.
PA (DAHL/) DAHL E.
PA (STAU/) STAUB E.
PA (PILA/) PILARSKY C.
PA (SPEC/) SPECHT T.
Percent Similarity: 39.45% Conservative: 42
Best Local Similarity: 24.91% Mismatches: 132
Query Match: 12.93% Indels: 43
RESULT 910
ID ABL22880 standard; DNA; 8410 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 20113.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 38.84% Conservative: 49
Best Local Similarity: 23.85% Mismatches: 121
Query Match: 12.93% Indels: 79
RESULT 911
ID ADH71829 standard; DNA; 2902 BP.
DE Human gene of the invention NOV29ae SEQ ID NO:725.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.71% Conservative: 47
Best Local Similarity: 26.84% Mismatches: 126
Query Match: 12.87% Indels: 75
RESULT 912
ID ADH71815 standard; DNA; 2902 BP.
DE Human gene of the invention NOV29x SEQ ID NO:711.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.71% Conservative: 47
Best Local Similarity: 26.84% Mismatches: 126
Query Match: 12.87% Indels: 75
RESULT 913
ID ADH71819 standard; DNA; 7831 BP.
DE Human gene of the invention NOV29z SEQ ID NO:715.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 914
ID ABS51089 standard; cDNA; 7876 BP.
DE cDNA encoding human NOV12a protein.
PN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 915
ID ADJ83054 standard; DNA; 7876 BP.

DE Human NOVX NOV12a DNA.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERR/) ZERRHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SEK/) SEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 916
ID ADH71843 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29al SEQ ID NO:739.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 917
ID ADH71769 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29a SEQ ID NO:665.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 918
ID ADH71839 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29aj SEQ ID NO:735.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 919
ID ADH71847 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29an SEQ ID NO:743.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35% Conservative: 46
Best Local Similarity: 26.90% Mismatches: 132
Query Match: 12.85% Indels: 72
RESULT 920
ID ADH71853 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29aq SEQ ID NO:749.
PN WO2003102155-A2.
PD 11-DEC-2003.

PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 921
ID ADH71841 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29ak SEQ ID NO:737.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 922
ID ADH71845 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29am SEQ ID NO:741.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 923
ID ADH71849 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29ao SEQ ID NO:745.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 924
ID ADH71835 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29ah SEQ ID NO:731.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 925
ID ADH71851 standard; DNA; 7876 BP.
DE Human gene of the invention NOV29ap SEQ ID NO:747.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 926
ID ADH71837 standard; DNA; 7877 BP.
DE Human gene of the invention NOV29ai SEQ ID NO:733.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 927
ID ABS51094 standard; cDNA; 8270 BP.
DE cDNA encoding human NOV12f protein.
FN WO200250277-A2.
PD 27-JUN-2002.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 928
ID ADJ361064 standard; DNA; 8270 BP.
DE Human NOVX NOV12f DNA.
FN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.

PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (PERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 929
ID ADH71821 standard; DNA; 8270 BP.
DE Human gene of the invention NOV29aa SEQ ID NO:717.
FN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 40.35%
Best Local Similarity: 26.90%
Query Match: 12.85%
Conservative: 46
Mismatches: 132
Indels: 72
RESULT 930
ID ABX10231 standard; cDNA; 11796 BP.
DE Human cDNA encoding protein NOV9.
FN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Percent Similarity: 39.55%
Best Local Similarity: 28.30%
Query Match: 12.85%
Conservative: 35
Mismatches: 128
Indels: 60
RESULT 931
ID AAV40528 standard; cDNA; 3442 BP.
DE Homo sapiens DL185_1 clone secreted protein coding region.
FN WO9830695-A2.
PD 16-JUL-1998.
PA (GEMY-) GENETICS INST INC.
Percent Similarity: 42.01%
Best Local Similarity: 26.74%
Query Match: 12.79%
Conservative: 44
Mismatches: 135
Indels: 32
RESULT 932
ID ADQ38613 standard; DNA; 13650 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 276.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.79%
Conservative: 40
Mismatches: 148
Indels: 42
RESULT 933
ID ADQ38612 standard; DNA; 13711 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 275.
FN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91%
Best Local Similarity: 26.05%
Query Match: 12.79%
Conservative: 40
Mismatches: 148
Indels: 42

Query Match: 12.79% Indels: 42
RESULT 934
ID AD038614 standard; DNA; 13793 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 277.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.79% Indels: 42
RESULT 935
ID AD038611 standard; DNA; 14194 BP.
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 274.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.79% Indels: 42
RESULT 936
ID AAT87074 standard; cDNA; 2869 BP.
DE Rat Dmk receptor cDNA.
PN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.13% Conservative: 45
Best Local Similarity: 25.16% Mismatches: 145
Query Match: 12.76% Indels: 51
RESULT 937
ID AAT90472 standard; cDNA; 2869 BP.
DE Rat muscle-specific kinase (MusK) cDNA.
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.13% Conservative: 45
Best Local Similarity: 25.16% Mismatches: 145
Query Match: 12.76% Indels: 51
RESULT 938
ID ABD33038 standard; cDNA; 8455 BP.
DE Mouse cancer-associated cDNA WR22-025.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 38.78% Conservative: 39
Best Local Similarity: 25.51% Mismatches: 103
Query Match: 12.78% Indels: 77
RESULT 939
ID ABD32650 standard; cDNA; 10976 BP.
DE Human cancer-associated cDNA HR13-036.1.
PN WO2004074320-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 36.96% Conservative: 50
Best Local Similarity: 24.30% Mismatches: 134
Query Match: 12.76% Indels: 116
RESULT 940
ID AAT87073 standard; DNA; 2610 BP.
DE Human Dmk receptor gene.
PN US5656473-A.
PD 12-AUG-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.88% Conservative: 44
Best Local Similarity: 26.17% Mismatches: 138
Query Match: 12.74% Indels: 55
RESULT 941
ID AAT90473 standard; cDNA; 2610 BP.
DE Human muscle-specific kinase (MusK) cDNA.
PN WO9721811-A2.
PD 19-JUN-1997.
PA (REGE-) REGENERON PHARM INC.
Percent Similarity: 39.88% Conservative: 44
Best Local Similarity: 26.17% Mismatches: 138
Query Match: 12.74%

RESULT 942
ID AD089843 standard; DNA; 2610 BP.
DE Antagonist of cell cycle progression nucleotide sequence #137.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Percent Similarity: 39.88% Conservative: 44
Best Local Similarity: 26.17% Mismatches: 138
Query Match: 12.74% Indels: 55
RESULT 943
ID ADL13698 standard; DNA; 13182 BP.
DE Osteoarthritis-associated polymorphic nucleotide #230.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.74% Indels: 42
RESULT 944
ID ADL13697 standard; DNA; 13793 BP.
DE Osteoarthritis-associated polymorphic nucleotide #229.
PN WO2003054166-A2.
PD 03-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.74% Indels: 42
RESULT 945
ID ADL35757 standard; DNA; 13793 BP.
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) DNA.
PN WO2004019893-A2.
PD 11-MAR-2004.
PA (RIGE-) RIGEL PHARM INC.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.74% Indels: 42
RESULT 946
ID AAS87452 standard; cDNA; 14586 BP.
DE DNA encoding novel human diagnostic protein #23256.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 38.91% Conservative: 40
Best Local Similarity: 26.05% Mismatches: 148
Query Match: 12.74% Indels: 42
RESULT 947
ID ADM03329 standard; cDNA; 2004 BP.
DE Human cDNA of the invention SEQ ID NO:2014.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Percent Similarity: 37.60% Conservative: 36
Best Local Similarity: 27.58% Mismatches: 146
Query Match: 12.71% Indels: 78
RESULT 948
ID ACN42337 standard; cDNA; 6144 BP.
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1212.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Percent Similarity: 39.74% Conservative: 44
Best Local Similarity: 25.64% Mismatches: 139
Query Match: 12.71% Indels: 49
RESULT 949
ID ADL16583 standard; cDNA; 6487 BP.
DE Human 282PIG3 polynucleotide #16.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74% Conservative: 44
Best Local Similarity: 25.64% Mismatches: 139
Query Match: 12.71% Indels: 49
RESULT 950

ID ADL16581 standard; cDNA; 6487 BP.	DE Human 282PIG3 polynucleotide #10.
DE Human 282PIG3 polynucleotide #14.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 951	
ID ADL16430 standard; cDNA; 6487 BP.	ID ADL16617 standard; cDNA; 7570 BP.
DE Human 282PIG3 polynucleotide #4.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 952	
ID ADL16587 standard; cDNA; 7329 BP.	ID ADL16619 standard; cDNA; 7570 BP.
DE Human 282PIG3 polynucleotide #17.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 953	
ID ADL16432 standard; cDNA; 7329 BP.	ID ADL16434 standard; cDNA; 7602 BP.
DE Human 282PIG3 polynucleotide #5.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 954	
ID ADL16589 standard; cDNA; 7329 BP.	ID ADL16593 standard; cDNA; 7602 BP.
DE Human 282PIG3 polynucleotide #19.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 955	
ID ADL16601 standard; cDNA; 7527 BP.	ID ADL16595 standard; cDNA; 7602 BP.
DE Human 282PIG3 polynucleotide #25.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 956	
ID ADL16436 standard; cDNA; 7527 BP.	ID ADL16576 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #7.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 957	
ID ADL16599 standard; cDNA; 7527 BP.	ID ADL16582 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #23.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49
RESULT 958	
ID ADL16442 standard; cDNA; 7570 BP.	ID ADL16612 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #30.	PN WO2004016734-A2.
PD 26-FEB-2004.	PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%	Conservative: 44
Best Local Similarity: 25.64%	Mismatches: 139
Query Match: 12.71%	Indels: 49

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PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 967
ID ADL16426 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #2.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 968
ID ADL16594 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #21.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 969
ID ADL16588 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #18.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 970
ID ADL16618 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #33.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 971
ID ADL16600 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #24.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 972
ID ADL16606 standard; cDNA; 7650 BP.
DE Human 282PIG3 polynucleotide #27.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 973
ID ADL16631 standard; cDNA; 7651 BP.
DE Human 282PIG3 polynucleotide #35.
PN WO2004016734-A2.
PD 26-FEB-2004.
PA (AGEN-) AGENSYS INC.
Percent Similarity: 39.74%
Best Local Similarity: 25.64%
Query Match: 12.71%
Conservative: 44
Mismatches: 139
Indels: 49
RESULT 974
ID ADQ97818 standard; DNA; 109661 BP.
DE Human cancer associated sequence HD11-002, SEQ ID 795.
PN WO2004060304-A2.

PD 22-JUL-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Percent Similarity: 39.94%
Best Local Similarity: 26.15%
Query Match: 12.71%
Conservative: 48
Mismatches: 130
Indels: 79
RESULT 975
ID ADG39785 standard; cDNA; 11796 BP.
DE Human cDNA encoding NOV9.
PN US2003203843-A1.
PD 30-OCT-2003.
PA (PENA/) PENA C E A.
PA (GUOX/) GUO X.
PA (SHIM/) SHIMKETS R A.
PA (PADI/) PADIGARU M.
PA (KEKU/) KEKUDA R.
PA (SEYT/) SPYTEK K A.
PA (MEHR/) MEHRABAN F.
PA (TOPP/) TOPPER J N.
PA (MALY/) MALYANKAR U M.
PA (WASS/) WASSERMAN S M.
PA (EDIN/) EDINGER S R.
PA (SWIT/) SMITHSON G.
PA (GUNT/) GUNTHER E.
PA (KOMU/) KOMUVES L.
Percent Similarity: 39.55%
Best Local Similarity: 27.97%
Query Match: 12.68%
Conservative: 36
Mismatches: 128
Indels: 60
RESULT 976
ID AAS92794 standard; cDNA; 4452 BP.
DE DNA encoding novel human diagnostic protein #28598.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 33.24%
Best Local Similarity: 24.10%
Query Match: 12.62%
Conservative: 33
Mismatches: 137
Indels: 104
RESULT 977
ID AAS80523 standard; cDNA; 4452 BP.
DE DNA encoding novel human diagnostic protein #16327.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 33.24%
Best Local Similarity: 24.10%
Query Match: 12.62%
Conservative: 33
Mismatches: 137
Indels: 104
RESULT 978
ID ABN59991 standard; cDNA; 4009 BP.
DE Novel human coding sequence SEQ ID NO: 402.
PN WO200222660-A2.
PD 21-MAR-2002.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 39.43%
Best Local Similarity: 25.71%
Query Match: 12.57%
Conservative: 48
Mismatches: 146
Indels: 66
RESULT 979
ID ABT17394 standard; DNA; 4045 BP.
DE Human IG gene related nucleic acid SEQ ID No 20.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 39.43%
Best Local Similarity: 25.71%
Query Match: 12.57%
Conservative: 48
Mismatches: 146
Indels: 66
RESULT 980
ID ACN37528 standard; cDNA; 4045 BP.
DE Tumour-associated antigenic target (TAT) cDNA DNA323962, SEQ ID NO:476.
PN WO2004030615-A2.
PD 15-APR-2004.
PA (GETH ) GENENTECH INC.
Percent Similarity: 39.43%
Best Local Similarity: 25.71%
Query Match: 12.57%
Conservative: 48
Mismatches: 146
Indels: 66
RESULT 981
```

Best Local Similarity:	25.32%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 989			
ID ADP28189 standard; DNA; 4752 BP.			
DE Human secreted protein encoding sequence SEQ ID #187.			
PN WO2004035732-A2.			
PD 29-APR-2004.			
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 990			
ID ADP28123 standard; DNA; 4752 BP.			
DE Human secreted protein encoding sequence SEQ ID #21.			
PN WO2004035732-A2.			
PD 29-APR-2004.			
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 991			
ID AAS84195 standard; cDNA; 5298 BP.			
DE DNA encoding novel human diagnostic protein #19999.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 992			
ID AAS86818 standard; cDNA; 5298 BP.			
DE DNA encoding novel human diagnostic protein #22622.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 993			
ID AAS76204 standard; cDNA; 6040 BP.			
DE DNA encoding novel human diagnostic protein #12008.			
PN WO200175067-A2.			
PD 11-OCT-2001.			
PA (HYSE-) HYSEQ INC.			
Percent Similarity:	35.35%	Conservative:	52
Best Local Similarity:	22.22%	Mismatches:	145
Query Match:	12.43%	Indels:	111
RESULT 994			
ID ADL16575 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #11.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 995			
ID ADL16577 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #13.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 996			
ID ADL16428 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #3.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49
RESULT 997			
ID ADL16428 standard; cDNA; 7491 BP.			
DE Human 282PIG3 polynucleotide #3.			
PN WO2004016734-A2.			
PD 26-FEB-2004.			
PA (AGEN-) AGENSYS INC.			
Percent Similarity:	39.42%	Conservative:	44
Best Local Similarity:	25.33%	Mismatches:	140
Query Match:	12.43%	Indels:	49

Query Match: 12.43% Indels: 49
 RESULT 997
 ID ADL15033 standard; DNA; 7642 BP.
 DE Human neural cell adhesion molecule DNA for cancer treatment.
 PN WO2003068268-A2.
 PD 21-AUG-2003.
 PA (BIOI-) BIOINVENT INT AB.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 998
 ID ADJ75061 standard; DNA; 7642 BP.
 DE Marker gene SEQ ID NO:313.
 PN EP1394274-A2.
 PD 03-MAR-2004.
 PA (GENO-) GENOX RES INC.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 999
 ID ADN04061 standard; cDNA; 7642 BP.
 DE Antipsoriatic cDNA sequence #230.
 PN WO2004028479-A2.
 PD 08-APR-2004.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 1000
 ID ADQ19765 standard; DNA; 7642 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 2584.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 1001
 ID ADQ23905 standard; DNA; 7642 BP.
 DE Human soft tissue sarcoma-upregulated DNA - SEQ ID 6725.
 PN WO2004048938-A2.
 PD 10-JUN-2004.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 1002
 ID ADRI14750 standard; DNA; 7642 BP.
 DE Nucleotide sequence of human MAPCAX orthologue #8.
 PN WO2004066948-A2.
 PD 12-AUG-2004.
 PA (EXEL-) EXELIXIS INC.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 1003
 ID ADI61707 standard; cDNA; 7647 BP.
 DE Human cDNA downregulated in Alzheimer's disease, INCYTE 334247.2.
 PN US668288-B1.
 PD 27-JAN-2004.
 PA (INCY-) INCYTE CORP.
 Percent Similarity: 39.42%
 Best Local Similarity: 25.32%
 Mismatches: 140
 Indels: 49
 Query Match:
 RESULT 1004
 ID AAS66304 standard; cDNA; 1464 BP.
 DE DNA encoding novel human diagnostic protein #2108.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.25%
 Best Local Similarity: 25.50%
 Mismatches: 137
 Indels: 82
 Query Match:

RESULT 1005
 ID AAS90766 standard; cDNA; 1464 BP.
 DE DNA encoding novel human diagnostic protein #26570.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.25%
 Best Local Similarity: 25.50%
 Mismatches: 137
 Indels: 82
 Query Match:
 RESULT 1006
 ID AAS72490 standard; cDNA; 1802 BP.
 DE DNA encoding novel human diagnostic protein #8294.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.25%
 Best Local Similarity: 25.50%
 Mismatches: 137
 Indels: 82
 Query Match:
 RESULT 1007
 ID AAS66206 standard; cDNA; 2214 BP.
 DE DNA encoding novel human diagnostic protein #2010.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Percent Similarity: 37.25%
 Best Local Similarity: 25.50%
 Mismatches: 137
 Indels: 82
 Query Match:
 RESULT 1008
 ID AAK94785 standard; cDNA; 2500 BP.
 DE Human full-length cDNA, SEQ ID NO: 3892.
 PN EP1130094-A2.
 PD 05-SEP-2001.
 PA (HELI-) HELIX RES INST.
 Percent Similarity: 37.90%
 Best Local Similarity: 23.89%
 Mismatches: 127
 Indels: 68
 Query Match:
 RESULT 1009
 ID ADL31859 standard; cDNA; 2500 BP.
 DE Full length human cDNA clone SeqID 3892.
 PN EP1396543-A2.
 PD 10-MAR-2004.
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.
 Percent Similarity: 37.90%
 Best Local Similarity: 23.89%
 Mismatches: 127
 Indels: 68
 Query Match:
 RESULT 1010
 ID AAX37725 standard; cDNA; 3598 BP.
 DE Human PRO335 DNA fragment #2.
 PN WO9914241-A2.
 PD 25-MAR-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Mismatches: 148
 Indels: 146
 Query Match:
 RESULT 1011
 ID AAX52264 standard; DNA; 3662 BP.
 DE Protein PRO335 cDNA clone DNA41388-1234.
 PN WO9914328-A2.
 PD 25-MAR-1999.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Mismatches: 148
 Indels: 146
 Query Match:
 RESULT 1012
 ID AAZ52206 standard; cDNA; 3662 BP.
 DE Human PRO335 protein encoding cDNA, UNQ287V.
 PN WO200015797-A2.
 PD 23-MAR-2000.
 PA (GETH) GENENTECH INC.
 Percent Similarity: 33.03%
 Best Local Similarity: 20.73%
 Mismatches: 148
 Indels: 146
 Query Match:
 RESULT 1013

ID ADC78601 standard; cDNA; 3662 BP.
DE Human PRO335 cDNA.
FN WO200015796-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 37.90% Conservative: 44
Best Local Similarity: 23.89% Mismatches: 127
Query Match: 12.40% Indels: 68
RESULT 1014
ID AAF72422 standard; cDNA; 3662 BP.
DE Human PRO335 cDNA.
FN WO200104311-A1.
PD 18-JAN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1015
ID AA500161 standard; cDNA; 3662 BP.
DE Human cDNA clone DNA41388-1234 encoding PRO335 (UNQ287).
FN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1016
ID ACA60239 standard; cDNA; 3662 BP.
DE Human cDNA for secreted/transmembrane protein PRO335.
FN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1017
ID AC007639 standard; cDNA; 3662 BP.
DE Novel human secreted and transmembrane protein PRO335 cDNA.
FN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1018
ID ABX71687 standard; cDNA; 3662 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO335.
FN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1019
ID ACH07019 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane polypeptide PRO335 cDNA.
FN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1020
ID ABX96256 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #52.
FN US2002160374-A1.
PD 31-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1021
ID ACA05577 standard; cDNA; 3662 BP.

DE cDNA encoding human secreted protein PRO335.
FN US2003023054-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1022
ID ACD20244 standard; cDNA; 3662 BP.
DE Human secreted / transmembrane polypeptide PRO335 cDNA.
FN US2003036060-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1023
ID ACA55047 standard; cDNA; 3662 BP.
DE Novel human secreted and transmembrane protein PRO335 cDNA.
FN US2003017463-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1024
ID ACD19882 standard; cDNA; 3662 BP.
DE Human secreted / transmembrane polypeptide PRO335 cDNA.
FN US2003027143-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1025
ID ADB29494 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
FN US2003092002-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1026
ID ADA18350 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
FN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1027
ID ACD67029 standard; cDNA; 3662 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO335.
FN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1028
ID ACD83190 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
FN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1029
ID ADA16325 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.

PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1030
ID ADA42470 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1031
ID ACD23368 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1032
ID ADA16749 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1033
ID ADA13178 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1034
ID ADA42046 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003082540-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1035
ID ADA17393 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1036
ID ADA42896 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1037
ID ACD23730 standard; cDNA; 3662 BP.
DE Human PRO polynucleotide #50.
PN US2003064923-A1.

PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1038
ID ADB77815 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1039
ID ADB74951 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1040
ID ADC28597 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1041
ID ADC39797 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1042
ID ADC40311 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1043
ID ADC19135 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1044
ID ADC34435 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1045
ID ADC29490 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003049676-A1.
PD 13-MAR-2003.

Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1054			
ID	ADD03670 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003108983-A1.		
PD	12-JUN-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1055			
ID	ADE334922 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003077593-A1.		
PD	24-APR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1056			
ID	ADH59405 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003039972-A1.		
PD	27-FEB-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1057			
ID	ADI38184 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003054352-A1.		
PD	20-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1058			
ID	ACA59135 standard; cDNA; 3662 BP.		
DE	Human PRO polynucleotide #50.		
FN	U52002146709-A1.		
PD	10-OCT-2002.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1059			
ID	ACA58532 standard; cDNA; 3662 BP.		
DE	cDNA encoding human PRO polypeptide #50.		
FN	U52002192659-A1.		
PD	13-DEC-2002.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1060			
ID	ADJ26452 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003054349-A1.		
PD	20-MAR-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1061			
ID	ADE79367 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003135025-A1.		
PD	17-JUL-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146
RESULT 1062			
ID	ADJ26452 standard; cDNA; 3662 BP.		
DE	Human secreted/transmembrane protein CDNA, #54.		
FN	U52003135025-A1.		
PD	17-JUL-2003.		
PA	(GETH) GENENTECH INC.		
Percent Similarity:	33.03%	Conservative:	54
Best Local Similarity:	20.73%	Mismatches:	148
Query Match:	12.40%	Indels:	146

Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2003180312-A1.
RESULT 1062		PD 25-SEP-2003.
ID ADE79791 standard; cDNA; 3662 BP.		PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #54.		Percent Similarity: 33.03%
PN US2003130489-A1.		Best Local Similarity: 20.73%
PD 10-JUL-2003.		Query Match: 12.40%
PA (GETH) GENENTECH INC.		RESULT 1070
Percent Similarity: 33.03%	Conservative: 54	ID ADF73542 standard; cDNA; 3662 BP.
Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2003166051-A1.
RESULT 1063		PD 04-SEP-2003.
ID ADE73467 standard; cDNA; 3662 BP.		PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #54.		Percent Similarity: 33.03%
PN US2003129592-A1.		Best Local Similarity: 20.73%
PD 10-JUL-2003.		Query Match: 12.40%
PA (GETH) GENENTECH INC.		RESULT 1071
Percent Similarity: 33.03%	Conservative: 54	ID ADG92385 standard; cDNA; 3662 BP.
Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2003027145-A1.
RESULT 1064		PD 06-FEB-2003.
ID ADE74002 standard; cDNA; 3662 BP.		PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #54.		Percent Similarity: 33.03%
PN US2003148370-A1.		Best Local Similarity: 20.73%
PD 07-AUG-2003.		Query Match: 12.40%
PA (GETH) GENENTECH INC.		RESULT 1072
Percent Similarity: 33.03%	Conservative: 54	ID ADG92812 standard; cDNA; 3662 BP.
Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2003027146-A1.
RESULT 1065		PD 06-FEB-2003.
ID ADE99556 standard; cDNA; 3662 BP.		PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #54.		Percent Similarity: 33.03%
PN US2003211576-A1.		Best Local Similarity: 20.73%
PD 13-NOV-2003.		Query Match: 12.40%
PA (GETH) GENENTECH INC.		RESULT 1073
Percent Similarity: 33.03%	Conservative: 54	ID ADH20601 standard; cDNA; 3662 BP.
Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2004005553-A1.
RESULT 1066		PD 08-JAN-2004.
ID ADE98675 standard; cDNA; 3662 BP.		PA (GETH) GENENTECH INC.
DE Human secreted/transmembrane protein cDNA, #54.		Percent Similarity: 33.03%
PN US2003211569-A1.		Best Local Similarity: 20.73%
PD 13-NOV-2003.		Query Match: 12.40%
PA (GETH) GENENTECH INC.		RESULT 1074
Percent Similarity: 33.03%	Conservative: 54	ID ADH07456 standard; cDNA; 3662 BP.
Best Local Similarity: 20.73%	Mismatches: 148	DE Human secreted/transmembrane protein cDNA, #54.
Query Match: 12.40%	Indels: 146	PN US2004006211-A1.
RESULT 1067		PD 08-JAN-2004.
ID ADE99102 standard; cDNA; 3662 BP.		PA (DESN/) DESNOYERS L.
DE Human secreted/transmembrane protein cDNA, #54.		PA (GODD/) GODDARD A.
PN US2003211568-A1.		PA (GODO/) GODOWSKI P J.
PD 13-NOV-2003.		PA (GURN/) GURNEY A L.
PA (GETH) GENENTECH INC.		PA (MATH/) MATHER J P.
Percent Similarity: 33.03%	Conservative: 54	PA (WILL/) WILLIAMS P M.
Best Local Similarity: 20.73%	Mismatches: 148	PA (WOOD/) WOOD W I.
Query Match: 12.40%	Indels: 146	RESULT 1068
ID ADG40572 standard; cDNA; 3662 BP.		ID ADH07029 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.		DE Human secreted/transmembrane protein cDNA, #54.
PN US2003225253-A1.		PN US2003215904-A1.
PD 04-DEC-2003.		PD 20-NOV-2003.
PA (DESN/) DESNOYERS L.		PA (GETH) GENENTECH INC.
PA (GODD/) GODDARD A.		Percent Similarity: 33.03%
PA (GODO/) GODOWSKI P J.		Best Local Similarity: 20.73%
PA (GURN/) GURNEY A L.		Query Match: 12.40%
PA (MATH/) MATHER J P.		RESULT 1076
PA (WILL/) WILLIAMS P M.		ID ADH07029 standard; cDNA; 3662 BP.
PA (WOOD/) WOOD W I.		DE Human secreted/transmembrane protein cDNA, #54.
Percent Similarity: 33.03%	Conservative: 54	PN US2004005665-A1.
Best Local Similarity: 20.73%	Mismatches: 148	PD 08-JAN-2004.
Query Match: 12.40%	Indels: 146	PA (DESN/) DESNOYERS L.
RESULT 1069		
ID ADF73966 standard; cDNA; 3662 BP.		

PA (GODD//) GODDARD A.	PD 02-OCT-2003.		
PA (GODO//) GODOWSKI P J.	PA (GETH) GENENTECH INC.		
PA (GURN//) GURNEY A L.	Percent Similarity: 33.03%	Conservative: 54	
PA (MATH//) MATHER J P.	Best Local Similarity: 20.73%	Mismatches: 148	
PA (WILL//) WILLIAMS P M.	Query Match: 12.40%	Indels: 146	
PA (WOOD//) WOOD W I.	RESULT 1084		
Percent Similarity: 33.03%	ID ADM25252 standard; cDNA; 3662 BP.		
Best Local Similarity: 20.73%	DE Human secreted/transmembrane protein cDNA, #54.		
Query Match: 12.40%	PN US2003096233-A1.		
RESULT 1077	PD 22-MAY-2003.		
ID AD118771 standard; cDNA; 3662 BP.	PA (GETH) GENENTECH INC.		
DE Human secreted/transmembrane protein cDNA, #54.	Percent Similarity: 33.03%	Conservative: 54	
PN US2003152399-A1.	Best Local Similarity: 20.73%	Mismatches: 148	
PD 14-AUG-2003.	Query Match: 12.40%	Indels: 146	
PA (GETH) GENENTECH INC.	RESULT 1085		
Percent Similarity: 33.03%	ID ADM30002 standard; cDNA; 3662 BP.		
Best Local Similarity: 20.73%	DE Human secreted/transmembrane protein cDNA, #54.		
Query Match: 12.40%	PN US2003190611-A1.		
RESULT 1078	PD 09-OCT-2003.		
ID AD137750 standard; cDNA; 3662 BP.	PA (GETH) GENENTECH INC.		
DE Human secreted/transmembrane protein cDNA, #54.	Percent Similarity: 33.03%	Conservative: 54	
PN US2003096340-A1.	Best Local Similarity: 20.73%	Mismatches: 148	
PD 22-MAY-2003.	Query Match: 12.40%	Indels: 146	
PA (GETH) GENENTECH INC.	RESULT 1086		
Percent Similarity: 33.03%	ID ADO06324 standard; cDNA; 3662 BP.		
Best Local Similarity: 20.73%	DE Human PRO polynucleotide #52.		
Query Match: 12.40%	PN US6686451-B1.		
RESULT 1079	PD 03-FEB-2004.		
ID ADH97550 standard; cDNA; 3662 BP.	PA (GETH) GENENTECH INC.		
DE Human secreted/transmembrane protein cDNA, #54.	Percent Similarity: 33.03%	Conservative: 54	
PN US2003190610-A1.	Best Local Similarity: 20.73%	Mismatches: 148	
PD 09-OCT-2003.	Query Match: 12.40%	Indels: 146	
PA (GETH) GENENTECH INC.	RESULT 1087		
Percent Similarity: 33.03%	ID ADRI1176 standard; cDNA; 3662 BP.		
Best Local Similarity: 20.73%	DE Human secreted/transmembrane protein cDNA, #54.		
Query Match: 12.40%	PN US2004137561-A1.		
RESULT 1080	PD 15-JUL-2004.		
ID ADI65918 standard; cDNA; 3662 BP.	PA (GETH) GENENTECH INC.		
DE Human secreted/transmembrane protein cDNA, #54.	Percent Similarity: 33.03%	Conservative: 54	
PN US2003148371-A1.	Best Local Similarity: 20.73%	Mismatches: 148	
PD 07-AUG-2003.	Query Match: 12.40%	Indels: 146	
PA (GETH) GENENTECH INC.	RESULT 1088		
Percent Similarity: 33.03%	ID ADRI8085 standard; cDNA; 3662 BP.		
Best Local Similarity: 20.73%	DE Human secreted/transmembrane protein cDNA, #54.		
Query Match: 12.40%	PN US2004147017-A1.		
RESULT 1081	PD 29-JUL-2004.		
ID ADH60661 standard; cDNA; 3662 BP.	PA (ASHK//) ASHKENAZI A.		
DE Human secreted/transmembrane protein cDNA, #54.	PA (BOTS//) BOTSTEIN D.		
PN US2004023331-A1.	PA (DESN//) DESNOYERS L.		
PD 05-FEB-2004.	PA (EATO//) EATON D L.		
PA (GODD//) GODDARD A.	PA (FERR//) FERRARA N.		
PA (GODO//) GODOWSKI P J.	PA (FILV//) FILVAROFF E.		
PA (GURN//) GURNEY A L.	PA (FONG//) FONG S.		
PA (MATH//) MATHER J P.	PA (GAOW//) GAO W.		
PA (WILL//) WILLIAMS P M.	PA (GERB//) GERBER H.		
PA (WOOD//) WOOD W I.	PA (GERR//) GERRITSEN M E.		
Percent Similarity: 33.03%	PA (GODD//) GODDARD A.		
Best Local Similarity: 20.73%	PA (GODO//) GODOWSKI P J.		
Query Match: 12.40%	PA (GRIM//) GRIMALDI C J.		
RESULT 1082	PA (GURN//) GURNEY A L.		
ID ADJ99718 standard; cDNA; 3662 BP.	PA (HILL//) HILLAN K J.		
DE Human secreted/transmembrane protein cDNA, #54.	PA (KLJA//) KLJAVIN I J.		
PN US2003187238-A1.	PA (MATH//) MATHER J P.		
PD 02-OCT-2003.	PA (PANJ//) PAN J.		
PA (GETH) GENENTECH INC.	PA (PAON//) PAONI N F.		
Percent Similarity: 33.03%	PA (ROYM//) ROY M A.		
Best Local Similarity: 20.73%	PA (STEW//) STEWART T A.		
Query Match: 12.40%	PA (TUMA//) TUMAS D.		
RESULT 1083	PA (WILL//) WILLIAMS P M.		
ID ADL08911 standard; cDNA; 3662 BP.	PA (WOOD//) WOOD W I.		
DE Human secreted/transmembrane protein cDNA, #54.	Percent Similarity: 33.03%	Conservative: 54	
PN US2003186358-A1.	Best Local Similarity: 20.73%	Mismatches: 148	
	Query Match: 12.40%	Indels: 146	

RESULT 1089
ID ADT03761 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane protein cDNA, #54.
PN US2003152322-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1090
ID ADS74724 standard; cDNA; 3662 BP.
DE Human secreted/transmembrane cDNA #54.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PRON/) PRONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUNA/) TUNAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1091
ID AAX37743 standard; cDNA; 3807 BP.
DE Human PRO326 DNA fragment #2.
PN WO9914241-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1092
ID AAX52266 standard; DNA; 4053 BP.
DE Protein PRO326 cDNA clone DNA37140-1234.
PN WO9914328-A2.
PD 25-MAR-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1093
ID AA252208 standard; cDNA; 4053 BP.
DE Human PRO326 protein encoding cDNA, UNQ287.
PN WO200015797-A2.
PD 23-MAR-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1094
ID AAF72424 standard; cDNA; 4053 BP.
DE Human PRO326 cDNA.
PN WO200104311-A1.
PD 18-JAN-2001.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1095
ID AAC84422 standard; cDNA; 4053 BP.
DE Human PRO326 polypeptide encoding cDNA.
PN WO200075316-A1.
PD 14-DEC-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1096
ID AAS00163 standard; cDNA; 4053 BP.
DE Human cDNA clone DNA37140-1234 encoding PRO326 (UNQ287).
PN WO200119991-A1.
PD 22-MAR-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1097
ID AAS21419 standard; cDNA; 4053 BP.
DE Human cDNA sequence encoding for PRO326 polypeptide.
PN WO200140466-A2.
PD 07-JUN-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1098
ID ACA60241 standard; cDNA; 4053 BP.
DE Human cDNA for secreted/transmembrane protein PRO326.
PN US2003003530-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1099
ID ACD07641 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2002197671-A1.
PD 26-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1100
ID ACA03778 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003036180-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1101
ID ABX71689 standard; cDNA; 4053 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO326.
PN US2002132240-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1102
ID ACH07021 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane polypeptide PRO326 cDNA.
PN US2003044839-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.

Query Match: 12.40% Indels: 146
RESULT 1119
ID ADB15943 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087350-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1120
ID ADA47729 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003073215-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1121
ID ADAL8354 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003039971-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1122
ID ACD67031 standard; cDNA; 4053 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO326.
PN US2003045693-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1123
ID ADA67524 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068795-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1124
ID ADB30531 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003068794-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1125
ID ADA85827 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082693-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1126
ID ADA97039 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082705-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146

RESULT 1127
ID ADA79343 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082763-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1128
ID ADA87482 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087345-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1129
ID ADB16684 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087349-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1130
ID ACD83192 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2003044793-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1131
ID ADA16329 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049621-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1132
ID ADA91776 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082694-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1133
ID ADB14839 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087351-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1134
ID ADB18800 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1135
ID ADB18800 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003073211-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146

ID ADA94015 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US200307722-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1136

ID ADB19911 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1137

ID ADB13223 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1138

ID ACD98599 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1139

ID ADA74477 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1140

ID ADA42474 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054401-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1141

ID ADB24710 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US200307713-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1142

ID ADA82234 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1143

ID ADA75197 standard; cDNA; 4053 BP.
DE

DE Human PRO polynucleotide #176.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1144

ID ADA85275 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1145

ID ADA84723 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1146

ID ACD23370 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2003064367-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1147

ID ADB29979 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1148

ID ADA80507 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1149

ID ADA75749 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1150

ID ADA46974 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1151

ID ADB25270 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
DE

PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1152
ID ADA93446 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1153
ID ADB26796 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1154
ID ADB31083 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1155
ID ADAG1011 standard; cDNA; 4053 BP.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1156
ID ADB24158 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1157
ID ADA96487 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1158
ID ADA81059 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1159
ID ADA95935 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082759-A1.

PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1160
ID ADB26244 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1161
ID ADB21729 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1162
ID ADA77508 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1163
ID ADB18248 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1164
ID ADA86931 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1165
ID ADA16753 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003039969-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1166
ID ADA13182 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049622-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1167
ID ADA42050 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082540-A1.
PD 01-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1168
ID ADA88034 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1169
ID ADA46422 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1170
ID ADA17397 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
FN US2003017498-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1171
ID ADA42900 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
FN US2003054351-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1172
ID ADB28452 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1173
ID ADB29004 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1174
ID ADA76956 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1175
ID ADA88586 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003073213-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1176
ID ADA97591 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003082686-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1177
ID ADB27348 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
FN US2003022239-A1.
PD 30-JAN-2003.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1178
ID ADB22281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003087344-A1.
PD 08-MAY-2003.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1179
ID ACD23732 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
FN US2003064923-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1180
ID ADA66972 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003068793-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1181
ID ADB22833 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
FN US2003077711-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1182
ID ADB23606 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
FN US2003077712-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1183
ID ADA92328 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
FN US2003082712-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146

RESULT 1184
ID ADB15391 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087352-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1185
ID ADB38643 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082766-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1186
ID ADB38091 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087347-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1187
ID ADB66563 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082689-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1188
ID ADB9643 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082698-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1189
ID ADB90375 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082762-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1190
ID ADB77819 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003077654-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1191
ID ADB39476 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082764-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1192
ID ADB36124 standard; cDNA; 4053 BP.

ID ADB74955 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082542-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1193
ID ADB47099 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1194
ID ADB86706 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1195
ID ADB77311 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1196
ID ADB34468 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1197
ID ADB35572 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1198
ID ADB3916 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1199
ID ADB35020 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide SEQ ID NO 351.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1200
ID ADB36124 standard; cDNA; 4053 BP.

DE Human PRO polynucleotide SEQ ID NO 351.
PN US200307720-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1201
ID ADC46519 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1202
ID ADC28601 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059772-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1203
ID ADC39801 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1204
ID ADC40315 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1205
ID ADC19139 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1206
ID ADC34439 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1207
ID ADC29494 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1208
ID ADC29025 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003087365-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1209
ID ADC40910 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1210
ID ADC19567 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1211
ID ADC34015 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073077-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1212
ID ADC13085 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003073079-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1213
ID ADC50392 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092106-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1214
ID ADC71939 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092107-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1215
ID ADC59918 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092105-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1216
ID ADC52925 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087365-A1.

PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1217
ID ADC57279 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087366-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1218
ID ADC60470 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087367-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1219
ID ADC50945 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087361-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1220
ID ADC65472 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003087362-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1221
ID ADC54570 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087363-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1222
ID ADC53531 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087364-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1223
ID ADC59054 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087359-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1224
ID ADC55932 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087360-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1225
ID ADC58502 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein cDNA Seq ID351.
PN US2003087346-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1226
ID ADC12537 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003082541-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1227
ID ADD03176 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092104-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1228
ID ADC90168 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087348-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1229
ID ADC69587 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003194770-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1230
ID ADC48476 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194773-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1231
ID ADD10005 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1232
ID ADD04580 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1233
ID ADC80536 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1234
ID ADD11043 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1235
ID ADC47924 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1236
ID ADD05092 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003104469-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1237
ID ADC79984 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1238
ID ADD09453 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1239
ID ADD04098 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003104381-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1240
ID ADD03674 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003108983-A1.
PD 12-JUN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54

Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1241
ID ADD41166 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1242
ID ADD5305 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1243
ID ADD53045 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1244
ID ADD53597 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1245
ID ADD51753 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003194779-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1246
ID ADD02552 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203431-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1247
ID ADD01986 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203430-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1248
ID ADD54168 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003203432-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148

Query Match: 12.40% Indels: 146
RESULT 1249
ID ADD92485 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199030-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1250
ID ADE91381 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199055-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1251
ID ADE03995 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199057-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1252
ID ADE32292 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194765-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1253
ID ADE22224 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003199056-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1254
ID ADD79448 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003203428-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1255
ID ADE41984 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1256
ID ADE17801 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:

RESULT 1257
ID ADD91933 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1258
ID ADE33396 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1259
ID ADE33948 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1260
ID ADE80000 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1261
ID ADD93037 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1262
ID ADE19457 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1263
ID ADE34926 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003077583-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1264
ID ADE18905 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1265
ID ADE17801 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:

ID AD543101 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1266

ID AD95890 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1267

ID AD22776 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1268

ID AD78894 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1269

ID AD32844 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1270

ID AD842536 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1271

ID AD80552 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1272

ID AD9580 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199028-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1273

ID ADE40864 standard; cDNA; 4053 BP.

DE Human PRO polynucleotide #176.
PN US2003199031-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1274

ID AD804663 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199034-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1275

ID AD92792 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194777-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1276

ID ADG21501 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207355-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1277

ID ADG23142 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207384-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1278

ID ADF97477 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207370-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1279

ID ADG80541 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207373-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1280

ID ADG79989 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207372-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1281

ID ADH59409 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.

PN US2003039972-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1282
ID ADH55281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207381-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1283
ID ADH55833 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207379-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1284
ID ADH3188 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054352-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1285
ID ADH4052 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207385-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1286
ID ADH65001 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207386-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1287
ID ADH6500 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207387-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1288
ID ADH81914 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1289
ID ADH81362 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207377-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1290
ID ACA59137 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #52.
PN US2002146709-A1.
PD 10-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1291
ID ACD24028 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003032156-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1292
ID ACA58534 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #52.
PN US2002192659-A1.
PD 19-DEC-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1293
ID ACA67169 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003004311-A1.
PD 02-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1294
ID ADJ26456 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003054349-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1295
ID ADM82531 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1296
ID ADN15930 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
RESULT 1297
ID ADN16559 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087385-A1.
PD 08-MAY-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1298
ID ADN15378 standard; cDNA; 4053 BP.
DE Human secreted and transmembrane protein PRO326 cDNA.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1299
ID ADN14826 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1300
ID ADC81088 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1301
ID ADE79371 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003135025-A1.
PD 17-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1302
ID ADD76536 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1303
ID ADD87900 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003092113-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1304
ID ADD86304 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203440-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1305
ID ADE79795 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003130489-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1306
ID ADE75752 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003211571-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1307
ID ADE73471 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003129592-A1.
PD 10-JUL-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1308
ID ADE23328 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003092108-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1309
ID ADE23880 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003092110-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1310
ID ADE24523 standard; cDNA; 4053 BP.
DE CDNA encoding human PRO polypeptide #176.
PN US2003092111-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1311
ID ADD87348 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003203439-A1.
PD 30-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1312
ID ADE89214 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199062-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1313
ID ADE74006 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003148370-A1.
PD 07-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%

Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1314
ID ADEL8353 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194794-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1315
ID ADE88662 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199054-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1316
ID ADE99560 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211576-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1317
ID ADE94682 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199027-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1318
ID ADE91093 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199061-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1319
ID ADE95234 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199052-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1320
ID ADE93344 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199060-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1321
ID ADE34925 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003199029-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1322
ID ADE98679 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1323
ID ADE92240 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1324
ID ADE90541 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1325
ID ADE91688 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1326
ID ADE99106 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1327
ID ADG40576 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1328
ID ADF73970 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1329
ID ADG02267 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.

Query Match: 12.40% Indels: 146
RESULT 1322
ID ADE98679 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211569-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1323
ID ADE92240 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1324
ID ADE90541 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1325
ID ADE91688 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1326
ID ADE99106 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003211568-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1327
ID ADG40576 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003225253-A1.
PD 04-DEC-2003.
PA (DESN) DESNOYERS L.
PA (GODD) GODDARD A.
PA (GODO) GODOWSKI P J.
PA (GURN) GURNEY A L.
PA (MATH) MATHER J P.
PA (WILL) WILLIAMS P M.
PA (WOOD) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1328
ID ADF73970 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003180312-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1329
ID ADG02267 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.

PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1330
ID ADG22053 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1331
ID ADG20123 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1332
ID ADF98029 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1333
ID ADG24246 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1334
ID ADF98600 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1335
ID ADG03431 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207351-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1336
ID ADF99152 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207353-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1337
ID ADG16737 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207359-A1.

PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1338
ID ADG05196 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207375-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1339
ID ADG19463 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207425-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1340
ID ADF73546 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003166051-A1.
PD 04-SEP-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1341
ID ADG13300 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207357-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1342
ID ADG08357 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207424-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1343
ID ADG15527 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003219885-A1.
PD 27-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1344
ID ADF96925 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207371-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Conservative: 54
Mismatches: 148
Indels: 146
Query Match:
RESULT 1345
ID ADG06110 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207374-A1.
PD 06-NOV-2003.

PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1346
ID ADG23694 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207389-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1347
ID ADG03983 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207423-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1348
ID ADG24884 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207427-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1349
ID ADG07181 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207350-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1350
ID ADG07733 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207356-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1351
ID ADG55228 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003194778-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1352
ID ADG60892 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207390-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1353
ID ADG61996 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207428-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1354
ID ADG92389 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003027145-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1355
ID ADG82197 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207358-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1356
ID ADG57436 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207362-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1357
ID ADG56884 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207364-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1358
ID ADG55780 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207365-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1359
ID ADG58540 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207368-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1360
ID ADG70906 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207420-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1361
ID ADG92816 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003027146-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Conservative: 54
Mismatches: 148
Indels: 146

Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1362
ID ADG57988 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207363-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1363
ID ADG53572 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207415-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1364
ID ADG71458 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207421-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1365
ID ADG81645 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003207805-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1366
ID ADH30607 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003077723-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1367
ID ADH11974 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207419-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1368
ID ADG52396 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207414-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1369
ID ADG54124 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207416-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146

RESULT 1370
ID ADG81093 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003194793-A1.
PD 16-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1371
ID ADG56332 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207366-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1372
ID ADH12598 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207378-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1373
ID ADG61444 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207429-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1374
ID ADH28531 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2003022331-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1375
ID ADG54676 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207367-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1376
ID ADG59716 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207369-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1377
ID ADH20605 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146
RESULT 1378
ID ADH20605 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005553-A1.
PD 08-JAN-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73% Mismatches: 54
Query Match: 12.40% Indels: 146

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ID ADH07460 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004006211-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1379
ID ADH60005 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003215904-A1.
PD 20-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1380
ID ADH07033 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004005665-A1.
PD 08-JAN-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1381
ID ADH18140 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003207361-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1382
ID ADH18775 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003152999-A1.
PD 14-AUG-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1383
ID ADH37754 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003096340-A1.
PD 22-MAY-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1384
ID ADG09883 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009548-A1.
PD 15-JAN-2004.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1385
ID ADH97554 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003190610-A1.
PD 09-OCT-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1386
ID ADH15354 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207382-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1387
ID ADG09231 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004009547-A1.
PD 15-JAN-2004.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1388
ID ADH65922 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003148371-A1.
PD 07-AUG-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1389
ID ADH14686 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207383-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1390
ID ADH60665 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004023331-A1.
PD 05-FEB-2004.
PA (DESN//) DESNOYERS L.
PA (GODD//) GODDARD A.
PA (GODO//) GODOWSKI P J.
PA (GURN//) GURNEY A L.
PA (MATH//) MATHER J P.
PA (WILL//) WILLIAMS P M.
PA (WOOD//) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1391
ID ADH18281 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207349-A1.
PD 06-NOV-2003.
PA (GETH//) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1392
ID ADJ99722 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
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PN US2003187238-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1393
ID ADL08915 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003186358-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1394
ID ADM25256 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003096233-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1395
ID ADJ63562 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2004039164-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1396
ID ADM30006 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003190611-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1397
ID ADJ77457 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #176.
PN US2004038336-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1398
ID ADJ65579 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2004038335-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1399
ID ADM27715 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2004048333-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1400
ID ADM42439 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2004058424-A1.

PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1401
ID ADO06328 standard; cDNA; 4053 BP.
DE Human PRO polynucleotide #54.
PN US6686451-B1.
PD 03-FEB-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1402
ID ADM28301 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2004077064-A1.
PD 22-APR-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1403
ID ADR11180 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004137561-A1.
PD 15-JUL-2004.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1404
ID ADR18089 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2004147017-A1.
PD 29-JUL-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOVERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANG/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146
RESULT 1405
ID ADI95783 standard; cDNA; 4053 BP.
DE cDNA encoding human PRO polypeptide #176.
PN US2003077659-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03%
Best Local Similarity: 20.73%
Query Match: 12.40%
Conservative: 54
Mismatches: 148
Indels: 146

RESULT 1406
ID AD196335 standard; cDNA; 4053 BP.
DE Novel human secreted and transmembrane protein PRO326 cDNA.
PN US2003207354-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1407
ID AD703765 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane protein cDNA, #56.
PN US2003152922-A1.
PD 14-AUG-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1408
ID AD574728 standard; cDNA; 4053 BP.
DE Human secreted/transmembrane cDNA #56.
PN US2004185531-A1.
PD 23-SEP-2004.
PA (ASHK/) ASHKENAZI A.
PA (BOTS/) BOTSTEIN D.
PA (DESN/) DESNOYERS L.
PA (EATO/) EATON D L.
PA (FERR/) FERRARA N.
PA (FILV/) FILVAROFF E.
PA (FONG/) FONG S.
PA (GAOW/) GAO W.
PA (GERB/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J.
PA (GRIM/) GRIMALDI C J.
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (KLJA/) KLJAVIN I J.
PA (MATH/) MATHER J P.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (ROYM/) ROY M A.
PA (STEW/) STEWART T A.
PA (TUMA/) TUMAS D.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
Percent Similarity: 33.03% Conservative: 54
Best Local Similarity: 20.73% Mismatches: 148
Query Match: 12.40% Indels: 146
RESULT 1409
ID ABA06424 standard; cDNA; 2667 BP.
DE Human cDNA SEQ ID NO: 90.
PN WO200154474-A2.
PD 02-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 37.92% Conservative: 34
Best Local Similarity: 25.28% Mismatches: 123
Query Match: 12.38% Indels: 45
RESULT 1410
ID ABV83761 standard; cDNA; 2667 BP.
DE Human polynucleotide SEQ ID NO 90.
PN US2002090672-A1.
PD 11-JUL-2002.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (BARA/) BARASH S C.
Percent Similarity: 37.92% Conservative: 34
Best Local Similarity: 25.28% Mismatches: 123
Query Match: 12.38% Indels: 45
RESULT 1411
ID ABX34664 standard; cDNA; 1213 BP.
DE Human mddt cDNA SEQ ID 225.

PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Percent Similarity: 38.94% Conservative: 38
Best Local Similarity: 26.40% Mismatches: 123
Query Match: 12.35% Indels: 62
RESULT 1412
ID AAZ33346 standard; cDNA; 1417 BP.
DE Human secreted protein clone cw1000_2 nucleotide sequence SEQ ID NO:61.
PN WO9957132-A1.
PD 11-NOV-1999.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.25% Conservative: 61
Best Local Similarity: 25.07% Mismatches: 153
Query Match: 12.35% Indels: 52
RESULT 1413
ID ADR28012 standard; cDNA; 3540 BP.
DE Long form full-length IGSF9 protein encoding cDNA.
PN WO2004066933-A2.
PD 12-AUG-2004.
PA (MCLA/) MCLACHLAN K.
PA (GLAS/) GLASER S.
PA (PEAC/) PEACH R J.
PA (ROWE/) ROWE I.
Percent Similarity: 39.48% Conservative: 51
Best Local Similarity: 24.78% Mismatches: 144
Query Match: 12.35% Indels: 66
RESULT 1414
ID ADP28247 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #245.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 40.81% Conservative: 49
Best Local Similarity: 25.55% Mismatches: 142
Query Match: 12.29% Indels: 48
RESULT 1415
ID ADP28237 standard; DNA; 3018 BP.
DE Human secreted protein encoding sequence SEQ ID #235.
PN WO2004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Percent Similarity: 40.81% Conservative: 49
Best Local Similarity: 25.55% Mismatches: 142
Query Match: 12.29% Indels: 48
RESULT 1416
ID ADH72193 standard; DNA; 3333 BP.
DE Human gene of the invention NOV51d SEQ ID NO:1089.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Percent Similarity: 39.25% Conservative: 40
Best Local Similarity: 24.15% Mismatches: 111
Query Match: 12.29% Indels: 50
RESULT 1417
ID ABL23498 standard; DNA; 7171 BP.
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 21567.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Percent Similarity: 36.66% Conservative: 43
Best Local Similarity: 24.05% Mismatches: 115
Query Match: 12.29% Indels: 101
RESULT 1418
ID AAA43911 standard; cDNA; 971 BP.
DE Human secreted expressed sequence tag SEQ ID NO:486.
PN WO200021991-A1.
PD 20-APR-2000.
PA (GEMY) GENETICS INST INC.
Percent Similarity: 42.34% Conservative: 53
Best Local Similarity: 26.43% Mismatches: 128
Query Match: 12.24% Indels: 65
RESULT 1419

ID AAS86820 standard; cDNA; 2948 BP.
DE DNA encoding novel human diagnostic protein #22624.
FN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Percent Similarity: 37.77%
Best Local Similarity: 25.75%
Query Match: 12.24%
Indels: 38
Conservative: 28
Mismatches: 107
Indels: 38
RESULT 1420
ID AAV31988 standard; cDNA; 6413 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM2 cDNA.
FN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity: 40.25%
Best Local Similarity: 28.63%
Query Match: 12.24%
Indels: 22
Conservative: 28
Mismatches: 122
Indels: 22
RESULT 1421
ID AAV31981 standard; cDNA; 6604 BP.
DE Human Down syndrome-cell adhesion molecule DS-CAM1 cDNA.
FN WO9817795-A1.
PD 30-APR-1998.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
Percent Similarity: 40.25%
Best Local Similarity: 28.63%
Query Match: 12.24%
Indels: 22
Conservative: 28
Mismatches: 122
Indels: 22
RESULT 1422
ID ADK71086 standard; DNA; 6649 BP.
DE Human MP21 polypeptide encoding DNA.
FN WO2004015073-A2.
PD 19-FEB-2004.
PA (EXEL-) EXELIXIS INC.
Percent Similarity: 40.25%
Best Local Similarity: 28.63%
Query Match: 12.24%
Indels: 22
Conservative: 28
Mismatches: 122
Indels: 22
RESULT 1423
ID ADR41293 standard; cDNA; 1153 BP.
DE Human CD-like molecule HATCZ07 cDNA, SEQ ID NO:92.
FN WO200226930-A2.
PD 04-APR-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1424
ID AAS80677 standard; cDNA; 1329 BP.
DE Human secreted protein #11 nucleotide sequence SEQ ID #137.
FN WO200029435-A1.
PD 25-MAY-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1425
ID ADA27145 standard; cDNA; 1329 BP.
DE Human novel secreted protein from gene 11 cDNA #3.
FN US200305231-A1.
PD 20-MAR-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENV/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
PA (LIUD/) LIU D.
PA (CROC/) CROCKER P R.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1426
ID ADE86686 standard; cDNA; 1329 BP.
DE Novel human secreted protein #11 associated cDNA #1.
FN US2003129685-A1.
PD 10-JUL-2003.
PA (NIJ/) NI J.
PA (YOUN/) YOUNG P E.
PA (KENV/) KENNY J J.
PA (OLSE/) OLSEN H S.
PA (MOOR/) MOORE P A.
PA (WEIY/) WEI Y.
PA (GREE/) GREENE J M.
PA (RUBE/) RUBEN S M.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1427
ID AAX80055 standard; cDNA; 1413 BP.
DE Human PRO355 nucleotide sequence.
FN WO9928462-A2.
PD 10-JUN-1999.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1428
ID AAA49563 standard; cDNA; 1413 BP.
DE Human PRO355 cDNA.
FN WO200032776-A2.
PD 08-JUN-2000.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1429
ID AAS45941 standard; cDNA; 1413 BP.
DE Human DNA encoding PRO polypeptide sequence #17.
FN WO200168848-A2.
PD 20-SEP-2001.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1430
ID ACA89391 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO polypeptide #17.
FN US2003036141-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1431
ID ACA73401 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
FN US2003036146-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1432
ID ACA05716 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
FN US2003036162-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Indels: 45
Conservative: 54
Mismatches: 135
Indels: 45
RESULT 1433
ID ACA66550 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO protein #17.
FN US2003036137-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.

Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1434
ID ACF20125 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040063-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1435
ID ACF19511 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040064-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1436
ID ACD21799 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003027267-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1437
ID ACF12964 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036160-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1438
ID ACD25067 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003044925-A1.
PD 06-MAR-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1439
ID ACF00116 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003054474-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1440
ID ABX96814 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein PRO355.
PN US2002173463-A1.
PD 21-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1441
ID ACA72173 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032114-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1442
ID ACD04697 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032101-A1.

PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1443
ID ACD18158 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036124-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1444
ID ACD08165 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003040054-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1445
ID ABX78468 standard; cDNA; 1413 BP.
DE DNA encoding Novel human secreted protein PRO355.
PN US2002150976-A1.
PD 17-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1446
ID ACB88599 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036133-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1447
ID ACA70041 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036134-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1448
ID ACD12263 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022294-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1449
ID ACC74178 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027275-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1450
ID ACD15806 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003027324-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1451
ID ACD25374 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036118-A1.

PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1452
ID ACD17851 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036123-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1453
ID ACC88138 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036148-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1454
ID ACD21492 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003040060-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1455
ID ACD18559 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003044916-A1.
PD 06-MAR-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1456
ID ABX77102 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO355 protein.
PN US2002142958-A1.
PD 03-OCT-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1457
ID ABX98169 standard; cDNA; 1413 BP.
DE Human cDNA encoding a secreted/transmembrane protein, SEQ ID 33.
PN US2003036156-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1458
ID ACD13920 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032117-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1459
ID ACD09700 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036128-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1460
ID ACC88445 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.

PN US2003027266-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1461
ID ACD21185 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1462
ID ABX75557 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO355.
PN US2003022298-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1463
ID ABX97760 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032102-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1464
ID ACA97236 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036117-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1465
ID ACA57699 standard; cDNA; 1413 BP.
DE Human PRO355 cDNA.
PN US2003036143-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1466
ID ACD14227 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003032130-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1467
ID ACC91010 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1468
ID ACC89752 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003036132-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1469
ID ACD06949 standard; cDNA; 1413 BP.

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DE Human PRO polynucleotide #17.
PN US2003008353-A1.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1470
ID ACA67400 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003017542-A1.
PD 23-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1471
ID ACC81455 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US200302137-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1472
ID ACC89059 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027369-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1473
ID ACC86415 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027268-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1474
ID ACC89673 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027274-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1475
ID ACC92852 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1476
ID ACA72480 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003022295-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1477
ID ACA88998 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003022297-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1478
ID ACA69734 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032105-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1479
ID ACA96877 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032123-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1480
ID ACA90873 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032108-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1481
ID ACA70655 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032111-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1482
ID ACA95165 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1483
ID ACC86108 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027263-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1484
ID ACC89980 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027271-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1485
ID ACD12588 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003036125-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1486
ID ACF19818 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003040068-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22%
Best Local Similarity: 26.18%
Query Match: 12.21%
Conservative: 54
Mismatch: 135
Indels: 45
RESULT 1487
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ID ABX75933 standard; cDNA; 1413 BP.
DE Human cDNA encoding secreted/transmembrane protein, PRO355.
PN US2002132981-A1.
PD 19-SEP-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1488
ID ABX76762 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003027280-A1.
PD 06-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1489
ID ACA73094 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022300-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1490
ID ACA68637 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036136-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1491
ID ACA74481 standard; cDNA; 1413 BP.
DE cDNA encoding human PRO polypeptide #17.
PN US2003036138-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1492
ID ACA70348 standard; cDNA; 1413 BP.
DE Human secreted/transmembrane protein (PRO) cDNA #17.
PN US2003032109-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1493
ID ACD14534 standard; cDNA; 1413 BP.
DE Human PRO polynucleotide #17.
PN US2003040056-A1.
PD 27-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1494
ID ABX89644 standard; cDNA; 1413 BP.
DE cDNA encoding novel secreted and transmembrane protein PRO355.
PN US2002168715-A1.
PD 14-NOV-2002.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1495
ID ACA68206 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003032104-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45

RESULT 1496
ID ABX98671 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036157-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1497
ID ACC81148 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003032120-A1.
PD 13-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1498
ID ACA95472 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003036155-A1.
PD 20-FEB-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1499
ID ACD04390 standard; cDNA; 1413 BP.
DE Novel human secreted and transmembrane protein PRO355 cDNA.
PN US2003022296-A1.
PD 30-JAN-2003.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45
RESULT 1500
ID ACC87831 standard; cDNA; 1413 BP.
DE Human secreted polypeptide PRO355-encoding cDNA, SEQ ID NO:33.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Percent Similarity: 43.22% Conservative: 54
Best Local Similarity: 26.18% Mismatches: 135
Query Match: 12.21% Indels: 45

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 30, 2005, 07:24:31 ; Search time 3856 Seconds
(without alignments)
3395.775 Million cell updates/sec

Title: US-10-017-084A-523

Perfect score: 1806

Sequence: 1 MKTIQPKHNSISWAIFTGL.....RRAGCVWLLPLVLHLLKPF 344

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US10017084/runat_28102005_112601_9167/app query fasta_1.519
-DB=EST_QFMT=fasCap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1500
-DOCALIGN=200 -THR SCORE=500 -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017084.cGCGN 1.1 4352 @runat_28102005_112601_9167 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gsl.*
9: gb_gsl2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1780	98.6	1808	3	AK045973 Mus muscu
2	1780	98.6	1808	3	AK046377 Mus muscu
3	1506	83.4	874	9	AY406347 Homo sapi
4	1488	82.4	874	9	AY406349 Mus muscu
5	1324	73.3	773	9	AY406348 Pan trogl
6	1321	73.1	1450	7	C0635648 Contig266
7	1254	69.4	765	6	CD354474 UI-M-GMO-
8	1199.5	66.4	856	5	BUI55617 AGENCOURT
9	1167	64.6	1039	2	BE798585 601581610

10	1117.5	61.9	748	7	CN362539
11	1112	61.6	890	6	CD327172
12	1094.5	60.6	759	7	CF737474
13	1062.5	58.8	1027	1	AL533026
14	1062.5	58.8	2512	3	CR602526
15	1047	58.0	740	5	BUI38328
16	1042	57.7	840	5	BUI320256
17	1005.5	55.7	849	4	BUI75360
18	982.5	54.4	865	4	B166583
19	973	53.9	601	6	CB582386
20	952	52.7	600	7	CR548212
21	932.5	51.6	1017	9	AY406971
22	929	51.4	793	5	BUI35385
23	926.5	51.3	1017	9	AY406973
24	926	51.3	545	2	BE263639
25	925.5	51.2	979	4	BG261691
26	920	50.9	737	7	CN533076
27	916.5	50.7	2768	3	AK030681
28	912	50.5	732	4	B1551784
29	910	50.4	553	2	BE864555
30	908.5	50.3	1015	9	AY406972
31	907	50.2	524	2	BE014142
32	902.5	50.0	859	6	CD325278
33	900	49.8	636	7	CR540711
34	894	49.5	2467	3	AK044845
35	890	49.3	784	4	B1549918
36	881	48.8	768	1	AU080629
37	875	48.4	754	4	B1550038
38	869	48.1	580	4	B1548566
39	868	48.1	680	7	CR751151
40	862.5	47.8	661	4	BM009450
41	862.5	47.8	953	4	BM423716
42	858.5	47.5	1033	4	BM807426
43	855.5	47.4	1083	4	BM809227
44	843.5	46.7	2330	3	BC080168
45	830	46.0	729	6	BU277649
46	818	45.3	738	6	CD353574
47	814.5	45.1	1138	4	BM556708
48	814	45.1	804	7	CN232247
49	811.5	44.9	557	4	BM256660
50	805	44.6	2096	3	AK035218
51	801	44.4	705	4	BG704152
52	799	44.2	1953	3	AK030503
53	795	44.0	660	6	BY723873
54	793.5	43.9	759	7	CN094277
55	791.5	43.8	764	5	BM945665
56	781.5	43.3	780	7	CK133831
57	774.5	42.9	724	7	CK312152
58	772.5	42.8	849	6	CA472810
59	771.5	42.7	533	4	B1341675
60	770	42.6	671	2	BB644996
61	767.5	42.5	582	5	BP194945
62	763	42.2	437	6	CB724811
63	761.5	42.2	858	6	CD325821
64	761	42.1	663	4	BM724307
65	759	42.0	2534	3	AK039193
66	748	41.4	690	7	CN233126
67	743	41.1	613	7	CR540607
68	742	41.1	827	6	CA306798
69	730	40.4	633	4	BG706987
70	727	40.3	677	5	BQ444788
71	726.5	40.2	1304	5	BM911516
72	709	39.3	815	5	BU230452
73	707.5	39.2	819	5	BU750937
74	707.5	39.2	823	5	BU750936
75	706	39.1	754	4	B1598759
76	705	39.0	934	7	CN015939
77	703.5	39.0	778	7	CN078143
78	697	38.6	683	2	BB640070
79	697	38.6	3166	3	AK042854
80	695	38.5	470	7	CR537991
81	688	38.1	695	7	CN228731
82	688	38.1	754	7	C0043662

83	687.5	38.1	2798	3	AK028345	Mus muscu	156	498	27.6	611	6	CA355517	CA355517	627428 NC
84	685.5	38.0	602	2	BB611718	BB611718	157	498	27.6	914	5	BM843874	BM843874	BM843874
85	682	37.8	870	5	BUS15609	AGENCOURT	158	497	27.5	768	5	BM868437	BM868437	BM868437
86	672	37.2	534	4	BM686717	UI-E-C00-	C 159	492.5	27.3	753	1	AI589824	AI589824	AI589824
87	671	37.2	643	5	B0390882	603807132	160	490	27.1	599	7	CN229507	CN229507	CN229507
88	671	37.2	806	1	AU051132	AU051132	161	488.5	27.0	835	5	BM881962	BM881962	BM881962
89	670.5	37.1	660	7	CR543517	CR543517	162	486	26.9	290	7	F05894	F05894	F05894
90	666.5	36.9	796	7	C0399311	AGENCOURT	C 163	485	26.9	578	2	BE121132	BE121132	BE121132
91	666	36.9	764	4	B1752729	603028343	164	484	26.8	456	6	CD803885	CD803885	CD803885
92	665	36.8	563	6	CB296974	12822045	165	483	26.7	347	7	CN094278	CN094278	CN094278
93	661	36.6	548	2	BE015245	127482 MA	166	483	26.7	755	5	BM843874	BM843874	BM843874
94	654	36.2	880	6	CD303536	AGENCOURT	167	480.5	26.6	664	7	CN362538	CN362538	CN362538
95	651	36.0	704	7	CN228803	RJB061B04	168	480	26.6	795	1	AU080106	AU080106	AU080106
96	644.5	35.7	640	7	CR545244	DKF2p459F	169	478	26.5	566	7	CF977262	CF977262	CF977262
97	637.5	35.3	496	5	BP201259	BP201259	170	477	26.4	478	5	BY245406	BY245406	BY245406
98	632.5	35.0	621	5	BM312928	BM312928	171	476	26.4	661	6	CA452139	CA452139	CA452139
99	632.5	35.0	1148	4	BM466102	AGENCOURT	172	475.5	26.3	392	2	BE651010	BE651010	BE651010
100	632	35.0	688	2	BM646531	BM646531	173	475	26.3	646	6	CA334396	CA334396	CA334396
101	629	34.8	674	6	CD767791	AGENCOURT	174	474.5	26.3	953	5	BUI16264	BUI16264	BUI16264
102	619.5	34.3	786	7	CO811192	AGENCOURT	175	473	26.2	284	7	CR543721	CR543721	CR543721
103	616	34.1	867	6	CD300857	AGENCOURT	176	468.5	25.9	703	7	CF530869	CF530869	CF530869
104	614.5	34.0	511	5	BM493152	DKF2p781G	C 177	468.5	25.9	772	7	CK776016	CK776016	CK776016
105	613	33.9	513	5	BM279850	BM279850	178	468	25.9	936	5	BO227365	BO227365	BO227365
106	612.5	33.9	858	7	CO914076	AGENCOURT	179	467.5	25.9	617	6	BY730405	BY730405	BY730405
107	607.5	33.6	492	2	AW967001	EST379075	180	467	25.9	390	4	BM719375	BM719375	BM719375
108	607	33.6	587	7	CN088583	EC2BBA30B	181	467	25.9	390	5	BM719757	BM719757	BM719757
109	604.5	33.5	639	7	CV030684	CV030684	182	467	25.9	390	5	BM931279	BM931279	BM931279
110	603	33.4	656	7	CK619540	mk25d06.Y	C 183	467	25.9	394	4	BM684112	BM684112	BM684112
111	591	32.7	528	4	B1553032	603193672	C 184	467	25.9	394	5	BM684852	BM684852	BM684852
112	591	32.7	678	5	BUS224639	UI-H-FG1-	C 185	467	25.9	734	5	BQ184395	BQ184395	BQ184395
113	590	32.7	672	6	CA444805	UI-H-DH1-	C 186	467	25.9	394	5	BQ184512	BQ184512	BQ184512
114	590	32.7	926	6	CD325412	AGENCOURT	C 187	467	25.9	394	7	CK300895	CK300895	CK300895
115	589	32.6	697	6	CD217649	pglin.pk0	C 188	467	25.9	403	4	BM684212	BM684212	BM684212
116	589	32.6	697	5	BQ021243	UI-H-DH1-	C 189	467	25.9	608	5	BQ188988	BQ188988	BQ188988
117	577	31.9	652	7	CN078144	EC2BBA14C	190	467	25.9	700	5	BQ189788	BQ189788	BQ189788
118	575	31.8	567	2	BF078551	228917 MA	191	467	25.9	734	5	BQ187606	BQ187606	BQ187606
119	569.5	31.5	1084	6	CD255729	AGENCOURT	192	466.5	25.8	884	5	B0323269	B0323269	B0323269
120	569	31.5	611	7	CN075612	EC2BBA10C	C 193	463.5	25.7	564	7	CO602836	CO602836	CO602836
121	567	31.4	655	4	B1548049	603196558	194	463	25.6	666	5	BM951674	BM951674	BM951674
122	565.5	31.3	528	2	BM856778	BM856778	195	461	25.5	795	7	CO395735	CO395735	CO395735
123	564.5	31.3	896	5	BQ890272	AGENCOURT	C 196	460	25.5	572	2	BF407747	BF407747	BF407747
124	564	31.2	708	7	CN083621	EC2BBA22D	197	459	25.4	282	7	R75391	R75391	R75391
125	561.5	31.1	519	7	CV038761	4136000 B	198	459	25.3	858	2	BF676478	BF676478	BF676478
126	561	31.1	726	5	BX912600	BX912600	199	457.5	25.3	718	6	CB460692	CB460692	CB460692
127	560.5	31.0	719	7	CK465166	936244 MA	C 200	455	25.2	456	1	AI369684	AI369684	AI369684
128	559.5	31.0	572	6	CB265380	1004285 H	201	453.5	25.1	651	2	AW327110	AW327110	AW327110
129	559	31.0	2296	3	CR592222	full-leng	202	448	24.8	257	2	BM726997	BM726997	BM726997
130	558	30.9	656	6	CA307492	UI-H-FT1-	203	448	24.8	909	5	BUI32565	BUI32565	BUI32565
131	554.5	30.7	625	2	BM643056	BM643056	204	445.5	24.7	637	6	CB528708	CB528708	CB528708
132	553	30.6	636	7	CK843444	UI-R-BJ2-	205	444	24.6	894	6	CB199088	CB199088	CB199088
133	552.5	30.6	670	7	CN083622	EC2BBA22D	206	443.5	24.6	791	7	CK308721	CK308721	CK308721
134	548	30.3	862	7	CK397022	AGENCOURT	207	441.5	24.4	497	7	CV036959	CV036959	CV036959
135	545	30.2	560	2	CR545391	DKF2p459M	208	441	24.4	801	7	BUI357013	BUI357013	BUI357013
136	544	30.1	693	7	BM633037	BM633037	209	440.5	24.4	700	7	CN458398	CN458398	CN458398
137	543.5	30.1	647	7	CO351229	DR AOV FL	210	440	24.4	445	5	BY269882	BY269882	BY269882
138	543.5	30.1	647	7	CV030870	10123 Ful	211	433.5	24.0	584	5	BP257486	BP257486	BP257486
139	541.5	30.0	415	7	R18841	YS22906.r1	212	432.5	23.9	892	5	BP462753	BP462753	BP462753
140	536	29.7	497	2	BM854833	BM854833	213	432	23.9	457	5	BY249728	BY249728	BY249728
141	535.5	29.7	906	5	BUI86468	AGENCOURT	C 214	427.5	23.7	580	7	CN089827	CN089827	CN089827
142	532.5	29.4	825	5	BP166655	BP166655	C 215	426	23.6	541	5	BUI35309	BUI35309	BUI35309
143	531.5	29.4	867	7	CO543917	LYEST116	C 216	426	23.6	544	6	CA439326	CA439326	CA439326
144	529	29.3	329	7	F06205	HSC10F041 n	217	423	23.4	481	5	BY256150	BY256150	BY256150
145	525	29.1	593	7	CK845949	968393 MA	218	416.5	23.1	496	7	CK693129	CK693129	CK693129
146	523.5	29.0	923	1	AL583491	AL583491	C 219	413	22.9	494	1	AA548396	AA548396	AA548396
147	518	28.7	565	2	BE663866	147903 MA	220	411.5	22.8	617	4	B0622933	B0622933	B0622933
148	512.5	28.4	535	9	AY409767	Homo sapi	221	407.5	22.6	778	7	CK315507	CK315507	CK315507
149	511	28.3	764	6	CA350929	621861 NC	222	407.5	22.6	788	4	BI011319	BI011319	BI011319
150	510	28.2	579	2	BM644523	BM644523	223	402	22.3	277	4	QV2-EN009	QV2-EN009	QV2-EN009
151	509.5	28.2	773	4	BG208674	RS278306	224	401.5	22.2	600	6	CA526928	CA526928	CA526928
152	508.5	28.2	535	9	AY409769	Mus muscu	225	396.5	22.0	862	5	BP462754	BP462754	BP462754
153	508	28.1	739	7	CK679857	ZF101-F00	C 226	394	21.8	598	1	AI815935	AI815935	AI815935
154	507	28.1	659	2	AW149545	xf39c10.x	227	390.5	21.6	771	7	CN528825	CN528825	CN528825
155	506.5	28.0	703	5	BUI17309	603138889	C 228	390	21.6	465	1	AI934791	AI934791	AI934791

229 389.5 21.6 878 5 BP165624 BP165624
230 389 21.5 450 5 BY263302 BY263302
231 388 21.5 294 7 W15256 ZC16H07.r1
232 388 21.5 357 5 BY303236 BY303236
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234 384.5 21.3 444 1 AA682970 ae89a04.r
235 380.5 21.1 775 4 B1199955 602761121
236 379.5 21.0 660 5 BW337636 BW337636
237 377.5 20.9 833 5 BP164129 BP164129
238 376.5 20.8 535 9 AY409768 Pan.trog1
239 376 20.8 470 6 A1580850 ta33e06.x
240 373.5 20.7 478 6 CA885050 B0115808-
241 372 20.6 511 1 A1415689 mc70a03.x
242 371.5 20.6 723 9 AG035406 Pan.trog1
243 370 20.5 863 3 CA475514 AGENCOURT
244 365.5 20.2 809 2 BP304194 601887043
245 364 20.2 268 1 AA296886 EST112650
246 363.5 20.1 801 5 BX852740 BX852740
247 363 20.1 519 1 AA828266 od03e04.r
248 362 20.0 229 1 AA450172 Zx42d09.r
249 358 19.8 855 5 BP158085 BP158085
250 357.5 19.8 483 7 CR536826 DKF2p459J
251 355.5 19.7 368 2 BP350775 OVO-H7036
252 355 19.7 348 7 R55964 Y989e11.r1
253 355 19.7 431 5 BY276402 BY276402
254 353 19.5 711 5 BU363662 603790080
255 352.5 19.5 729 2 BB585976 BB585976
256 351 19.4 429 5 BY272572 BY272572
257 350 19.4 504 5 BX281785 BX281785
258 348.5 19.3 868 5 BQ672092 AGENCOURT
259 342.5 19.0 960 5 BQ933325 AGENCOURT
260 341 18.9 525 1 AL919221 AL919221
261 339.5 18.8 825 5 BP464677 BP464677
262 338.5 18.7 514 4 BG814603 daF69d01.
263 338.5 18.7 807 5 BP168056 BP168056
264 331.5 18.4 801 7 CK303983 SB02022A1
265 331 18.3 594 5 BU400899 603481850
266 330 18.3 410 5 BY276506 BY276506
267 329 18.2 651 6 CB557691 AMGNNUC:N
268 327.5 18.1 458 7 CO667952 DK33-31f8
269 323.5 17.9 562 5 BU381982 603582664
270 320.5 17.7 470 5 BX954423 DKF2p781K
271 320.5 17.7 613 7 CF892168 AO106B07-
272 320 17.7 579 7 CN089828 CN089828
273 318.5 17.6 446 7 CO352257 DR.AOV.SU
274 315 17.4 422 1 A1288864 Q724f12.x
275 314 17.4 845 4 BN042630 603615963
276 312.5 17.3 641 2 AW379374 CM2-HT024
277 312 17.3 514 1 A1285235 qk59h04.x
278 311 17.2 378 2 BF601149 266043 MA
279 311 17.2 489 6 CB726015 AMGNNUC:N
280 310.5 17.2 527 5 BY243052 BY243052
281 310.5 17.2 552 4 B1337752 361275 MA
282 310.5 17.2 789 7 CR531801 CR531801
283 310 17.2 359 2 BE156390 QVO-HT036
284 310 17.2 415 5 BY263876 BY263876
285 310 17.2 461 2 BF463934 UI-M-CG0P
286 308 17.1 694 7 CF6599353 ZF101-P00
287 307.5 17.0 705 7 CN108877 EC3CAA32D
288 307 17.0 178 6 CB118055 K-ESTU0164
289 306.5 17.0 730 5 BX610460 BX610460
290 306.5 17.0 770 7 CR526028 CR526028
291 304 16.8 528 2 AW490008 UI-M-BH3-
292 303.5 16.8 790 5 BP141505 BP141505
293 302.5 16.7 394 9 AY400233 Homo.sapi
294 302.5 16.7 394 9 AY400233 Pan.trog1
295 300.5 16.6 481 5 BY247646 BY247646
296 300 16.6 377 7 CF977263 2-98-A10.
297 300 16.6 646 5 BW346790 BW346790
298 298 16.5 372 6 BY768835 BY768835
299 298 16.5 386 5 BY263646 BY263646
300 297 16.4 708 7 CK661144 LP20336.5
301 296.5 16.4 382 9 AY400235 Mus.muscu

302 296.5 16.4 417 6 CA884109
303 295 16.3 994 6 CD325921 AGENCOURT
304 294.5 16.3 451 1 AA933871 AL91d04.s
305 293 16.2 220 7 H16176 Ym21q09.r1
306 293 16.2 665 9 BX243020 Danio.rer
307 293 16.2 761 6 CD755145 AGENCOURT
308 291.5 16.1 899 5 BU134624 603119839
309 291 16.1 402 5 BY289266 BY289266
310 290.5 16.1 733 7 CO619752 DG9-1d13
311 290 16.1 585 7 CO628980 DG9-3m14
312 289.5 16.0 726 5 BU395513 603404749
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314 288 15.9 422 4 B1390270 P9p1c.pk0
315 285 15.8 691 7 CK661190 LP20417.5
316 285 15.8 693 7 CK657729 LP24251.5
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318 283 15.7 488 5 BX477962 DKF2p686N
319 282.5 15.6 2193 9 AY418859 Mus.muscu
320 282.5 15.6 2709 3 AK082621 AK082621
321 282.5 15.6 2713 3 AK051197 AK051197
322 278.5 15.4 473 5 BY261511 BY261511
323 278 15.4 2190 9 AY418858 Pan.trog1
324 276 15.3 2190 9 AY418857 Hom.sapi
325 275 15.2 583 6 CA353359 CA353359
326 273.5 15.1 344 7 CN075611 CN075611
327 271.5 15.0 316 1 A1884993 A1884993
328 269.5 14.9 452 1 A1262821 A1262821
329 269.5 14.9 656 2 BB617916 BB617916
330 268 14.8 402 2 AW522667 UI-R-B00-
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332 267.5 14.8 392 5 BY267956 BY267956
333 265.5 14.7 421 5 BY275639 BY275639
334 263 14.6 2397 3 AK033973 AK033973
335 263 14.6 2509 3 AK046800 AK046800
336 263 14.6 3880 3 AK043760 AK043760
337 263 14.6 3892 3 AK038842 AK038842
338 260 14.4 412 5 BY274659 BY274659
339 257.5 14.3 401 5 BY266910 BY266910
340 257.5 14.3 3315 3 HSM805302 HSM805302
341 257 14.2 1080 5 BM916998 AGENCOURT
342 256 14.2 336 5 BY134531 BY134531
343 254.5 14.1 763 1 A1427225 mc70a03.Y
344 253 14.0 456 5 BY249027 BY249027
345 253 14.0 760 6 CD636199 CD636199
346 253 14.0 929 5 BX409828 BX409828
347 251.5 13.9 700 6 CD636207 CD636207
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356 248.5 13.8 785 6 CD636241 CD636241
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358 246 13.6 385 5 BY275013 BY275013
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361 246 13.6 3198 9 AY416712 Homo.sapi
362 245.5 13.6 724 6 CD636193 CD636193
363 245.5 13.6 753 6 CD636243 CD636243
364 244.5 13.5 1871 3 BC029119 Homo.sapi
365 243.5 13.5 649 6 CD636211 CD636211
366 243.5 13.5 690 6 CD636247 CD636247
367 243.5 13.5 1946 3 BC028193 BC028193
368 242.5 13.4 354 2 BE826697 BE826697
369 242 13.4 668 6 CD636194 CD636194
370 241.5 13.4 732 6 CD636203 CD636203
371 241 13.3 633 9 BX190380 BX190380
372 240.5 13.3 629 6 CD636245 CD636245
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374 238.5 13.2 374 5 BY294857 BY294857

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H16176 Ym21q09.r1
BX243020 Danio.rer
CD755145 AGENCOURT
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CO628980 DG9-3m14
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AK046800 Mus.muscu
AK038842 Mus.muscu
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CD636207 56031034J
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BE826640 QV1-EN004
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CD636241 56038385J
CR749495 Homo.sapi
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BY294857 BY294857

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377 237.5 13.2 3133 9 AY416714 Mus muscu
378 237.5 13.2 3179 3 AK028527
379 237.5 13.2 3948 3 AK036116
380 236.5 13.1 646 4 B1393264
381 236 13.1 529 6 CD284927 G39161.77
382 235 13.0 479 2 AW524531 UI-R-B00-
383 235 13.0 711 7 CO669353 DG33-50b1
384 233 12.9 582 7 CO626674 DG9-278a2
385 232 12.8 747 7 CF743366 UI-M-GV0-
386 232 12.8 758 6 CB525885 UI-M-FY0-
387 231.5 12.8 3057 9 AY417678 Homo sapi
388 231.5 12.8 4327 3 BC033255 Homo sapi
389 231 12.8 3392 3 BC036338 Homo sapi
390 231 12.8 3480 9 AY418997 Homo sapi
391 230 12.7 339 2 B8828667
392 230 12.7 872 5 BU411493
393 229.5 12.7 705 6 CD636208 56031050H
394 229 12.7 782 8 A2731274 RPCI-24-1
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397 228.5 12.7 2530 3 AK018522 Mus muscu
398 228 12.6 194 4 B1337742
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408 224 12.4 4187 3 AK053044 Mus muscu
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417 220.5 12.2 1372 3 AK053839 Mus muscu
418 220 12.2 2126 3 AK013911 Mus muscu
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430 216.5 12.0 375 5 B292584 B292584
431 216.5 12.0 473 7 CO280999 EK155707
432 215.5 11.9 657 2 B8618284 BB18284
433 215.5 11.9 1311 3 CR731011 Tetraodon
434 214.5 11.9 734 6 CB4848011 702065 MA
435 214.5 11.9 742 7 CO393507 AGENCOURT
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440 214 11.8 2464 3 AK043507 Mus muscu
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444 213.5 11.8 1306 3 CR605082 full-leng
445 213.5 11.8 1315 3 CR733537 Tetraodon
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458 211.5 768 6 CD636212 56031066H
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477 207.5 11.5 2104 3 AK033487 Mus muscu
478 207.5 11.5 4441 3 AK081990 AK081990
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491 204.5 11.3 893 5 BU233040 AGENCOURT
492 204.5 11.3 1237 3 CR641398 Tetraodon
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508 201 11.1 1788 9 AY411536 Mus muscu
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514 200 1062 5 BX343871 BX343871
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c 517 199.5 11.0 1074 7 CR754275 CR754275
518 199.5 11.0 1267 3 CR634286 Tetraodon
519 199 816 1 AU117395 AU117395
520 199 954 1 AL551492 AL551492

521	199	11.0	2236	3	BC030834	Homo sapi	594	190.5	10.5	779	5	BU419715	603955627
522	199	11.0	2705	3	AK090377	Mus muscu	595	190.5	10.5	797	5	BU419715	603955627
523	199	11.0	4068	9	AY06427	Mus muscu	596	190.5	10.5	924	5	BQ882851	AGENCOURT
524	198.5	11.0	618	6	CD363200	560309668	597	190.5	10.5	1499	5	CR636336	Tetraodon
525	198.5	11.0	732	7	CN381875	170005328	598	190	10.5	514	5	EX111689	EX111689
526	198.5	11.0	796	6	CD620697	56100881J	599	190	10.5	769	5	EX857871	EX857871
527	198.5	11.0	4919	3	BC040674	Homo sapi	c 600	190	10.5	1463	8	CC288776	CH261-170
528	198	11.0	625	4	BJ032692	BJ032692	601	189.5	10.5	714	7	CN460823	UI-M-HB0-
529	198	11.0	728	7	CF728819	UI-M-HB0-	602	189.5	10.5	748	5	BU058289	UI-M-F00-
530	198	11.0	838	7	CK028945	AGENCOURT	603	189.5	10.5	946	4	BI549835	603194572
531	198	11.0	1104	7	CR755975	CR755975	604	189.5	10.5	2211	9	AY418471	Pan trogl
532	197.5	10.9	534	7	CR950627	Ha_mx0_36	605	189.5	10.5	3057	9	AY417679	Pan trogl
533	197.5	10.9	766	6	CA326802	UI-M-FY0-	606	189	10.5	609	6	CA381472	660987 NC
534	197.5	10.9	795	7	CN532710	UI-M-H00-	607	189	10.5	683	2	BBI38882	BB318882
535	197.5	10.9	1145	7	CR754709	CR754709	608	189	10.5	706	6	CA324144	UI-M-FY0-
536	197	10.9	433	4	BG515406	dae04h10.	609	189	10.5	710	7	CR638303	UI-M-H00-
537	197	10.9	474	2	BG682022	BB682022	610	189	10.5	938	5	EX708988	EX708988
538	197	10.9	631	4	BM426245	pgf2n.pk0	611	188.5	10.4	603	1	AL679324	AL679324
539	197	10.9	781	6	CD620693	56100781J	612	188.5	10.4	663	5	BU708530	UI-M-FY0-
540	196.5	10.9	582	5	BP355301	BP355301	613	188.5	10.4	720	3	CR644200	Tetraodon
541	196.5	10.9	686	6	CA372777	646750 NC	614	188.5	10.4	773	6	CD348004	CD348004
542	196.5	10.9	812	5	B0180027	UI-M-EW0-	615	188.5	10.4	839	4	BI851286	603377864
543	196.5	10.9	923	5	BU140452	603135370	616	188.5	10.4	922	4	BM802337	AGENCOURT
544	196.5	10.9	1272	3	CR731454	Tetraodon	617	188.5	10.4	4185	3	AK083540	Mus muscu
545	196.5	10.9	3647	3	BC046957	Mus muscu	618	188	10.4	313	2	AW430704	70599 MAR
546	196	10.9	895	7	CR761982	ID0AA3BG	619	188	10.4	558	6	CB448500	702638 MA
547	196	10.9	925	4	BG413088	602446318	620	188	10.4	722	7	CN530508	UI-M-H00-
548	196	10.9	987	6	CD507156	CD483-C12	621	188	10.4	833	6	CD636250	56038493H
549	196	10.9	4068	9	AY06425	Homo sapi	622	188	10.4	1121	7	CR755403	CR755403
550	195.5	10.8	576	1	AL699151	DKFZp886E	623	187.5	10.4	582	5	BP355339	BP355339
551	195.5	10.8	632	7	C0432230	UI-M-HX0-	624	187.5	10.4	652	8	BH269030	CH230-66P
552	195.5	10.8	675	7	CN060015	Salamande	625	187.5	10.4	655	1	AI980307	pat.pk002
553	195.5	10.8	787	6	CD802924	UI-M-GV0-	626	187.5	10.4	759	7	CN430206	170005315
554	195.5	10.8	857	6	CD520168	UI-M-GI0-	627	187.5	10.4	784	7	CK478969	AGENCOURT
555	195.5	10.8	1261	3	CR640626	Tetraodon	628	187	10.4	497	5	EX515241	EX515241
556	195.5	10.8	1263	3	CR647139	Tetraodon	629	187	10.4	616	7	CN532902	UI-M-H00-
557	195	10.8	617	5	BQ555199	H4032G01-	630	187	10.4	766	2	BE213159	IPbrn0200
558	195	10.8	666	7	CN832582	AGENCOURT	631	187	10.4	837	7	CF345598	Mus muscu
559	194.5	10.8	455	7	C0337067	EN13754.5	632	187	10.4	3531	3	AK035110	AGENCOURT
560	194.5	10.8	632	7	CR689464	ZF101-P00	633	187	10.4	3821	3	AK085461	Mus muscu
561	194.5	10.8	730	6	CA357629	630022 NC	634	186.5	10.3	664	4	BJ732469	BJ732469
562	194.5	10.8	763	6	CR519682	UI-M-GH0-	635	186.5	10.3	835	7	CK847657	970316 MA
563	194.5	10.8	852	7	CK422792	CD422792	636	186.5	10.3	923	3	BU326524	603489483
564	194	10.7	523	4	BI512632	BB160009B	637	186.5	10.3	1230	3	CR641410	Tetraodon
565	194	10.7	896	6	CD514588	AGENCOURT	638	186	10.3	644	6	CB518611	UI-M-GH0-
566	194	10.7	3424	3	AK044694	Mus muscu	639	186	10.3	648	5	BM935487	UI-M-BH3-
567	193.5	10.7	837	6	CD352315	UI-M-GI0-	640	186	10.3	727	7	CO431177	UI-M-HX0-
568	193.5	10.7	4178	3	AK087693	Mus muscu	641	186	10.3	752	7	CF741342	UI-M-GH0-
569	193	10.7	226	1	AA776056	ae79a07.s	642	186	10.3	788	7	CF737289	UI-M-HD0-
570	193	10.7	710	7	CN225540	WLA073F11	643	186	10.3	791	7	CO557024	AGENCOURT
571	193	10.7	808	5	BU746846	CH3#007 D	644	186	10.3	883	7	CN985580	CN985580 58560_126
572	192.5	10.7	614	6	CD636183	56020347J	645	186	10.3	1146	7	CR755551	CR755551
573	192.5	10.7	944	5	B0681009	AGENCOURT	646	186	10.3	1791	9	AY411534	AY411534 Homo sapi
574	192.5	10.7	945	9	CN504AD2	AL2811711	647	185.5	10.3	636	5	BU363294	603585969
575	192.5	10.7	1259	3	CR636055	Tetraodon	648	185.5	10.3	761	6	CA384559	665213 NC
576	192.5	10.7	2283	9	AY418472	Mus muscu	649	185.5	10.3	987	2	BF579256	602093426
577	192.5	10.7	4329	3	AK040765	Mus muscu	650	185.5	10.3	1215	9	AY421473	Homo sapi
578	192	10.6	534	7	CR556169	DKP2p459D	651	185.5	10.3	2299	9	AY418470	Homo sapi
579	192	10.6	730	7	CO505029	GGZE8B103	652	185	10.2	736	1	AA439246	LD13756.5
580	192	10.6	839	6	CD578410	UI-M-FY0-	653	185	10.2	951	5	BQ680360	AGENCOURT
581	192	10.6	877	5	BU322077	603850177	654	185	10.2	990	9	AY418720	Pan trogl
582	192	10.6	2132	3	BC045734	Homo sapi	655	185	10.2	3638	3	AK045373	Mus muscu
583	192	10.6	4068	9	AY406426	Pan trogl	656	184.5	10.2	644	5	BQ561052	H4068A05-
584	191.5	10.6	581	8	BH269028	CH230-66P	657	184.5	10.2	700	4	BM623297	170006874
585	191.5	10.6	702	7	CR359049	170004245	658	184.5	10.2	1497	3	AK053039	Mus muscu
586	191.5	10.6	779	8	BH292378	CH230-44D	659	184	10.2	565	4	BG732685	333483 MA
587	191.5	10.6	1291	3	CR641448	Tetraodon	660	184	10.2	662	4	BM624477	170006874
588	191.5	10.6	3157	9	AY403615	Pan trogl	661	184	10.2	669	7	CF745309	UI-M-GV0-
589	191	10.6	613	4	BM487940	pgm2n.pk0	662	184	10.2	670	4	BM117149	imageqc 5
590	191	10.6	754	7	CF530715	UI-M-FY0-	663	184	10.2	791	7	CO572836	AGENCOURT
591	191	10.6	1055	4	BM551034	AGENCOURT	664	184	10.2	838	6	CD636246	56038477H
592	190.5	10.5	643	6	CA385573	666709 NC	665	184	10.2	865	5	EX725298	EX725298
593	190.5	10.5	649	7	CO505951	GGZE8B103	666	184	10.2	940	7	CK871065	AGENCOURT

667	184	10.2	970	5	BU107306	BU107306 602954168	C	740	178	9.9	653	7	CF180026	CF180026 815076 MA
668	183.5	10.2	558	4	B1067163	BI067163 pGfIn.pk0	741	178	9.9	738	5	BU448181	BU448181 603764825	
669	183.5	10.2	774	6	CB247631	UI-M-F10-	742	178	9.9	871	7	CF551909	CF551909 AGENCOURT	
670	183.5	10.2	863	6	CD514529	AGENCOURT	743	178	9.9	883	2	BF792657	BF792657 602525386	
671	183.5	10.2	904	5	BU144883	603229681	744	178	9.9	893	9	CNS02MVY	AL204631 Tetraodon	
672	183.5	10.2	974	5	BU559792	AGENCOURT	745	178	9.9	1285	3	AK010350	AK010350 Mus muscu	
673	183.5	10.2	1064	5	BX343872	BX343872	746	178	9.9	3903	3	AK076423	AK076423 Mus muscu	
674	183	10.1	550	2	AW653843	102720 MA	747	178	9.9	4544	3	AK052489	AK052489 Mus muscu	
675	183	10.1	609	1	AL673319	AL673319	748	177.5	9.8	548	5	BQ636532	hd11a05.Y	
676	183	10.1	671	5	BU344752	603407056	749	177.5	9.8	593	5	EX676568	EX676568	
677	183	10.1	865	6	CA327194	UI-M-FY0-	750	177.5	9.8	714	2	BF575974	BF575974 602132952	
678	183	10.1	914	5	BU184213	AGENCOURT	751	177.5	9.8	726	4	BJ708729	BJ708729	
679	183	10.1	1064	5	BQ055710	AGENCOURT	752	177.5	9.8	734	2	BF529510	BF529510 602043274	
680	182.5	10.1	627	7	CF534081	UI-M-GH0-	753	177.5	9.8	814	7	CV121409	CV121409 AGENCOURT	
681	182.5	10.1	717	7	CF534534	UI-N-G10-	754	177.5	9.8	951	5	BQ919823	BQ919823 AGENCOURT	
682	182.5	10.1	743	6	CD636180	56005276H	755	177.5	9.8	1088	5	BQ062993	BQ062993 AGENCOURT	
683	182.5	10.1	799	6	CD620695	56100873J	756	177.5	9.8	1516	9	AY408377	AY408377 Mus muscu	
684	182.5	10.1	862	1	AA698836	HL05774.5	757	177	9.8	371	7	CO196400	EXK004112.	
685	182.5	10.1	1086	5	BQ071438	AGENCOURT	758	177	9.8	757	6	BI559288	BI559288 AGENCOURT	
686	182	10.1	496	4	BF995884	QV1-GN020	759	177	9.8	760	4	BI559288	603241144	
687	182	10.1	867	6	CB519811	UI-M-GH0-	760	177	9.8	908	6	CD796854	CD796854 EST668215	
688	182	10.1	900	5	EX350637	EX350637	761	177	9.8	909	5	BQ435144	BQ435144 AGENCOURT	
689	182	10.1	922	5	BQ948697	AGENCOURT	762	177	9.8	2942	3	AK031495	AK031495 Mus muscu	
690	182	10.1	2197	3	CR614873	full-leng	763	177	9.8	3865	3	AF077041	AF077041 Homo sapi	
691	181.5	10.0	563	6	CA370225	650349 NC	764	176.5	9.8	587	4	BM153637	TCBAP2B11	
692	181.5	10.0	629	7	CF723085	UI-M-GV0-	765	176.5	9.8	607	5	BU948358	io50a10.Y	
693	181.5	10.0	676	2	BE731113	601566330	766	176.5	9.8	652	6	CA376364	654703 NC	
694	181.5	10.0	731	4	BU712564	BU712564	767	176.5	9.8	671	7	CK003726	AGENCOURT	
695	181.5	10.0	740	7	CO881919	BovGen.10	768	176.5	9.8	674	4	BG722412	602693645	
696	181.5	10.0	2906	3	AK051027	Mus muscu	769	176.5	9.8	679	7	CR538523	DKF2P459F	
697	181	10.0	400	7	CO339200	EP01053.3	770	176.5	9.8	706	4	BI914768	603184148	
698	181	10.0	580	7	CK89202	SGP161216	771	176.5	9.8	787	6	CD636242	56038393H	
699	181	10.0	624	2	AV988998	AV988998	772	176.5	9.8	801	4	BI553374	603193319	
700	181	10.0	975	5	EX335437	EX335437	773	176.5	9.8	816	5	BQ881760	AGENCOURT	
701	181	10.0	4168	3	BC060216	Mus muscu	774	176.5	9.8	898	5	BQ951309	AGENCOURT	
702	181	10.0	4962	3	HSM804543	Homo sapi	775	176.5	9.8	1163	9	AY421474	Pan trogl	
703	180.5	10.0	588	4	BJ031875	BJ031875	776	176.5	9.8	2334	9	AY408375	Homo sapi	
704	180.5	10.0	713	5	BU311407	603543724	777	176	9.7	524	7	CN304965	170005325	
705	180.5	10.0	802	1	AU124625	AU124625	778	176	9.7	702	5	BX299781	BX299781	
706	180	10.0	290	2	BF362977	CM4-NN008	779	176	9.7	727	6	CA346240	677090 NC	
707	180	10.0	364	1	A1940007	QVO-CT001	780	176	9.7	744	7	CK693733	ZF101-P00	
708	180	10.0	434	1	A1279142	qm18e02.x	781	176	9.7	820	6	CD758447	AGENCOURT	
709	180	10.0	442	5	BF112198	BF112198	782	176	9.7	857	7	CK192396	CK192396 EST781711	
710	180	10.0	468	2	BF110673	7n55h10.x	783	176	9.7	2178	3	AK018613	Mus muscu	
711	180	10.0	502	1	AI796834	AI796834	784	176	9.7	2369	3	BC034042	Homo sapi	
712	180	10.0	523	2	B8550993	we22h06.x	785	176	9.7	2894	3	AK033581	Mus muscu	
713	180	10.0	583	6	CB588460	AMGNNUC:N	786	175.5	9.7	608	5	BQ582107	il12h03.Y	
714	180	10.0	585	2	AV959095	AV959095	787	175.5	9.7	631	5	BX709958	BX709958	
715	180	10.0	671	7	CF366096	836780 MA	788	175.5	9.7	675	6	CB722950	UI-M-GH0-	
716	180	10.0	713	7	CN442065	BE04028A1	789	175.5	9.7	675	6	CD625574	55147942H	
717	180	10.0	776	7	CK780892	UI-M-H80-	790	175.5	9.7	702	7	CK781415	UI-M-GV0-	
718	180	10.0	796	5	EX348968	EX348968	791	175.5	9.7	758	7	CK475728	AGENCOURT	
719	180	10.0	858	6	CB196421	AGENCOURT	792	175.5	9.7	831	6	CD636244	56038469H	
720	180	10.0	866	7	CK872817	AGENCOURT	793	175.5	9.7	847	7	CK475175	AGENCOURT	
721	180	10.0	1135	7	CO27809	AGENCOURT	794	175.5	9.7	952	5	BU556507	AGENCOURT	
722	179.5	9.9	452	7	CO289807	EK072116.	795	175.5	9.7	2271	9	AY418467	Homo sapi	
723	179.5	9.9	747	7	CF948722	UI-N-HJ0-	796	175.5	9.7	2334	1	AY408376	Pan trogl	
724	179	9.9	594	4	BU489405	BU489405	797	175	9.7	324	1	AV349585	AV349585	
725	179	9.9	645	4	BM488779	pGm2n.pk0	798	175	9.7	303	1	AI422504	file0505.x	
726	179	9.9	794	7	CF533313	UI-M-FY0-	799	175	9.7	526	4	BI045435	BI045435 MR3-FN020	
727	179	9.9	811	6	CD636248	56038485H	800	175	9.7	606	6	CB273099	mai66h01.	
728	179	9.9	939	7	CK865923	AGENCOURT	801	175	9.7	631	4	BI553967	603193844	
729	179	9.9	2453	3	AK033574	Mus muscu	802	175	9.7	651	7	CK679637	ZF101-P00	
730	179	9.9	3939	3	AK036698	Mus muscu	803	175	9.7	660	5	BM986302	EST531210	
731	178.5	9.9	710	6	CA378084	656807 NC	804	175	9.7	714	6	CB527370	UI-M-FY0-	
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735	178.5	9.9	894	5	BQ642447	AGENCOURT	808	174.5	9.7	550	7	CF544600	DKF2p459F	
736	178.5	9.9	910	5	BQ895192	AGENCOURT	809	174.5	9.7	582	5	BP316461	BP316461	
737	178.5	9.9	912	5	BU154175	AGENCOURT	810	174.5	9.7	752	5	BU0707206	UI-M-FR0-	
738	178.5	9.9	967	1	AL538691	AL538691	811	174.5	9.7	775	1	AU006387	AU006387	
739	178	9.9	208	1	AU281844	AU281844	812	174.5	9.7	836	2	BE747501	601573016	

813 174.5 9.7 CF374272 AGENCOURT
814 174.5 9.7 847 5 BX403262
815 174 285 5 BX209637
816 174 581 5 BP2117876
817 174 625 1 AU134398
818 174 669 5 BX670963
819 174 736 8 AZ989621
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821 174 2756 3 AK038385
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823 174 4152 3 AK079332
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882 171 9.5 1386 3 CF608576
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884 170.5 9.4 484 5 BX099260
885 170.5 9.4 526 7 CN677790

886 170.5 9.4 585 5 BP377151
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954 167.5 9.3 573 1 AI685262
955 167.5 9.3 725 7 CK691938
956 167.5 9.3 736 7 CK367468
957 167.5 9.3 786 7 BU382983
958 167.5 9.3 798 7 CK481268

BP377151 BP377151
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CK481268 AGENCOURT

959 167.5 9.3 817 4 BG91J2522 602806620 BG91J2522 602806620 1032 164 9.1 1164 3 AK008187 Mus muscu
960 167.5 9.3 831 5 BU491858 604131047 BU491858 604131047 1033 164 9.1 1639 3 AK032833 Mus muscu
961 167.5 9.3 930 7 CK407450 AUF Iflvzr CK407450 AUF Iflvzr 1034 164 9.1 1701 3 AK013156 Mus muscu
962 167.5 9.3 981 5 BG964950 AGENCOURT BG964950 AGENCOURT 1035 164 9.1 1930 3 AK003326 Mus muscu
963 167.5 9.3 1469 3 AK044527 Mus muscu AK044527 Mus muscu 1036 164 9.1 2814 3 CR593108 full-leng
964 167 9.2 514 6 CB716703 AMGNNUC:N CB716703 AMGNNUC:N 1037 163.5 9.1 469 2 AW414520 48011 MAR
965 167 9.2 608 6 CD636186 56020455H CD636186 56020455H 1038 163.5 9.1 584 6 CB586237 AMGNNUC:M
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979 166 9.2 583 4 BG223754 1M00018F0 BG223754 1M00018F0 1052 163.5 9.1 923 7 CN322132 AGENCOURT
980 166 9.2 647 7 CK781448 UI-M-GV0- CK781448 UI-M-GV0- 1053 163.5 9.1 934 7 CK868656 AGENCOURT
981 166 9.2 656 7 CK659672 LPI7591.5 CK659672 LPI7591.5 1054 163.5 9.1 951 7 CK866211 AGENCOURT
982 166 9.2 680 7 CF899461 A0303E02- CF899461 A0303E02- 1055 163.5 9.1 1776 3 AK010153 Mus muscu
983 166 9.2 740 4 BJ720179 BJ720179 1056 163.5 9.1 3248 3 AK004821 Mus muscu
984 166 9.2 796 6 CD653854 AGENCOURT CD653854 AGENCOURT 1057 163.5 9.1 3590 3 AY402969 Homo sapi
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987 166 9.2 910 5 BX324896 BX324896 1060 163 9.0 444 9 AY402971 Mus muscu
988 165.5 9.2 420 6 CB798880 AMGNNUC:N CB798880 AMGNNUC:N 1061 163 9.0 548 7 CO323280 EKI90105.
989 165.5 9.2 517 6 CD290273 St-Pu538. CD290273 St-Pu538. 1062 163 9.0 557 7 CK541739 Mus muscu
990 165.5 9.2 589 1 AA606149 f616d03.8 AA606149 f616d03.8 1063 163 9.0 569 4 BM090970 i918e09.x
991 165.5 9.2 634 6 CD803622 UI-M-GV0- CD803622 UI-M-GV0- 1064 163 9.0 635 1 AL878745 AL878745
992 165.5 9.2 654 7 CF744226 UI-M-GV0- CF744226 UI-M-GV0- 1065 163 9.0 645 5 BX276614 BX276614
993 165.5 9.2 699 6 CD802719 UI-M-GV0- CD802719 UI-M-GV0- 1066 163 9.0 658 5 BX260070 BX260070
994 165.5 9.2 797 7 CK670310 AGENCOURT CK670310 AGENCOURT 1067 163 9.0 661 1 AL872179 AL872179
995 165.5 9.2 793 7 CK636666 UI-M-HN0- CK636666 UI-M-HN0- 1068 163 9.0 730 5 BU709173 UI-M-EV0-
996 165.5 9.2 798 7 CK870327 AGENCOURT CK870327 AGENCOURT 1069 163 9.0 744 4 BJ780707 BJ780707
997 165.5 9.2 886 5 BU528897 AGENCOURT BU528897 AGENCOURT 1070 163 9.0 790 1 AU006391 AU006391
998 165.5 9.2 939 5 BQ646105 AGENCOURT BQ646105 AGENCOURT 1071 163 9.0 803 7 CK311931 SB02010A2
999 165.5 9.2 1057 5 BX396408 BX396408 1072 163 9.0 904 4 BG760809 BG760809
1000 165.5 9.2 1138 7 CK030399 AGENCOURT CK030399 AGENCOURT 1073 163 9.0 935 4 BG923654 602823392
1001 165 9.1 618 4 B1065024 p6fin.pk0 B1065024 p6fin.pk0 1074 163 9.0 1181 3 CR722859 Tetraodon
1002 165 9.1 624 1 AL968116 AL968116 1075 163 9.0 1694 3 AK040711 Mus muscu
1003 165 9.1 641 1 AL892168 AL892168 1076 162.5 9.0 562 1 AV614571 AV614571
1004 165 9.1 645 1 AL846277 AL846277 1077 162.5 9.0 580 4 BG710895 BG710895
1005 165 9.1 693 7 CK781175 UI-M-GV0- CK781175 UI-M-GV0- 1078 162.5 9.0 590 7 CK824237 I918e09.y
1006 165 9.1 700 5 BX331242 BX331242 1079 162.5 9.0 601 1 AL703664 DKF2p686A
1007 165 9.1 748 6 CD079492 MA3-9999U CD079492 MA3-9999U 1080 162.5 9.0 685 7 CN537909 UI-M-HS0-
1008 165 9.1 775 7 CN532584 UI-M-HQ0- CN532584 UI-M-HQ0- 1081 162.5 9.0 699 7 CF536456 UI-M-G10-
1009 165 9.1 780 7 CF539770 UI-M-GV0- CF539770 UI-M-GV0- 1082 162.5 9.0 708 6 CA439206 UI-H-D10-
1010 165 9.1 786 7 CF216645 AGENCOURT CF216645 AGENCOURT 1083 162.5 9.0 728 5 BX495682 DKF2p779H
1011 165 9.1 898 7 CF223675 AGENCOURT CF223675 AGENCOURT 1084 162.5 9.0 755 7 CK018234 AGENCOURT
1012 165 9.1 912 7 CN093676 EC2BBA8CB CN093676 EC2BBA8CB 1085 162.5 9.0 763 4 BG921356 BG921356
1013 165 9.1 1137 6 CD507144 CDA83-C06 CD507144 CDA83-C06 1086 162.5 9.0 763 4 BI080254 602824217
1014 164.5 9.1 559 5 BP370855 BP370855 1087 162.5 9.0 779 6 CD636252 60249016H
1015 164.5 9.1 561 7 CK618594 mk14a07.y CK618594 mk14a07.y 1088 162.5 9.0 814 7 CO810649 AGENCOURT
1016 164.5 9.1 604 5 BUI02167 PRODIGID BUI02167 PRODIGID 1089 162.5 9.0 856 5 BUI130635 603118991
1017 164.5 9.1 683 4 B1393255 p6pin.pk0 B1393255 p6pin.pk0 1090 162.5 9.0 860 6 CB193630 AGENCOURT
1018 164.5 9.1 743 6 CD494572 CDA11-E10 CD494572 CDA11-E10 1091 162.5 9.0 925 4 BI872091 BI872091
1019 164.5 9.1 836 8 BH044916 RPT-24-3 BH044916 RPT-24-3 1092 162.5 9.0 930 7 CK409630 AUF Iflvzr
1020 164.5 9.1 839 7 CO922821 AGENCOURT CO922821 AGENCOURT 1093 162.5 9.0 933 5 BU856183 AGENCOURT
1021 164.5 9.1 859 4 B1413783 602987688 B1413783 602987688 1094 162.5 9.0 3905 3 AK083069 Mus muscu
1022 164 9.1 387 7 CO298825 EK173933. CO298825 EK173933. 1095 162 9.0 455 4 BG358967 BOVNS1-00
1023 164 9.1 599 8 A2585520 1M0390E18 A2585520 1M0390E18 1096 162 9.0 571 7 CK707773 2F2701-P00
1024 164 9.1 627 7 CN983254 51876.126 CN983254 51876.126 1097 162 9.0 625 5 BP277969 BP277969
1025 164 9.1 644 6 CD372018 UI-R-GO0- CD372018 UI-R-GO0- 1098 162 9.0 660 7 CF532017 UI-M-FX0-
1026 164 9.1 651 6 CD806831 UI-M-GW0- CD806831 UI-M-GW0- 1099 162 9.0 699 7 CF366889 841594 MA
1027 164 9.1 720 6 CB520196 UI-M-G10- CB520196 UI-M-G10- 1100 162 9.0 870 4 BI197164 602756667
1028 164 9.1 767 4 BG570299 602838903 BG570299 602838903 1101 162 9.0 891 6 CB194073 AGENCOURT
1029 164 9.1 883 8 BZ222298 BZ230-324 BZ222298 BZ230-324 1102 162 9.0 962 6 CD080179 CD080179
1030 164 9.1 924 5 BQ933843 AGENCOURT BQ933843 AGENCOURT 1103 162 9.0 1056 5 BM925845 AGENCOURT
1031 164 9.1 964 5 BQ715124 AGENCOURT BQ715124 AGENCOURT 1104 161.5 8.9 581 5 BP346467 BP346467

AK008187 Mus muscu
AK032833 Mus muscu
AK013156 Mus muscu
AK003326 Mus muscu
CR593108 full-leng
AW414520 48011 MAR
CB586237 AMGNNUC:M
B1654678 603285596
CN537405 UI-M-HS0-
BB525933 BB525933
B1662853 603286287
CK951501 4091020 B
CF998350 AGENCOURT
CF996540 AGENCOURT
CK867184 AGENCOURT
CF996588 AGENCOURT
CA382308 662081 NC
B1554904 602326202
CN501295 AGENCOURT
CF266068 AGENCOURT
CN322132 AGENCOURT
CK868656 AGENCOURT
CK866211 AGENCOURT
AK010153 Mus muscu
AK004821 Mus muscu
AY402969 Homo sapi
AY402970 Pan trogl
AY402971 Mus muscu
CO323280 EKI90105.
CK541739 Mus muscu
BM090970 i918e09.x
AL878745 AL878745
BX276614 BX276614
BX260070 BX260070
AL872179 AL872179
UI-M-EV0-
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AU006391 AU006391
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BG760809 602717170
BG923654 602823392
CR722859 Tetraodon
AK040711 Mus muscu
AV614571 AV614571
BG710895 p6lin.pk0
CK824237 I918e09.y
AL703664 DKF2p686A
CN537909 UI-M-HS0-
CF536456 UI-M-G10-
CA439206 UI-H-D10-
BX495682 DKF2p779H
CK018234 AGENCOURT
BG921356 602824217
BI080254 60249016H
CD636252 60249016H
CO810649 AGENCOURT
BUI130635 603118991
CB193630 AGENCOURT
BI872091 BI872091
CK409630 AUF Iflvzr
BU856183 AGENCOURT
AK083069 Mus muscu
BG358967 BOVNS1-00
CK707773 2F2701-P00
BP277969 BP277969
CF532017 UI-M-FX0-
CF366889 841594 MA
BI197164 602756667
CB194073 AGENCOURT
CD080179 MA3-9999U
BM925845 AGENCOURT
BP346467 BP346467

1105	161.5	8.9	583	5	BF347694	BP347694	1178	159.5	8.8	641	7	CK693848	CK693848	ZFI101-P00
c1106	161.5	8.9	622	2	BE864980	UI-M-BH1-	1179	159.5	8.8	699	4	BM728584	UI-E-E30-	BM728584
1107	161.5	8.9	679	7	CF900715	A0319A05-	c1180	159.5	8.8	717	5	BQ206762	UI-R-D21-	BQ206762
1108	161.5	8.9	694	7	CF792923	AGENCOURT	1181	159.5	8.8	801	7	CF182513	UI-M-EY0-	CF182513
c1109	161.5	8.9	708	5	EX881610	EX881610	1182	159.5	8.8	806	4	BI762516	603048638	BI762516
1110	161.5	8.9	723	4	BG974950	602844949	1183	159.5	8.8	808	4	BI833165	603090890	BI833165
1111	161.5	8.9	731	7	CN528054	UI-M-HQ0-	1184	159.5	8.8	832	2	BE563419	603133546	BE563419
1112	161.5	8.9	733	4	BG545860	602573145	1185	159.5	8.8	850	1	AU133135	AU133135	AU133135
1113	161.5	8.9	819	7	CK865025	AGENCOURT	1186	159.5	8.8	882	7	BK728325	BK728325	BK728325
1114	161.5	8.9	820	6	CD620694	60100873H	1187	159.5	8.8	938	7	CK866851	AGENCOURT	CK866851
1115	161.5	8.9	855	6	CS588927	AGENCOURT	1188	159.5	8.8	940	5	EX369835	EX369835	EX369835
1116	161.5	8.9	874	7	CO733078	SILF02C04	1189	159.5	8.8	941	5	BU912943	AGENCOURT	BU912943
1117	161.5	8.9	878	5	BQ887533	AGENCOURT	1190	159.5	8.8	947	5	BQ644258	AGENCOURT	BQ644258
1118	161.5	8.9	910	5	BQ850842	AGENCOURT	1191	159.5	8.8	2748	3	AK036352	Mus muscu	AK036352
1119	161.5	8.9	979	4	BG420574	602448438	1192	159	8.8	259	2	BB607028	BB607028	BB607028
1120	161	8.9	489	2	BF705825	268993 MA	1193	159	8.8	451	1	AL119880	DKF2P761M	AL119880
1121	161	8.9	556	7	CR452315	CR452315	1194	159	8.8	557	6	CA563258	K0311H02-	CA563258
1122	161	8.9	581	4	BU070444	BU070444	1195	159	8.8	599	4	BU058708	BU058708	BU058708
1123	161	8.9	670	7	CN538094	UI-M-HS0-	1196	159	8.8	692	6	CB526667	UI-M-FY0-	CB526667
1124	161	8.9	673	7	CN366089	170005313	1197	159	8.8	719	6	CB724268	UI-M-FY0-	CB724268
1125	161	8.9	714	7	CN366080	170004243	1198	159	8.8	738	7	CR564541	CR564541	CR564541
1126	161	8.9	717	5	BU321343	603854520	1199	159	8.8	931	5	EX336244	EX336244	EX336244
1127	161	8.9	730	7	CN366076	170005331	1200	159	8.8	934	5	BU903988	AGENCOURT	BU903988
1128	161	8.9	732	7	CN304969	170005325	1201	159	8.8	1013	3	CN801753	ILLUMIGEN	CN801753
1129	161	8.9	738	4	BG864104	602797704	1202	159	8.8	1677	3	AK030635	Mus muscu	AK030635
1130	161	8.9	757	7	CN304990	170004240	1203	159	8.8	3687	3	AK076215	Mus muscu	AK076215
1131	161	8.9	766	5	EX869908	EX869908	1204	158.5	8.8	569	5	BP377634	BP377634	BP377634
1132	161	8.9	770	5	B0444091	UI-M-EX0-	1205	158.5	8.8	574	2	BP540423	BP540423	BP540423
1133	161	8.9	879	6	CD557080	AGENCOURT	1206	158.5	8.8	582	5	BP208357	BP208357	BP208357
1134	161	8.9	887	7	CK408075	AUF_ILFVr	1207	158.5	8.8	583	5	BP357634	BP357634	BP357634
1135	161	8.9	901	7	CN319156	AGENCOURT	1208	158.5	8.8	586	5	BP254888	BP254888	BP254888
1136	161	8.9	902	7	CR442151	CR442151	1209	158.5	8.8	600	5	BU918743	5033-34 M	BU918743
1137	161	8.9	905	5	BU182251	AGENCOURT	1210	158.5	8.8	652	1	AL846235	AL846235	AL846235
1138	161	8.9	908	5	BX386931	BX386931	1211	158.5	8.8	760	6	CA319537	UI-M-FW0-	CA319537
1139	161	8.9	922	5	BQ894075	AGENCOURT	1212	158.5	8.8	828	7	CV077258	AGENCOURT	CV077258
1140	161	8.9	939	4	BM451147	BM451147	1213	158.5	8.8	853	5	BQ719866	BQ719866	BQ719866
1141	161	8.9	1673	3	CR617412	full-leng	1214	158.5	8.8	906	5	BU916159	AGENCOURT	BU916159
1142	161	8.9	3533	1	BC057284	Hom sapi	c1215	158.5	8.8	964	9	CNS05CLJ	Tetraodon	AL331264
1143	160.5	8.9	460	1	AA155245	Hom sapi	1216	158.5	8.8	1057	5	BK398530	BK398530	BK398530
1144	160.5	8.9	486	7	CR746947	CR746947	1217	158.5	8.8	1154	6	CD503211	CD503211	CD503211
1145	160.5	8.9	530	2	BE226313	ia19a09.Y	1218	158.5	8.8	1296	7	CF110468	Shultzomi	CF110468
1146	160.5	8.9	582	5	BP361289	BP361289	1219	158.5	8.8	1580	9	AY411535	Pan trogl	AY411535
1147	160.5	8.9	592	7	AV617433	AV617433	1220	158.5	8.8	3751	9	AY404031	Homo sapi	AY404031
1148	160.5	8.9	602	1	CF727943	UI-M-HB0-	1221	158	8.7	382	6	CB809130	AMGNUG:C	CB809130
1149	160.5	8.9	606	5	BP505184	BP505184	1222	158	8.7	448	6	BY568324	BY568324	BY568324
1150	160.5	8.9	711	4	BG115636	602316760	1223	158	8.7	450	6	BY6731087	ma81a06.	BY6731087
1151	160.5	8.9	715	7	CN426880	170005321	1224	158	8.7	453	6	BY565338	BY565338	BY565338
1152	160.5	8.9	782	7	CK026234	AGENCOURT	1225	158	8.7	539	7	CN679683	E0127F05-	CN679683
1153	160.5	8.9	798	6	CD656120	AGENCOURT	1226	158	8.7	582	5	BP251115	BP251115	BP251115
1154	160.5	8.9	800	5	BU319927	603487913	1227	158	8.7	595	2	BE291062	601083890	BE291062
1155	160.5	8.9	884	4	BI771277	603054624	c1228	158	8.7	614	1	AI809639	wf31g05.X	AI809639
1156	160.5	8.9	889	7	CF266344	AGENCOURT	1229	158	8.7	670	4	BG085642	H3115G08-	BG085642
1157	160.5	8.9	966	7	CF995094	AGENCOURT	1230	158	8.7	671	1	AL859372	AL859372	AL859372
1158	160.5	8.9	3146	3	AK084850	Mus muscu	1231	158	8.7	716	5	BU281132	BU281132	BU281132
1159	160	8.9	456	7	CF796349	892593 NC	1232	158	8.7	716	6	CA376321	654651 NC	CA376321
1160	160	8.9	630	6	CA376096	654336 NC	1233	158	8.7	717	7	CF724990	UI-M-G20-	CF724990
1161	160	8.9	721	6	CA749345	UI-M-FY0-	1234	158	8.7	790	7	CK677667	ZFI101-P00	CK677667
1162	160	8.9	727	7	CK457803	UI-M-HN0-	1235	158	8.7	818	5	BU306680	BU306680	BU306680
1163	160	8.9	740	7	CF533274	UI-M-FY0-	c1236	158	8.7	822	7	CO870384	CO870384	CO870384
1164	160	8.9	819	5	BK424510	BK424510	1237	158	8.7	827	4	BI463685	603207357	BI463685
1165	160	8.9	820	7	CO395177	AGENCOURT	1238	158	8.7	899	7	CK866029	AGENCOURT	CK866029
1166	160	8.9	824	5	BQ444246	UI-M-EX0-	1239	158	8.7	914	5	BK089809	BK089809	BK089809
1167	160	8.9	824	7	CK470323	AGENCOURT	1240	158	8.7	935	5	BK853896	BK853896	BK853896
1168	160	8.9	865	1	AI134784	GHI2331.5	1241	157.5	8.7	582	5	BP250662	BP250662	BP250662
1169	160	8.9	1092	7	CN642862	ILLUMIGEN	1242	157.5	8.7	600	5	BU922970	BU922970	BU922970
1170	160	8.9	3811	3	AK031246	Mus muscu	1243	157.5	8.7	617	5	BQ359313	7042-78 M	BQ359313
1171	159.5	8.8	383	1	AA401292	zv63g05.r	c1244	157.5	8.7	636	5	BU011548	PRODIGID	BU011548
1172	159.5	8.8	493	6	CD739385	4027892.1	1245	157.5	8.7	650	4	BM049915	BM049915	BM049915
1173	159.5	8.8	538	2	BF022068	uy46d08.Y	1246	157.5	8.7	664	4	BI373259	RE60514.5	BI373259
1174	159.5	8.8	582	5	BP315255	BP315255	1247	157.5	8.7	666	2	BE392233	601308119	BE392233
1175	159.5	8.8	600	5	BU101549	PRODIGID	1248	157.5	8.7	721	5	BQ769295	UI-M-F10-	BQ769295
1176	159.5	8.8	615	4	BI067145	pgfin.pk0	1249	157.5	8.7	755	7	CK868145	AGENCOURT	CK868145
1177	159.5	8.8	629	1	AL657340	AL657340	1250	157.5	8.7	762	7	CK397238	AGENCOURT	CK397238

1251	157.5	8.7	776	7	CF737877	CF737877	UI-M-HDO-	1324	156	8.6	477	7	CN359280	CN359280	170005319
1252	157.5	8.7	796	5	BX923146	BX923146	BX923146	1325	156	8.6	596	1	AL5599774	AL5599774	DKF720313M
1253	157.5	8.7	818	5	CK968629	CK968629	AGENCOURT	1326	156	8.6	628	4	BJ685150	BJ685150	BJ685150
1254	157.5	8.7	860	6	CD627471	CD627471	56067512J	1327	156	8.6	653	7	CK003476	CK003476	AGENCOURT
1255	157.5	8.7	901	5	BQ8881261	BQ8881261	AGENCOURT	1328	156	8.6	691	1	AV384111	AV384111	AV384111
1256	157.5	8.7	904	5	BQ685640	BQ685640	AGENCOURT	1329	156	8.6	729	4	BM6211283	BM6211283	170006874
1257	157.5	8.7	932	5	BX452370	BX452370	BX452370	1330	156	8.6	740	7	CN531505	CN531505	UI-M-HQO-
1258	157.5	8.7	952	5	BX514323	BX514323	AGENCOURT	1331	156	8.6	760	7	CN531514	CN531514	UI-M-HQO-
1259	157.5	8.7	953	7	CK865103	CK865103	AGENCOURT	1332	156	8.6	767	2	AW175139	AW175139	fi32f09.y
1260	157.5	8.7	958	2	BF795536	BF795536	602259467	1333	156	8.6	775	6	CD080814	CD080814	MA3-9999U
1261	157.5	8.7	987	5	BX375028	BX375028	BX375028	1334	156	8.6	780	5	BX444240	BX444240	EX444240
1262	157.5	8.7	1008	5	BX424991	BX424991	BX424991	1335	156	8.6	784	6	CA350777	CA350777	621665 NC
1263	157.5	8.7	1046	4	BM552640	BM552640	AGENCOURT	1336	156	8.6	795	7	CO248560	CO248560	AGENCOURT
1264	157.5	8.7	1072	7	CN642560	CN642560	ILLUMIGEN	1337	156	8.6	810	7	CO799885	CO799885	AGENCOURT
1265	157.5	8.7	1488	3	CK608619	CK608619	full-leng	1338	156	8.6	1096	7	CN642525	CN642525	ILLUMIGEN
1266	157.5	8.7	1594	3	CK617107	CK617107	full-leng	1339	156	8.6	2036	3	AK089498	AK089498	Mus muscu
1267	157.5	8.7	1742	9	AY413879	AY413879	Mus muscu	1340	156	8.6	2850	3	AK047868	AK047868	Mus muscu
1268	157.5	8.7	2090	3	AK003152	AK003152	Mus muscu	1341	156	8.6	3312	3	AK004947	AK004947	Mus muscu
1269	157.5	8.7	2209	3	AK017447	AK017447	Mus muscu	1342	156	8.6	3449	3	AK041299	AK041299	Mus muscu
1270	157.5	8.7	2735	3	AK029024	AK029024	Mus muscu	1343	156	8.6	3559	9	AY404032	AY404032	Pan trogl
1271	157.5	8.7	3652	3	AK030851	AK030851	Mus muscu	1344	156	8.6	3687	3	AK079247	AK079247	Mus muscu
1272	157.5	8.7	4118	3	AK031391	AK031391	Mus muscu	1345	155.5	8.6	409	2	BE226893	BE226893	UG74A09.Y
1273	157	8.7	578	5	BP368062	BP368062	BP368062	1346	155.5	8.6	581	5	BP193219	BP193219	BP193219
1274	157	8.7	608	5	BX917921	BX917921	BX917921	1347	155.5	8.6	581	5	BP195771	BP195771	BP195771
1275	157	8.7	612	4	BM795050	BM795050	K-BST0076	1348	155.5	8.6	605	7	CF368297	CF368297	852930 MA
1276	157	8.7	641	2	BB664453	BB664453	BB664453	1349	155.5	8.6	617	5	BM305475	BM305475	BM305475
1277	157	8.7	690	6	CD636219	CD636219	56031467J	1350	155.5	8.6	638	6	CD629100	CD629100	56059934H
1278	157	8.7	695	7	CK949734	CK949734	4074697 B	1351	155.5	8.6	649	1	AL864304	AL864304	AL864304
1279	157	8.7	722	6	CD805128	CD805128	UI-M-GWO-	1352	155.5	8.6	702	9	CNS02PTU	CNS02PTU	Tetraodon
1280	157	8.7	727	7	CK961924	CK961924	4076329 B	1353	155.5	8.6	718	6	CD636336	CD636336	56048995J
1281	157	8.7	737	4	BI915307	BI915307	603184382	1354	155.5	8.6	727	4	BM290618	BM290618	EST577152
1282	157	8.7	757	6	CB519019	CB519019	UI-M-GHO-	1355	155.5	8.6	769	7	CN505057	CN505057	AGENCOURT
1283	157	8.7	781	6	CD348686	CD348686	UI-M-FYO-	1356	155.5	8.6	786	7	CN302526	CN302526	170006001
1284	157	8.7	805	1	AU131165	AU131165	AU131165	1357	155.5	8.6	796	5	BX923150	BX923150	EX923150
1285	157	8.7	826	6	CB165550	CB165550	BEQ603160	1358	155.5	8.6	796	5	EX926278	EX926278	EX926278
1286	157	8.7	848	7	CN020324	CN020324	AGENCOURT	1359	155.5	8.6	797	6	CD642524	CD642524	AGENCOURT
1287	157	8.7	850	5	BX739790	BX739790	BX739790	1360	155.5	8.6	850	5	BP264898	BP264898	BP264898
1288	157	8.7	876	7	CK948326	CK948326	4073246 B	1361	155.5	8.6	850	7	CO557070	CO557070	AGENCOURT
1289	157	8.7	886	5	BQ945091	BQ945091	AGENCOURT	1362	155.5	8.6	861	6	CD636209	CD636209	56031050J
1290	157	8.7	896	5	BX379273	BX379273	BX379273	1363	155.5	8.6	880	5	BU542115	BU542115	AGENCOURT
1291	157	8.7	910	5	BU192138	BU192138	AGENCOURT	1364	155.5	8.6	979	7	CN642097	CN642097	ILLUMIGEN
1292	157	8.7	930	7	CN315936	CN315936	AGENCOURT	1365	155.5	8.6	1039	5	BQ057979	BQ057979	AGENCOURT
1293	157	8.7	933	9	AY417086	AY417086	Mus muscu	1366	155.5	8.6	1091	7	CK232190	CK232190	ILLUMIGEN
1294	157	8.7	1020	4	BM548873	BM548873	AGENCOURT	1367	155.5	8.6	1376	3	CK635265	CK635265	Tetraodon
1295	157	8.7	1034	1	AL553289	AL553289	AL553289	1368	155.5	8.6	4017	3	AK028983	AK028983	Mus muscu
1296	157	8.7	1071	5	BU503048	BU503048	AGENCOURT	1369	155.5	8.6	5635	9	AY412619	AY412619	Mus muscu
1297	157	8.7	1127	1	AL549623	AL549623	AL549623	1370	155	8.6	427	7	CO436236	CO436236	ddPCR2_17
1298	157	8.7	1514	3	CK617300	CK617300	full-leng	1371	155	8.6	545	4	BM440456	BM440456	pgr1n.pk0
1299	157	8.7	1867	3	AK087272	AK087272	Mus muscu	1372	155	8.6	571	4	BJ124803	BJ124803	BJ124803
1300	157	8.7	1892	3	CK622259	CK622259	full-leng	1373	155	8.6	602	6	CA317092	CA317092	UI-M-FWO-
1301	157	8.7	2791	3	BC013698	BC013698	Homo sapi	1374	155	8.6	617	6	CD636187	CD636187	56020455J
1302	156.5	8.7	568	1	AI629069	AI629069	fc09b12.y	1375	155	8.6	669	5	BU696122	BU696122	LL21n1269
1303	156.5	8.7	618	4	BI065290	BI065290	pgr1n.pk0	1376	155	8.6	694	6	CD345249	CD345249	UI-M-FYO-
1304	156.5	8.7	627	4	BJ112590	BJ112590	BJ112590	1377	155	8.6	705	7	CK753907	CK753907	CR753907
1305	156.5	8.7	630	1	AI295266	AI295266	LP08849.5	1378	155	8.6	710	7	CN053418	CN053418	Salamande
1306	156.5	8.7	630	5	BQ390372	BQ390372	NISC mc12	1379	155	8.6	726	7	CN302510	CN302510	170005318
1307	156.5	8.7	684	6	CA354756	CA354756	626578 NC	1380	155	8.6	739	7	CN302524	CN302524	170004710
1308	156.5	8.7	725	4	BI736575	BI736575	603361039	1381	155	8.6	755	7	CN302501	CN302501	170005322
1309	156.5	8.7	740	5	BU058190	BU058190	UI-M-F00-	1382	155	8.6	778	7	CK634628	CK634628	UI-M-HNO-
1310	156.5	8.7	751	5	BP673676	BP673676	BP673676	1383	155	8.6	781	5	BU772811	BU772811	603581533
1311	156.5	8.7	768	7	CN172200	CN172200	AGENCOURT	1384	155	8.6	792	4	BI378797	BI378797	603581533
1312	156.5	8.7	776	5	BQ442214	BQ442214	UI-M-EXO-	1385	155	8.6	793	7	CF288820	CF288820	AGENCOURT
1313	156.5	8.7	858	5	BU470108	BU470108	603365843	1386	155	8.6	833	1	AA941031	AA941031	LD23480.5
1314	156.5	8.7	914	7	CF594392	CF594392	AGENCOURT	1387	155	8.6	836	4	BI824985	BI824985	603033468
1315	156.5	8.7	928	5	BQ733716	BQ733716	AGENCOURT	1388	155	8.6	891	6	CD384890	CD384890	AGENCOURT
1316	156.5	8.7	937	7	CO248697	CO248697	AGENCOURT	1389	155	8.6	907	5	BQ928239	BQ928239	AGENCOURT
1317	156.5	8.7	1004	5	BU134013	BU134013	603121573	1390	155	8.6	913	2	BE912082	BE912082	601663261
1318	156.5	8.7	1014	6	CB206098	CB206098	AGENCOURT	1391	155	8.6	922	5	BU518914	BU518914	AGENCOURT
1319	156.5	8.7	1028	7	CN642108	CN642108	ILLUMIGEN	1392	155	8.6	933	9	AY417084	AY417084	Homo sapi
1320	156.5	8.7	1319	7	CV182470	CV182470	pan trogl	1393	155	8.6	941	5	BQ928243	BQ928243	AGENCOURT
1321	156.5	8.7	3465	9	AY418996	AY418996	AY418996	1394	155	8.6	993	1	AL560725	AL560725	AL560725
1322	156.5	8.7	3689	3	AK004723	AK004723	Mus muscu	1395	155	8.6	1047	7	CK230378	CK230378	ILLUMIGEN
1323	156.5	8.7	3865	3	AK087355	AK087355	Mus muscu	1396	155	8.6	1971	3	AK076123	AK076123	Mus muscu

1397	155	8.6	1992	3	AK034125	Mus muscu	AK034125	152.5	8.4	430	5	BU947992	io56ell.y	
1398	155	8.6	3133	3	AK085723	Mus muscu	AK085723	1471	152.5	8.4	548	5	BX271825	BW271825
1399	154.5	8.6	247	7	CR474371		CR474371	1472	152.5	8.4	594	5	BW221728	BW221728
1400	154.5	8.6	450	1	AA168307		AA168307	1473	152.5	8.4	668	4	BI394312	p9pln.pk0
1401	154.5	8.6	498	6	CB070225		CB070225	1474	152.5	8.4	709	5	BU116030	603488360
1402	154.5	8.6	506	7	CO328919		CO328919	1475	152.5	8.4	710	9	AG286398	Mus muscu
1403	154.5	8.6	598	1	AL856990		AL856990	1476	152.5	8.4	723	6	CB526860	UI-M-FY0-
1404	154.5	8.6	648	8	AK379719		AK379719	1477	152.5	8.4	745	4	BI080347	602876784
1405	154.5	8.6	670	5	BX622375		BX622375	1478	152.5	8.4	768	5	EX918182	EX918182
1406	154.5	8.6	677	5	BU204691		BU204691	1479	152.5	8.4	769	5	BX856025	BX856025
1407	154.5	8.6	689	7	CF533968		CF533968	1480	152.5	8.4	822	6	CB245137	UI-M-FY0-
1408	154.5	8.6	702	6	CD620688		CD620688	1481	152.5	8.4	833	7	CN837756	AGENCOURT
1409	154.5	8.6	715	4	BA487033		BA487033	1482	152.5	8.4	867	6	CA788252	AGENCOURT
1410	154.5	8.6	732	4	BW292745		BW292745	1483	152.5	8.4	912	6	CD515059	AGENCOURT
1411	154.5	8.6	778	5	BQ745865		BQ745865	1484	152.5	8.4	950	1	AL523470	AL523470
1412	154.5	8.6	783	6	CD636195		CD636195	1485	152.5	8.4	1004	9	CN642068	ILLUMIGEN
1413	154.5	8.6	808	4	BI253511		BI253511	1486	152.5	8.4	1028	9	CNS0070A	ILLUMIGEN
1414	154.5	8.6	811	7	CF5339481		CF5339481	1487	152.5	8.4	2338	3	AK032604	Mus muscu
1415	154.5	8.6	840	5	BX729243		BX729243	1488	152.5	8.4	4050	3	AK049704	Mus muscu
1416	154.5	8.6	1002	4	BM472841		BM472841	1489	152.5	8.4	5655	9	AY412618	Pan trogl
1417	154.5	8.6	1029	7	BN642582		BN642582	1490	152	8.4	530	7	CK580486	IST WIS 2
1418	154.5	8.6	1311	5	BP938160		BP938160	1491	152	8.4	602	5	BU741589	UI-E-EO1-
1419	154.5	8.6	5724	9	AY412617		AY412617	1492	152	8.4	622	8	BH374792	AG-ND-138
1420	154	8.5	513	4	EM152259		EM152259	1493	152	8.4	717	4	BM622248	170006874
1421	154	8.5	525	5	BX317406		BX317406	1494	152	8.4	731	6	CA750190	UI-M-FD0-
1422	154	8.5	563	5	BQ637244		BQ637244	1495	152	8.4	808	7	CF744297	UI-M-GV0-
1423	154	8.5	588	2	AW977089		AW977089	1496	152	8.4	878	7	CN643444	ILLUMIGEN
1424	154	8.5	595	4	BJ071900		BJ071900	1497	152	8.4	888	5	BQ945830	AGENCOURT
1425	154	8.5	620	1	AL876779		AL876779	1498	152	8.4	919	7	CN646263	ILLUMIGEN
1426	154	8.5	620	1	AL892876		AL892876	1499	152	8.4	925	6	CA982594	AGENCOURT
1427	154	8.5	659	7	CK639629		CK639629	1500	152	8.4	979	7	CN642895	ILLUMIGEN
1428	154	8.5	677	7	CV027585		CV027585							
1429	154	8.5	684	6	CA307499		CA307499							
1430	154	8.5	692	7	CN302521		CN302521							
1431	154	8.5	723	6	CD217761		CD217761							
1432	154	8.5	735	4	BG468165		BG468165							
1433	154	8.5	814	7	CR871988		CR871988							
1434	154	8.5	2151	3	AK011949		AK011949							
1435	154	8.5	3754	9	AY404033		AY404033							
1436	153.5	8.5	529	7	CO302094		CO302094							
1437	153.5	8.5	553	7	CV067547		CV067547							
1438	153.5	8.5	569	7	CK554083		CK554083							
1439	153.5	8.5	657	5	BQ078813		BQ078813							
1440	153.5	8.5	692	5	BW437745		BW437745							
1441	153.5	8.5	745	6	CD802869		CD802869							
1442	153.5	8.5	765	7	CN080626		CN080626							
1443	153.5	8.5	772	5	BP686752		BP686752							
1444	153.5	8.5	806	7	CO248525		CO248525							
1445	153.5	8.5	866	7	CR414240		CR414240							
1446	153.5	8.5	915	5	BU914386		BU914386							
1447	153.5	8.5	916	5	BQ682463		BQ682463							
1448	153.5	8.5	933	6	CA979380		CA979380							
1449	153.5	8.5	1090	7	CR232196		CR232196							
1450	153.5	8.5	2265	9	AY418468		AY418468							
1451	153.5	8.5	2931	3	AK033723		AK033723							
1452	153	8.5	457	2	AW487927		AW487927							
1453	153	8.5	560	7	CO315167		CO315167							
1454	153	8.5	573	7	CF977921		CF977921							
1455	153	8.5	579	5	BP253163		BP253163							
1456	153	8.5	609	1	AV611538		AV611538							
1457	153	8.5	629	4	BG638272		BG638272							
1458	153	8.5	644	5	BX299780		BX299780							
1459	153	8.5	646	6	CA969841		CA969841							
1460	153	8.5	707	7	CH853558		CH853558							
1461	153	8.5	708	4	BU508410		BU508410							
1462	153	8.5	717	6	CD625578		CD625578							
1463	153	8.5	752	7	CN302505		CN302505							
1464	153	8.5	817	7	CO431094		CO431094							
1465	153	8.5	826	7	CN988932		CN988932							
1466	153	8.5	844	7	CN987704		CN987704							
1467	153	8.5	866	7	CN978018		CN978018							
1468	153	8.5	941	5	BQ917338		BQ917338							
1469	153	8.5	2802	9	AY416713		AY416713							

ALIGNMENTS	1808 bp	mRNA	linear	HTC 03-APR-2004
AK045973	Mus musculus adult male corpora quadrigenmina cDNA, RIKEN			
LOCUS	full-length enriched library, clone:B230328N06 product:NEUROTRIMIN			
DEFINITION	PRECUSOR (GP65), homolog [Rattus norvegicus], full insert sequence.			
ACCESSION	AK045973.1	GI:26337738		
VERSION	HTC; CAP trapper.			
KEYWORDS	Mus musculus (house mouse)			
SOURCE	Mus musculus			
ORGANISM	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
REFERENCE	1			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	High-efficiency full-length cDNA cloning			
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)			
MEDLINE	99279253			
PUBMED	10349636			
REFERENCE	2			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	3			
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Iishi, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamanoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.			
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer			
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)			

ALIGNMENTS

RESULT 1	AK045973	1808 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK045973				
DEFINITION	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length enriched library, clone:B203328N06 product:NEUROTRIMIN PRECURSOR (GP65), homolog [Rattus norvegicus], full insert sequence.				
ACCESSION	AK045973.1	GI:263377738			
VERSION	AK045973.1	GI:263377738			
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	92279253				
REFERENCE	10349636				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
REFERENCE	11042159				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuina, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format				
JOURNAL	sequencing pipeline with 384 multicapillary sequencer				
	Genome Res. 10 (11), 1757-1771 (2000)				

MEDLINE PUBMED REFERENCE AUTHORS	20530913 11076861 4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
TITLE JOURNAL REFERENCE AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 1808)
TITLE JOURNAL REFERENCE AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hangaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuura, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE JOURNAL	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
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Db	264	CGGCTCTGTGCTCTTTTCCAAGGAGTGCCGGTGGTAGCGAGATGCCACCTTTCCAAA	323
Qy	41	AlaMetAspAsnValThrValArgGlnGlyCysSerAlaThrLeuArgCysThrIleAsp	60
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Qy	61	AsnArgValThrArgValAlaTTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
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Db 1104 CTGGGTCAACCAACGCCAGCATCATGCTATTGTGTCGCCGTGTGTCAAGTCAAC 1163
Qy 321 AenGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340
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Qy 341 LeuLeuLysPhe 344
Db 1224 CTCCTCAATTT 1235

RESULT 3
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LOCUS Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406347
VERSION AY406347.1 GI:39762321
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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/mol_type="genomic DNA"
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gene
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Alignment Scores: 4.01e-166 Length: 874
Pred. No.: 1506.00 Matches: 288
Score: 99.31% Conservative: 0
Percent Similarity: 99.31% Mismatches: 0
Best Local Similarity: 83.39% Indels: 2
Query Match: 9 Gaps: 1
DB: 1

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Qy 341 LeuLeuLysPhe 344
Db 1224 CTCCTCAATTT 1235

RESULT 3
AY406347 874 bp DNA linear GSS 12-DEC-2003
LOCUS Homo sapiens HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY406347
VERSION AY406347.1 GI:39762321
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 874)
AUTHORS Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source location/Qualifiers
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gene
ORIGIN
Alignment Scores: 4.01e-166 Length: 874
Pred. No.: 1506.00 Matches: 288
Score: 99.31% Conservative: 0
Percent Similarity: 99.31% Mismatches: 0
Best Local Similarity: 83.39% Indels: 2
Query Match: 9 Gaps: 1
DB: 1

US-10-017-084a-523 (1-344) x AY406347 (1-874)
Qy 57 CysThrIleAenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyr 76
Db 2 TGCACATATTGACAAACCGGGTCAACCGGGTGGCTTAAACCGCAGCACCATCTCTAT 61
Qy 77 AlaGlyAenAspLysTyrCysLeuAspProArgValValLeuLeuSerAenThrGlnThr 96
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RESULT 4
 AY406349 874 bp DNA linear GSS 12-DEC-2003
 LOCUS Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY406349
 VERSION AY406349.1 GI:39762323
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 874)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBLISHED 14671302
 REFERENCE 2 (bases 1 to 874)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

TITLE This sequence was made by sequencing genomic exons and ordering
 JOURNAL them based on alignment.
 COMMENT Location/Qualifiers
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 source 1..874
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 Percent Similarity: 97.24% Mismatches: 1
 Best Local Similarity: 82.39% Indels: 2
 Query Match: 9 Gaps: 1
 DB: 1

US-10-017-084A-523 (1-344) x AY406349 (1-874)

Qy 57 CysThrIleAepAsnArgValThrArgValAlaTrrpLeuAenArgSerThrIleLeuTyr 76
 Db 2 TGCACAAATTGACACCGAGTCACCGGGTGGCTGGCTTAACCCGAGTACCATCTCTAT 61

Qy 77 AlaGlyAenAspLysTrrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
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Qy 335 LeuLeuValLeuHisLeuLeuLeuLysPhe 344
 Db 842 CTTCTGCTCTTACACCTGCTCTCAAAATTT 871

RESULT 5
 AY406348 773 bp DNA linear GSS 12-DEC-2003
 LOCUS Pan troglodytes HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AY406348
 VERSION AY406348.1 GI:39762322
 KEYWORDS GSS.
 SOURCE Pan troglodytes (chimpanzee)
 ORGANISM Pan troglodytes

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
 1 (bases 1 to 773)
 Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Inferring nonneutral evolution from human-chimp-mouse orthologous
 gene trios
 Science 302 (5652), 1960-1963 (2003)

JOURNAL PUBLISHED 14671302
 REFERENCE 2 (bases 1 to 773)
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
 Adams,M.D. and Cargill,M.
 Direct Submission
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
 Rockville, MD 20850, USA

TITLE This sequence was made by sequencing genomic exons and ordering
 JOURNAL them based on alignment.
 COMMENT Location/Qualifiers
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 source 1..874
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 gene <1..>874
 /locus_tag="HCM2527"

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 Pred. No.: 1488.00 Matches: 282
 Score: 98.97% Conservative: 5
 Percent Similarity: 97.24% Mismatches: 1
 Best Local Similarity: 82.39% Indels: 2
 Query Match: 9 Gaps: 1
 DB: 1

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14671302
2 (bases 1 to 773)
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submision
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 Weet Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
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/locus_tag="HCM2527"
gene
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Score: 1324.00 Matches: 253
Percent Similarity: 98.44% Conservative: 0
Best Local Similarity: 98.44% Mismatches: 2
Query Match: 73.31% Indels: 2
DB: 9 Gaps: 1
US-10-017-084A-523 (1-344) x AY406348 (1-773)
Qy 57 CysThrIleAspAsnArgValThrArgValAlaTIpLeuAsnArgSerThrIleLeuTyr 76
Db 2 TGCACATATTGACACCGGGTACCCGGGTGGCTGGCTTAACCCGAGCAGCATCTCTAT 61
Qy 77 AlaGlyAsnAspLysTIpCysLeuAspProArgValValLeuLeuLeuSerAsnThrGlnThr 96
Db 62 GCTGGGAATGACNAGTGGTCTGATCTCGCGTGGTCTCTTCGAGCAACACCCAAAGC 121
Qy 97 GlnTyrSerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSer 116
Db 122 CAGTACACGATCGAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCG 181
Qy 117 ValGlnThrAspAsnHisProLysThrSerArgValHisLeuLeuValGlnValSerPro 136
Db 182 GTGCAGACAGACACACCCAAAGACCTCTAGGTCCACCTCATTTGTCNNNTATCTCCC 241
Qy 137 LysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThr 156
Db 242 AAAATTGTAGAGATTCTTCAGATATCTCCATTAACGAAGGGAACAATATCAGCCTCACC 301
Qy 157 CysIleAlaThrGlyArgProGluProThrValThrTIpArgHisIleSerProLys--- 175
Db 302 TGCATAGCAACTGGTGTAGACACGAGCCTACGGTTACTTGGAGACACATCTCCCCAAACCC 361
Qy 176 ---AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyThrArgGlu 194
Db 362 GCAGCGGTGGCTTTGTGAGTGAAGCAAAATCTTGGAAATTCAGGGCATCACCCGGGAG 421
Qy 195 GlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaProValValArgArg 214
Db 422 CAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGGCGCGCGCGGTGACGGAGA 481
Qy 215 ValIysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValPro 234
Db 482 GTAAGAGTTCACCGTGAATATATCCACCATACATTTTCAAGAGCAAGGGTACAGGGTCCCC 541
Qy 235 ValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGln 254
Db 542 GTGGGACAAAAGGGGACACTGCAGTGTGAGCCTCAGCAGTCCCTCAGCAGAAATTCAG 601
Qy 255 TrpTyrLysAspAspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArg 274
Db 602 TGGTACAAGGATGACAAAGACTGATTTCAGAGAAAGAAAGGGGTCAAAAGTGGAAACAGA 661
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Qy 275 PropheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThr 294
Db 662 CTTTCTCTCAAAACTCATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACTACT 721
Qy 295 CysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPhe 311
Db 722 TGGTGGCCTCCAAACAAGCTGGGCCACCAATGCCAGCATCATGCTATT 772
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LOCUS Contig2663 WL/RJ Phraped ESTs Gallus gallus cdna 5', mRNA sequence.
DEFINITION CO635648
ACCESSION CO635648
VERSION CO635648.1 GI:50538871
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1450)
AUTHORS Fitzsimmons,C.J., Savolainen,P., Amini,B., Hjalms,G., Lundeberg,J.
and Andersson,L.
TITLE Detection of sequence polymorphisms in red junglefowl and White
Leghorn ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Carolyn Fitzsimmons
Leif Andersson IMBIM/Dept. Animal Breeding and Genetics
Uppsala University/Swedish University of Agricultural Sciences
Box 597, SE-751 24 Uppsala, SWEDEN
Tel: 00 46 (0)18 471 4593
Fax: 00 46 (0)18 471 4833
Email: Carolyn.fitzsimmons@bmc.uu.se
This EST is a consensus sequence obtained from a Phrap assembly of
4 cdna libraries. The consensus sequence is submitted because SNP
data in the publication 'Detection of sequence polymorphisms in red
junglefowl and White Leghorn ESTs', is reported with reference to
positions in the Phrap consensus sequence.
Seq primer: (5'-end) M13 reverse.
FEATURES
source Location/Qualifiers
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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Red junglefowl/White Leghorn"
/db_xref="taxon:9031"
/sex="female/male"
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/clone_lib="WL/RJ Phraped ESTs"
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III; Site 2: EcoRI; The cdna libraries were created with
the Superscript Plasmid System (Invitrogen)."
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ORIGIN

Alignment Scores:

Pred. No.:	5,27e-144	Length:	1450
Score:	1321.00	Matches:	255
Percent Similarity:	87.58%	Conservative:	27
Best Local Similarity:	79.19%	Mismatches:	34
Query Match:	73.15%	Indels:	6
DB:	7	Gaps:	2

US-10-017-084A-523 (1-344) x CO635648 (1-1450)

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Qy 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46
Db 308 CAAGGAGTCCCGTCGCGCAGCGAGATGCCACCTTCCCAAGCTATGGACAACGTGACT 367
Qy 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66
Db 368 GTGGGCAAGGGGAGAGTGGCCACCTCAGGTGCTCCGTGGGACACCGCGTCGCCCGGTG 427
Qy 67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86
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Db 428 GCCTGGCTGAAACCGCAGCATCTCTATCCGCGCAATGACAGTGGTGTGGACCCG 487
Qy 87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106
Db 488 AGGTGGTGGTCTCTGGCCACACCAACACCATGATCCAGATCCAGATCCAGATGGAC 547
Qy 107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126
Db 548 GTGTACGATGAAGGCCCTACACCTGCTCCGTGCAGACAGACAATCACCCCAAGACATCT 607
Qy 127 ArgValHisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSer 146
Db 608 CGCGTGCACCTCATGTGCAAGTGTCCGCGAAATATCCGAGATCTCTTGTGACATCTCC 667
Qy 147 IleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyValProGluProThr 166
Db 668 ATCAATGAAGTGGCAAGCTCAGCTCCTCAGTGCATAGCCAGCGGAGCCAGACCCACA 727
Qy 167 ValThrTrpArgHisIleSerProLysAlaValGly-PheValSerGluAspGluTyrLe 186
Db 728 ATCACTGGAGACACATCTGCCCAAGCTGTGGCCCTTCATCAGCAGGATGAGTACT 787
Qy 186 uGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAs 206
Db 788 GGAGATCACGGGCATCACACGGGAGCAGTCCGGCGAGTATGAGTGCAGTGTGTCAATGA 847
Qy 206 pValAlaAlaProValAlaArgValLysValThrValAsnTyrProTyrIleLe 226
Db 848 TGTGGCTCTCCAGATGTCCGGAAGTCAAGTCACTGTCACTACCCCGGTACATCTC 907
Qy 226 rGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSe 246
Db 908 CAATGCCAAGAACAACAGCGCCTCAGTGGGCCAGAGGCGCATCTCTGAGTCCGAGGCCCTC 967
Qy 246 rAlaValProSerAlaGluPheGlnTyrTyrLysAspLysArgLeuIleGluGlyLy 266
Db 968 GCCTGTTCCGTGGCAGAGTTTCAGTGGTTCAAGGAGGACACCAAGTTAGCAAAATGGGCT 1027
Qy 266 sLysGlyValLysValGluAsnArgProPheLeuSerLysLysLeuIlePhePheAsnValSe 286
Db 1028 GGAGGCGTGGCGATGGAGAGCAGGGCGGCTCTCGAGCGTGACCTTCTTCAATGTGTC 1087
Qy 286 rGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAl 306
Db 1088 GGAGAAGGACTATGGCAACTACACGTGTGTGGCCACAAACAAAGTTGGGCAACACCAATGC 1147
Qy 306 aSerIleMetLeuPhe-GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgA 326
Db 1148 CAGCATCATCTGTACGGGGCCCGGAGCGGTGCACAGACAGTGGCAATGCAGCCTCCCGGG 1207
Qy 326 rGAlaGly-----CysValTrpLeuLeuProLeuLeuValLeuHisLeuLeuLeuLysP 344
Db 1208 CAGCGCTGGGCTTGCCTCTGG-----GCCACCTCTCTCGCTGCCTCTCTCTCGACT 1261
Qy 344 he 344
Db 1262 TT 1263

RESULT 7
CD354474
LOCUS
DEFINITION
UI-M-GMO-C9d-g-16-0-UI.r1 NIH_BMAP_GMO Mus musculus cDNA clone
IMAGE:30361215 5', mRNA sequence.
ACCESSION
CD354474
VERSION
CD354474.1 GI:31146975
KEYWORDS
EST.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 765)
AUTHORS
NIH-MGC http://mgc.nci.nih.gov/.
```

```

TITLE
JOURNAL
COMMENT
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@email.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pYX-5.
Location/Qualifiers
1. 765
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clones IMAGE:30361215"
/tissue_type="whole brain"
/dev_stage="1, 5 and 15 days newborn"
/lab_host="DH10B (Ti phage resistant)"
/clone_lib="NIH_BMAP_GMO"
/notes="Organ: Brain; Vector: pYX- Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was size
selected according to mRNA size fraction, ligated with Ecor
I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTCAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
```

ORIGIN

Alignment Scores:

Pred. NO.:	1.55e-136	Length:	765
Score:	1254.00	Matches:	246
Percent Similarity:	97.24%	Conservative:	1
Best Local Similarity:	96.85%	Mismatches:	6
Query Match:	69.44%	Indels:	2
DB:	6	Gaps:	1

US-10-017-084A-523 (1-344) x CD354474 (1-765)

Qy 7 LysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe 26

Db 5 AAAATGGACAAATCTATCTGTGGCAATCTTACGGGGCTGGCGGCTCTGTGCTCTTC 64

Qy 27 GlnGlyValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThr 46

Db 65 CAAGGAGTGGCGGTGGTAGCGGAGATGCCACCTTTCCAAAGCTATGGACACGTCAGC 124

Qy 47 ValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgVal 66

Db 125 GTCAAGGAGGGGGAGAGCGCCACCTCAGGTGCAATTTGCAACCGAGTCCCGGGTG 184

Qy 67 AlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspPro 86

Db 185 GCCTGGCTTAACCCAGTACCATCTCTATGCTGGAAATGACAAGTGGTGGCTAGATCCT 244

Qy 87 ArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAsp 106

Db 245 CGTGTGGTCTCTCTGAGTAAACACCCAGACCCAGTACAGCATTTGAGATCCAGAAATGTGAT 304

Qy 107 ValTyrAspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSer 126

|||||

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1039)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCW79 row: d column: 04
 High quality sequence stop: 849.
 Location/Qualifiers
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 /tissue_type="small cell carcinoma"
 /cell_line="MGC3"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_7"
 /note="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
 ORIGIN
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 Pred. No.: 4,33e-126 Length: 1039
 Score: 1167.00 Matches: 243
 Percent Similarity: 80.71% Conservative: 8
 Best Local Similarity: 78.14% Mismatches: 24
 Query Match: 64.62% Indels: 37
 DB: 2 Gaps: 7
 US-10-017-084a-523 (1-344) x BE798585 (1-1039)
 Qy 56 ArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeu 75
 Db 66 AGGTGCATATTGACACCGGTGCGCGGTGGCTGGCTAAACCGCAGCACCATCCTC 125
 Qy 76 TyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGln 95
 Db 126 TATGCTGGGAATGACAAGTGGTGGCTGGATCTCGTGGTCTCTCTGAGCAACACCCAA 185
 Qy 96 ThrGlnTyrSerIleGluIleGlnAsnValAspValTyrAsnGluGlyProTyrThrCys 115
 Db 186 ACGAGTACAGATCGATCCAGAACGTGATGTATGACGAGGCGCTTACACCTGC 245
 Qy 116 SerValGlnThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSer 135
 Db 246 TCGGTGCAGACAGACACCAACCAAGACCTTAGGTCACCTCATTTGTGCAAGTATCT 305
 Qy 136 ProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeu 155
 Db 306 CCCAAATTTAGAGATTCTTCAGATATCTCCATTAATGAAGGGAAACAATATTAGCCTC 365
 Qy 156 ThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLys 175
 Db 366 ACCTCATAGCAACATGGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCCAAA 425
 Qy 176 AlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGln 195

Db 426 GCGGTTGGCTTTGTGAGTGAAGACCAATCTTGGAAATTCAGGGCATCACCGGAGCAG 485
 Qy 196 SerGlyAspTyrGluCysSerAlaSerAsnAspValAlaProValValArgVal 215
 Db 486 TCAGGGACTACGAGTACGAGTGGCTCAATGACGTGGCGCGCGGTGATCAGGAGAGTA 545
 Qy 216 LysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProVal 235
 Db 546 AAGGTCACCGTGAACATATCCACCATACATTTCAGAGCAAGGGTACAGGTGTCCCGTG 605
 Qy 236 GlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrp 255
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 Qy 256 TyrLysAspAspLysArgLeuIleGluGly---LysLysGlyValLysValGluAsnArg 274
 Db 666 TACAAGGATGACAAAGACTGATTGAAGGAAACAGACAGGGGTGAACAGTTGGAACACAGA 725
 Qy 275 ProPheLeuSerLysLeuIlePhe-----PheAsnValSer---GluHisAspTyr-Gl 291
 Db 726 CTTTTTCTCTCTCAAAAGTCATTCCTTCTTCAATGTCTCTGANCATCGACTATGGG 785
 Qy 291 YAsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAla----- 306
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 Qy 307 ----- 307
 Db 844 ACGTAATAGACAGACAGTAGAAGTGGTACCATGCGAGAGCCCAATGCCGATAGGA 903
 Qy 307 rIleMetLeuPheGlyProGlyAlaValSerGluValSerAsnGlyThrSerArg----- 325
 Db 904 CAGTCCAGTCTACAGCCCC---AGTGTGAGGAGCCCAAGAGAGAGCAGGCGCGGAGTG 960
 Qy 326 -----ArgAlaGly---CysValTrp 331
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 LOCUS 17000470517655 GRN_EB Homo sapiens cDNA 5', mRNA sequence.
 DEFINITION CN362539
 ACCESSION CN362539
 VERSION CN362539.1 GI:47362473
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 748)
 AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R., Lebkowski, J. and Stanton, L.W.
 TITLE Transcription characterization elucidates signaling networks that control human ES cell growth and differentiation
 JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)
 COMMENT Contact: Brandenberger R
 Regenerative Medicine
 Geron Corporation
 230 Constitution Drive, Menlo Park, CA 94025, USA
 Tel: 650 473 8658
 Fax: 650 473 7760
 Email: rbrandenberger@geron.com
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 Location/Qualifiers
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 /organism="Homo sapiens"
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 /db_xref="taxon:9606"
 /tissue_type="embryonic stem cells, embryonic bodies derived from H1, H7 and H9 cells"
 /clone_lib="GRN_EB"
 FEATURES source

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Qy 144 AspileSerileAsnGluGlyAsnAsnileSerLeuThrCysIleAlaThrGlyArgPro 163
Db 489 AATATTGCTGTTAATGAGGAGTAAATGTCAGCTGATTTGCTATTCGATTCGACCGGAGACCT 548
Qy 164 GluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheValSerGluAsp 183
Db 549 GAACCCGTAGTGAACCTGAGATACCTGTCCCTAAAGCACGGGGTTTTGTAAAGTGAAGAT 608
Qy 184 GluThrLeuGluIleGlnGlyIleThrArgGlnSerGlyAspTyrGluCysSerIle 203
Db 609 GAGTACCTCGGAATACACAGGAATCACTAGGAGCAGTCTGGAATATATGAAATGCAAGTCG 668
Qy 204 SerAsnAspValAlaAlaProValValArgArgValLysValThrValAsnTyrProPro 223
Db 669 TCCATGATGTCCTCGCACACAGATGTCGAGGGTTAAATTAACATTAATTAACCCACCA 728
Qy 224 TyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCys 243
Db 729 TACATTTCTGGATGCACAGAACATCGGGCTCCCTTGGCCATCGAGGTATTTTGCAGGT 788
Qy 244 GluAlaSerAlaValProSerAla-GluPheGlnTrpTyrLysAspAspLysArgLeuIle 263
Db 789 GAAGCCTCTGCTGTACCTGCGACCGGACTTCTCTGTGTACAGGAGAACAAAGGCTGAG 848
Qy 263 eGluGlyLysLys-GlyValLysValGlu 272
Db 849 TGATTCATGGAGGGGGGTCAAGTAGAG 877

RESULT 12
CF737474
LOCUS
DEFINITION
UI-M-HD0-cks-o-09-0-UI.r1 NIH_BMAP_HD0 Mus musculus cDNA clone
IMAGE:30614264 5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 759)
NIH-MGC <http://mgs.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousef1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1..759
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/mol_type="mRNA"
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/clone="IMAGE:30614264"
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/dev_stages="embryo 12.5,13.5,14.5 dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH BMAP_HD0"
/note="Organ: Eye; Vector: pYX- Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose

FEATURES
source

gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site .Double strand cDNA was
size selected according to mRNA size fraction .ligated
with EcoR I adaptor , digested with NotI and then cloned
directionally into pYX-Asc vector . The library tag
sequence located between the Not I site and the polyA tail
is TTATGGAAGT. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH). "

ORIGIN

Alignment Scores:
Pred. No.: 9.25e-118 Length: 759
Score: 1094.50 Matches: 216
Percent Similarity: 92.83% Conservative: 4
Best Local Similarity: 91.14% Mismatches: 14
Query Match: 60.60% Indels: 4
DB: 7 Gaps: 1

US-10-017-084A-523 (1-344) x CF737474 (1-759)

Qy 12 IleSerTrpAlaIlePheThrGlyLeuAlaAlaLeuCysLeuPhe-----GlnGly 28
Db 45 CTGCCCTGGAAGTCCCTCGTGTCTCTCAGGCTGCTATTCCTTGTATCCACACAGA 104
Qy 29 ValProValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArg 48
Db 105 GTGCGGTGCTAGCGGAGATGCCACCTTTCCCAAGCTATGGACACGTCACGGTCAGG 164
Qy 49 GlnGlyGluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrp 68
Db 165 CAGGGGAGAGCGCACCTCAGGTGCACAAATTCACCAACCGAGTCACCGGCTGGCTGG 224
Qy 69 LeuAsnArgSerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgVal 88
Db 225 CTAAACCGCAGTACCATCTCTATGTGTGGAATGACAAAGTGGTGTAGATCTCTGTGTG 284
Qy 89 ValLeuLeuSerAsnThrGlnThrGlnTyrSerIleGluIleGlnAsnValAspValTyr 108
Db 285 GTCTCTCTGAGTACACCCAGCCAGTACAGCATTCAGATCCAGAAATGTGATGTGTAC 344
Qy 109 AspGluGlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgVal 128
Db 345 GATGAGGGCCCTTATACCTGCTCGGTACAGACAGACCAACCACTTAAGACCTCCAGGTC 404
Qy 129 HisLeuIleValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsn 148
Db 405 CACCTCATTTGTACAAAGTATCTCCCAAAATTTGTAGAGATTTCTTCAGATATCTCCATTAA 464
Qy 149 GluGlyAsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThr 168
Db 465 GAAGGGAACAACATCAGCCCTCATTGTCATAGCCACAGGTAGACCGGAGCCTACAGTAACC 524
Qy 169 TrpArgHisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIle 188
Db 525 TGGAGACATATTTCTCCCAAGCGCTTGGCTTGTGTGAGTGAAGTACGTACCTGAGATC 584
Qy 189 GlnGlyIleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAla 208
Db 585 CAGGGCATCACTCGGGAAACAGTCAGGCGGAGTACAGGTGCAGCGCTCCAAAGACGTCGGC 644
Qy 209 AlaProValValArgArgValLysValThrValAsnTyrProTyrIleSerGluAla 228
Db 645 GCACAGTGTGACGAGAGTGAAGTCACTGACTGACTATCCACCATACATCTCAAGAGCT 704
Qy 229 LysGlyThrGlyValProValGlyGlnLysGlyThrLeuGlnCysGluAla 245
Db 705 AAGGGCACAGGTGTCCCGTGGGGCAAGANGGACT-CTGAGCTGTGAAGCT 754

RESULT 13

AL533026

LOCUS

1027 bp mRNA linear EST 24-MAR-2004

```

DEFINITION AL533026 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone
ACCESSION CS0DN005YD20 5-PRIME, mRNA sequence.
AL533026
VERSION AL533026.3 GI:45707932
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1027)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 13, 2001 this sequence version replaced gi:31070858.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 6387.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?e=CS0DN005YD20&e=6387.f.
FEATURES
source
1..1027
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN005YD20"
/tissue_type="ADULT BRAIN"
/dev_stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
ORIGIN
Alignment Scores:
Pred. No.: 8.59e-114 Length: 1027
Score: 1062.50 Matches: 211
Percent Similarity: 84.19% Conservative: 2
Best Local Similarity: 83.40% Mismatches: 0
Query Match: 58.83% Indels: 40
DB: 1 Gaps: 1
US-10-017-084A-523 (1-344) x AL533026 (1-1027)
QY 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db ::::
98 ATTAAGTATCTCCCAAAATGTAGAGATTTCTTCAGATATCTCCATTAATGAAGGAAC 157
QY 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
Db 158 AATATTAGCCTCACCCTGCATAGCAACTGGTAGACAGAGCCTACCGTTACTTGGAGACAC 217
QY 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
Db 218 ATCTCTCCCAAGCGGTTGGCTTTGTAGTAGAGAGCAATACTTGGAAATTCAGGGCATC 277
QY 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
Db 278 ACCCGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCAATGACGTGCGCCGCCGCTG 337
QY 212 ValArgArgValLysValThrValAsnTyrProTyrIleSerGluAlaLysGlyThr 231
Db 338 GTACCGAGAGTAAAGGTACCGGTGAACCTATCCACCATATTCAGAACCCAGGGTACA 397
QY 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251

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Db 398 GGTGTCCCGTGGGACAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 457
QY 252 GluPheGlnTrpTyrLysAspAsp-Lys----- 260
Db 458 GAATTCAGTGGTACAAGGATGACAAAAGAGAGCTGAAATCTCATTCACAGTTTGGTTATGA 517
QY 260 ----- 260
Db 518 TGGGAAGACTTCTCCCTCCCATGGTGGAGCAATGGTGTCAAAACGCCAGTCGGATCAATCA 577
QY 261 -----ArgLeuIleGluGlyLysGlyValGlyValGlyValGlyValGlyValGly 272
Db 578 GCCTGACTTGTCTCGACAATCTCCCGACTGATTGAAGGAAGAAAGGGGTGAAAGTGGGA 637
QY 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
Db 638 AAACAGACCTTTCCTCTCAAAACATCATCTTCTCAATGTCTCTGAACATGATATGGGAA 697
QY 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG1 312
Db 698 CTACACTTGGTGGCTTCCAACAAGCTGGGCCACCAATGCCAGCATCATGCTATTGG 757
QY 312 YProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLe 332
Db 758 TCCAGGCGCGCTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGCGAGGCTCGCTCGT 817
QY 332 uLeuProLeuValLeuHisLeuLeuLysPhe 344
Db 818 GCTGCCCTCTTCTGGTCTTGCACCTGCTTCTCAAAATTT 854
RESULT 14
LOCUS CR602526 2512 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DN005YD20 of Adult brain of Homo sapiens
(human).
ACCESSION CR602526
VERSION CR602526.1 GI:50483333
KEYWORDS HTC; CNSLT cDNA
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2512)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paraday Avenue
2 (bases 1 to 2512)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
1..2512
/organism="Homo sapiens"
/mol_type="mRNA"
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ORIGIN
Alignment Scores:
Pred. No.: 3.34e-113 Length: 2512

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Score: 1062.50 Matches: 211
Percent Similarity: 84.19% Conservative: 2
Best Local Similarity: 83.40% Mismatches: 0
Query Match: 58.83% Indels: 40
DB: 3 Gaps: 1

US-10-017-084A-523 (1-344) x CR602526 (1-2512)

Qy 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db ::::
97 ATTAAGTATCTCCCAAAATGTAGAGATTCTTCAGATATCTCCATTAATGAAGGAAC 156
Qy 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
Db ::::
157 AATATTAGCTTCACCTGCATAGCAACTGGTAGACAGAGCCCTACGGTTACTTGGAGAC 216
Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGlyIle 191
Db ::::
217 ATCTCTCCAAAGCGTTGGCTTTGTAGTGAAGACGATACTTGGAAATTCAGGGATC 276
Qy 192 ThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
Db ::::
277 ACCAGGAGCAGTCAGGGACTACGAGTGCACTGCTCCATGAGCTGGCGCGCCGGTG 336
Qy 212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
Db ::::
337 GTACGGAGAGTAAAGGTCCCGTGAACCTATCCACATACATATTCAGAACCCAGGTACA 396
Qy 232 GlyValProValGlyGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
Db ::::
397 GGTGTCCCGTGGGACAAAGGGGACACTGCGAGTGTGAAGCTCAGCAGTCCCTCAGCA 456
Qy 252 GluPheGlnTyrTyrLysAspAsp-Lys- 260
Db ::::
457 GAATTCAGTGTACAGGATGACAAAGAGCTGAATCTCATTCACAGTTTGGTTATGA 516
Qy 260 ----- 260
Db ::::
517 TGGGAAAGCTTCTCTCCCATGGTGGACGAATGGTGTCAAAACGCCAGTGGGATCAATCA 576
Qy 261 ----- 272
Db ::::
577 GCCTGACTTGTCTCGAGANTCTCCCGACTGATTGAAGGAAGAGGGGTGAAGTGA 636
Qy 272 uAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGlyAs 292
Db ::::
637 AAACAGACTTCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGGAA 696
Qy 292 nTyrThrCysValAlaSerAsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheG 312
Db ::::
697 CTACACTTGGTGGCTCCAAAGCTGGGCTCACCAAGTGGCCACACCAATGCCAGCATCTATTGG 756
Qy 312 yProGlyAlaValSerGluValSerAsnGlyThrSerArgAlaGlyCysValTrpLe 332
Db ::::
757 TCCAGGCGCCGTACAGCGAGGTGAGACAGCGACGTGCGAGGAGGCGAGCGTCTGCTGCT 816
Qy 332 uLeuProLeuLeuValLeuHisLeuLeuLysPhe 344
Db ::::
817 CTGCTCTCTTGTGCTTGTGACCTGCTTCTCAAAATTT 853

RESULT 15
BU368328
LOCUS BU368328.1
DEFINITION 603789424F1 CSEQCHN72 Gallus gallus cdna clone CHEST750p6 5', mRNA
sequence.
ACCESSION BU368328
VERSION BU368328.1
KEYWORDS Gr:25876329
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
```

REFERENCE 1 (bases 1 to 740)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PubMed 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
source
1..740
Location/Qualifiers
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CHEST750p6"
/sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="CSEQCHN72"
/notes="Organ: Brain; Vector: pBluescript II KS(+); Site: 1:
EcoRI; Site 2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

ORIGIN

Alignment Scores:
Pred. No.: 3,49e-112 Length: 740
Score: 1047.00 Matches: 192
Percent Similarity: 91.85% Conservative: 22
Best Local Similarity: 82.40% Mismatches: 19
Query Match: 57.97% Indels: 0
DB: 5 Gaps: 0
US-10-017-084A-523 (1-344) x BU368328 (1-740)
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 3 CAGATCCACGACGCTGGACGCTGTACGATGAAGGGCCCTACACCTCTCCGTGCAGACAGAC 62
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 63 AATCACCACCAAGACATCTCGGTGCACCTCATGTGTCAAGTGTCCGCAAAATTTACCGAG 122
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 123 ATCTCTTTCAGATCTCCATCAATGAAGTGGCAACGTCAGCCTCACCTGCATAGCCACG 182
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 183 GGCAGGCGCAGACCCCAATCACCTGGAGACACATCTCGCCAAAGCTGTGGGCTTCATC 242
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200
Db 243 ACCGAGGACGAGTACCTTGGAGATCACAGGCATCACAGGGAGGAGCTCGGGCGAGTACGAG 302

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Qy 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
303 TGCAGTGGCTCCNAGCAGCTGGCCGGCTGTCTGTCAGCGAGTCAAGTCACCGTCAAC 362
Qy 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
363 TACCCACCGTACATCTCGGATCGAAGAGACCGCGTGTCCGGTGGGGCAGAGGGCATC 422
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAspLys 260
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
423 CTGATGTGTGAAGCCTCCGCTGTGCCCTCCGCTGACTTCCAGTGGTACAAAGACGACAAG 482
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
483 CGGCTGGCTGAAGGACAGAAAGGCTGAAGTGGAAACAAAGCCTTCTTCCCGACTG 542
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
543 ACTTCTTCAACGTCTCCGAGCAGGACTACGGCAACTACACTGCGTGGCTCCCAACCCAG 602
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
603 CTAGGAACACCAACGCCAGCATGATCCTTATGGCCCCCGTGCAGTGCACGATGGCAAC 662
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeu 333
Db :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
663 AGCGGTGCGTGGCGCGGAGGAGCTGTGCTGCGTGTGCTG 701

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Search completed: October 30, 2005, 12:35:13
Job time : 4031 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: October 30, 2005, 09:21:27 ; Search time 216 Seconds
(without alignments)
2605.922 Million cell updates/sec

Title: US-10-017-084A-523
Perfect score: 1806
Sequence: 1 MKTIQPKHNSISWAIFTGL.....RRAGCVLLPLVLVLLLLK 344

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=1500 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10017084 @CGN 1 1 177 @runat_28102005_112603_9189 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTCUTS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1806	100.0	1032	4	US-09-700-397-1
2	1806	100.0	1693	4	US-09-700-397-2
3	1642	90.9	939	4	US-09-700-397-5
4	931.5	51.6	1195	4	US-09-976-594-403
5	926.5	51.3	1014	2	US-08-414-657D-5
6	926.5	51.3	1014	3	US-09-135-080-7
7	926.5	51.3	1238	3	US-08-414-657D-3
8	926.5	51.1	1238	3	US-09-135-080-3
9	923.5	51.1	977	2	US-08-414-657D-1
10	923.5	51.1	977	3	US-09-135-080-1
11	908	50.3	924	2	US-08-414-657D-7
12	907	50.2	945	2	US-08-414-657D-8

Sequence 6, Appli	912	49.9	902	13	US-08-414-657D-6	Sequence 6, Appli
Sequence 9, Appli	861	49.1	886.5	14	US-08-414-657D-9	Sequence 9, Appli
Sequence 10, Appl	861	49.0	885.5	15	US-08-414-657D-10	Sequence 10, Appl
Sequence 17, Appl	756	44.1	796.5	16	US-08-414-657D-17	Sequence 17, Appl
Sequence 18, Appl	756	44.0	795.5	17	US-08-414-657D-18	Sequence 18, Appl
Sequence 4587, Ap	1030	41.1	742.5	18	US-09-949-016-4587	Sequence 4587, Ap
Sequence 23289, A	333	30.2	545	19	US-09-513-999C-23289	Sequence 23289, A
Sequence 2775, Ap	352	19.0	344	20	US-09-513-999C-2775	Sequence 2775, Ap
Sequence 16329, A	113538	18.7	339	21	US-09-949-016-16329	Sequence 16329, A
Sequence 410, App	913	16.7	302.5	22	US-09-774-528-410	Sequence 410, App
Sequence 4676, Ap	2599	15.3	276	23	US-09-949-016-4676	Sequence 4676, Ap
Sequence 950, App	2633	15.2	275	24	US-09-023-655-950	Sequence 950, App
Sequence 245, App	5807	15.2	274	25	US-09-976-594-245	Sequence 245, App
Sequence 11659, A	2118	15.1	273.5	26	US-09-270-767-11659	Sequence 11659, A
Sequence 66, Appl	6814	14.6	263.5	27	US-09-484-370B-66	Sequence 66, Appl
Sequence 2, Appli	1266	14.2	256	28	US-08-659-984A-2	Sequence 2, Appli
Sequence 4, Appli	1335	14.2	256	29	US-08-660-531-2	Sequence 4, Appli
Sequence 4, Appli	1335	14.2	256	30	US-08-659-984A-4	Sequence 4, Appli
Sequence 5, Appli	4548	13.8	249.5	31	US-08-660-531-4	Sequence 5, Appli
Sequence 4450, Ap	3318	13.6	246.5	32	US-09-571-479C-5	Sequence 4450, Ap
Sequence 5, Appli	3360	13.6	246.5	33	US-08-408-093-5	Sequence 5, Appli
Sequence 5, Appli	3360	13.6	246.5	34	US-08-408-420A-5	Sequence 5, Appli
Sequence 5, Appli	3360	13.6	246.5	35	US-08-714-901-5	Sequence 5, Appli
Sequence 644, App	4723	13.4	241.5	36	US-08-040-741-5	Sequence 644, App
Sequence 350, App	4597	13.3	241	37	US-09-949-016-644	Sequence 350, App
Sequence 5173, Ap	219	13.2	237.5	38	US-09-799-451-350	Sequence 5173, Ap
Sequence 11, Appl	219	13.1	237	39	US-09-949-016-5173	Sequence 11, Appl
Sequence 12, Appl	219	13.1	237	40	US-08-414-657D-11	Sequence 12, Appl
Sequence 2, Appli	2869	12.8	230.5	41	US-08-414-657D-12	Sequence 2, Appli
Sequence 2, Appli	2869	12.8	230.5	42	US-08-374-834-2	Sequence 2, Appli
Sequence 17, Appl	2610	12.7	230	43	US-08-644-271-2	Sequence 17, Appl
Sequence 32, Appl	2610	12.7	230	44	US-09-077-955-2	Sequence 32, Appl
Sequence 14, Appl	1581	12.5	225.5	45	US-08-644-271-28	Sequence 14, Appl
Sequence 18, Appl	2580	12.5	225.5	46	PCT-US95-08493-14	Sequence 18, Appl
Sequence 20, Appl	2604	12.5	225.5	47	PCT-US95-08493-18	Sequence 20, Appl
Sequence 7, Appli	2607	12.4	225	48	PCT-US95-08493-20	Sequence 7, Appli
Sequence 75, Appl	7647	12.4	224.5	49	US-09-715-249-7	Sequence 75, Appl
Sequence 289, App	3662	12.4	224	50	US-09-556-921-75	Sequence 289, App
Sequence 289, App	3662	12.4	224	51	US-09-907-794A-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	52	US-09-905-125A-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	53	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	54	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	55	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	56	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	57	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	58	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	59	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	60	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	61	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	62	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	63	US-09-906-700-289	Sequence 289, App
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Sequence 289, App	3662	12.4	224	65	US-09-906-700-289	Sequence 289, App
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Sequence 289, App	3662	12.4	224	76	US-09-906-700-289	Sequence 289, App
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Sequence 289, App	3662	12.4	224	81	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	82	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	83	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	84	US-09-906-700-289	Sequence 289, App
Sequence 289, App	3662	12.4	224	85	US-09-906-700-289	Sequence 289, App

86	213.5	11.8	1718	4	US-09-778-510-5	Sequence 5, Appli	159	173.5	9.6	2550	1	US-08-481-130-10	Sequence 10, Appl
87	213	11.8	177	2	US-08-414-657D-13	Sequence 13, Appl	160	173.5	9.6	2550	1	US-08-656-984A-10	Sequence 10, Appl
88	212	11.7	177	2	US-08-414-657D-14	Sequence 14, Appl	161	173.5	9.6	2550	1	US-08-485-604-10	Sequence 10, Appl
89	211.5	11.7	5506	4	US-09-978-594-530	Sequence 530, App	162	173.5	9.6	2550	2	US-08-487-595-10	Sequence 10, Appl
90	211	11.7	1273	4	US-09-778-510-3	Sequence 3, Appli	163	173.5	9.6	2988	1	US-08-245-295-1	Sequence 1, Appli
c 91	210	11.6	577	4	US-07-770-767-1011	Sequence 1011, Ap	164	173.5	9.6	2988	1	US-08-481-130-1	Sequence 1, Appli
c 92	210	11.6	577	4	US-09-270-767-16293	Sequence 16293, A	165	173.5	9.6	2988	1	US-08-656-984A-1	Sequence 1, Appli
93	210	11.6	577	4	US-09-016-434-1120	Sequence 1120, Ap	166	173.5	9.6	2988	1	US-08-485-604-1	Sequence 1, Appli
94	210	11.6	5926	4	US-09-917-254-41	Sequence 41, Appl	167	173.5	9.6	2988	2	US-08-487-595-1	Sequence 1, Appli
95	209	11.6	3093	4	US-09-949-016-4183	Sequence 4183, Ap	168	173	9.6	3189	2	US-08-427-497E-3	Sequence 3, Appli
96	209	11.6	3145	4	US-09-949-016-1149	Sequence 1149, Ap	169	173	9.6	3774	2	US-08-341-843B-1	Sequence 1, Appli
97	205.5	11.4	1542	4	US-09-205-258-123	Sequence 123, App	170	173	9.6	3774	2	US-08-427-497E-1	Sequence 1, Appli
98	205	11.4	1820	4	US-09-778-510-1	Sequence 1, Appli	171	173	9.6	3774	2	US-08-427-497E-2	Sequence 2, Appli
99	203.5	11.3	5824	4	US-09-620-312D-72	Sequence 72, Appl	172	173	9.6	3888	3	US-08-506-296B-13	Sequence 13, Appl
100	202	11.2	4059	4	US-08-799-451-560	Sequence 560, App	173	172	9.5	1630	3	US-08-468-856B-2	Sequence 2, Appli
101	201	11.1	3398	5	PCT-US95-08493-12	Sequence 12, Appl	174	172	9.5	1630	3	US-08-468-859A-2	Sequence 2, Appli
102	200	11.1	1967	3	US-09-383-586-22	Sequence 22, Appl	175	172	9.5	2116	4	US-09-023-655-1256	Sequence 1256, Ap
103	200	11.1	1967	4	US-08-823-038A-22	Sequence 22, Appl	176	172	9.5	3461	3	US-08-468-856B-6	Sequence 6, Appli
104	199	11.0	4285	3	US-09-040-774-1	Sequence 1, Appli	177	172	9.5	3461	3	US-08-468-859A-6	Sequence 6, Appli
105	198	11.0	6718	4	US-09-949-016-4632	Sequence 4632, Ap	178	171.5	9.5	2352	1	US-08-232-538-17	Sequence 17, Appl
106	197.5	10.9	4608	3	US-08-041-886-24	Sequence 24, Appl	179	171.5	9.5	2352	2	US-08-786-164-17	Sequence 17, Appl
107	197.5	10.9	4608	5	PCT-US94-05277-1	Sequence 1, Appli	180	171.5	9.5	4014	4	US-09-119-014D-5	Sequence 5, Appli
108	196.5	10.9	5905	4	US-09-949-016-5625	Sequence 5625, Ap	181	171.5	9.5	7680	4	US-09-953-318-3	Sequence 3, Appli
109	196.5	10.9	6218	4	US-09-949-016-706	Sequence 706, App	182	171	9.5	1473	2	US-08-602-725-31	Sequence 31, Appl
110	196.5	10.9	6384	4	US-09-976-594-724	Sequence 724, App	183	171	9.5	1473	4	US-09-949-016-245	Sequence 245, App
c 111	196.5	10.9	6384	4	US-09-919-039-279	Sequence 279, App	184	171	9.5	1475	4	US-09-949-016-1654	Sequence 1654, Ap
112	194	10.7	3783	3	US-08-506-296B-20	Sequence 20, Appl	185	170	9.4	862	3	US-08-468-856B-4	Sequence 4, Appli
113	192.5	10.7	2481	3	US-08-877-730-15	Sequence 15, Appl	186	170	9.4	862	3	US-08-468-859A-4	Sequence 4, Appli
114	192.5	10.7	2715	3	US-09-877-730-5	Sequence 5, Appli	187	169	9.4	1339	3	US-08-468-856B-3	Sequence 3, Appli
115	192.5	10.7	2724	3	US-09-877-730-19	Sequence 19, Appl	188	169	9.4	1339	3	US-08-468-859A-3	Sequence 3, Appli
116	192.5	10.7	2958	3	US-09-877-730-9	Sequence 9, Appli	189	168	9.3	2383	1	US-08-232-538-18	Sequence 18, Appl
117	192.5	10.7	2976	3	US-09-877-730-11	Sequence 11, Appl	190	168	9.3	2383	1	US-08-786-164-18	Sequence 18, Appl
118	192.5	10.7	3192	3	US-09-412-554A-1	Sequence 1, Appli	c 191	167.5	9.3	842	4	US-09-270-767-11483	Sequence 11483, A
119	192.5	10.7	3210	3	US-09-877-730-1	Sequence 1, Appli	192	167	9.2	2264	1	US-08-232-538-16	Sequence 16, Appl
120	192.5	10.7	3219	3	US-09-877-730-17	Sequence 17, Appl	193	167	9.2	2264	2	US-08-786-164-16	Sequence 16, Appl
121	192.5	10.7	3453	3	US-09-877-730-7	Sequence 7, Appli	194	167	9.2	2292	3	US-09-142-956B-1	Sequence 1, Appli
122	192.5	10.7	3874	3	US-09-877-730-31	Sequence 31, Appl	195	167	9.2	4071	3	US-09-098-707A-1	Sequence 1, Appli
123	192.5	10.7	3943	3	US-08-506-296B-27	Sequence 27, Appl	196	167	9.2	4071	3	US-09-483-539-1	Sequence 1, Appli
124	192	10.6	2094	4	US-09-270-767-13304	Sequence 13304, A	197	167	9.2	4236	1	US-08-810-116-7	Sequence 7, Appli
c 125	191	10.6	601	4	US-09-949-016-163724	Sequence 163724, A	198	167	9.2	4236	2	US-07-930-348A-7	Sequence 7, Appli
126	190	10.6	6055	3	US-09-953-318-10	Sequence 10, Appl	199	167	9.2	5830	4	US-09-967-655-3	Sequence 3, Appli
127	187.5	10.4	3991	3	US-08-506-296B-3	Sequence 3, Appli	200	167	9.2	5830	4	US-09-949-016-327	Sequence 327, App
128	186	10.3	3551	4	US-09-620-312D-760	Sequence 760, App	201	167	9.2	5831	4	US-09-949-016-3982	Sequence 3982, Ap
129	185.5	10.3	957	2	US-08-633-148-3	Sequence 3, Appli	202	166.5	9.2	909	3	US-09-877-730-13	Sequence 13, Appl
130	185.5	10.3	1023	2	US-08-633-148-1	Sequence 1, Appli	203	166.5	9.2	1143	3	US-09-877-730-3	Sequence 3, Appli
131	185.5	10.3	1215	4	US-09-949-016-5154	Sequence 5154, Ap	204	166.5	9.2	1405	4	US-08-755-235-3	Sequence 3, Appli
132	185.5	10.3	2031	1	US-08-217-299-2	Sequence 2, Appli	205	166	9.2	2523	3	US-09-051-363-1	Sequence 1, Appli
133	185.5	10.3	2097	2	US-08-602-725-35	Sequence 35, Appl	206	165.5	9.2	1962	4	US-09-653-961-3	Sequence 3, Appli
134	185.5	10.3	2220	1	US-08-389-459A-16	Sequence 16, Appl	207	165.5	9.2	1962	4	US-09-653-961-5	Sequence 5, Appli
135	185.5	10.3	2220	3	US-08-987-867A-16	Sequence 16, Appl	208	165.5	9.2	2487	1	US-08-261-304-1	Sequence 1, Appli
136	185.5	10.3	2349	2	US-08-184-009-145	Sequence 145, App	209	165.5	9.2	2539	2	US-08-432-016-1	Sequence 1, Appli
137	185.5	10.3	2349	2	US-08-458-356-145	Sequence 145, App	210	165.5	9.2	2539	2	US-08-684-594-1	Sequence 1, Appli
138	185.5	10.3	2349	4	US-08-460-736-145	Sequence 145, App	211	165.5	9.2	2580	4	US-09-774-528-327	Sequence 327, App
139	185.5	10.3	2349	4	US-09-535-370-145	Sequence 145, App	212	165.5	9.2	3306	4	US-09-023-655-1434	Sequence 1434, Ap
140	185.5	10.3	2349	4	US-09-663-667-145	Sequence 145, App	213	165.5	9.2	3583	4	US-09-949-016-857	Sequence 857, App
141	185.5	10.3	2343	2	US-08-184-009-144	Sequence 144, App	214	165.5	9.2	4854	4	US-09-784-358-15	Sequence 15, Appl
142	185.5	10.3	2434	2	US-08-458-356-144	Sequence 144, App	215	165.5	9.2	5076	4	US-09-784-358-1	Sequence 1, Appli
143	185.5	10.3	2434	3	US-08-460-736-144	Sequence 144, App	216	165.5	9.2	7718	4	US-09-976-594-244	Sequence 244, App
144	185.5	10.3	2434	4	US-09-535-370-144	Sequence 144, App	217	165.5	9.2	8578	4	US-09-784-358-17	Sequence 17, Appl
145	185.5	10.3	2434	4	US-09-663-667-144	Sequence 144, App	218	165	9.1	2166	2	US-08-408-095-30	Sequence 30, Appl
146	185.5	10.3	2974	4	US-09-949-016-613	Sequence 613, App	219	164.5	9.1	2539	4	US-09-023-655-1496	Sequence 1496, Ap
147	185.5	10.3	2976	4	US-09-949-016-2297	Sequence 2297, Ap	220	164.5	9.1	2565	1	US-08-597-495B-29	Sequence 29, Appl
148	184.5	10.2	198	2	US-08-414-657D-15	Sequence 15, Appl	221	164.5	9.1	2565	3	US-09-068-051A-31	Sequence 31, Appl
149	184.5	10.2	198	2	US-08-414-657D-16	Sequence 16, Appl	222	164.5	9.1	2793	3	US-09-336-536-68	Sequence 68, Appl
150	184.5	10.2	1391	4	US-09-638-649-4	Sequence 4, Appli	223	164.5	9.1	2803	3	US-09-068-051A-33	Sequence 33, Appli
151	184.5	10.2	1391	4	US-09-638-648-4	Sequence 4, Appli	224	164	9.1	1378	4	US-09-419-788-3	Sequence 3, Appli
152	182	10.1	2346	4	US-09-949-016-1979	Sequence 1979, Ap	225	164	9.1	1742	3	US-09-383-586-23	Sequence 23, Appl
153	182	10.1	2350	4	US-09-949-016-342	Sequence 342, App	226	164	9.1	1742	4	US-09-823-038A-23	Sequence 23, Appl
154	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	227	164	9.1	1983	3	US-09-057-860A-8	Sequence 8, Appli
155	179.5	9.9	2839	3	US-08-468-856B-5	Sequence 5, Appli	228	164	9.1	2418	4	US-09-949-016-1694	Sequence 1694, Ap
c 156	174	9.6	785	4	US-09-270-767-1269	Sequence 1269, Ap	229	163.5	9.1	1950	4	US-09-653-961-1	Sequence 1, Appli
c 157	174	9.6	785	4	US-09-270-767-16551	Sequence 16551, A	230	163.5	9.1	2539	4	US-09-949-016-3677	Sequence 3677, Ap
158	173.5	9.6	2550	1	US-08-245-295-10	Sequence 10, Appl	231	163.5	9.1	2697	4	US-09-949-016-5335	Sequence 5335, Ap

232	163.5	9.1	4235	4	US-09-702-705-317	Sequence 317, App	305	159	8.8	6363	4	US-09-023-655-879	Sequence 879, App
233	163.5	9.1	4235	4	US-09-736-457-317	Sequence 317, App	306	158.5	8.8	4890	4	US-09-677-046A-3	Sequence 3, Appli
234	163.5	9.1	4235	4	US-09-614-124B-317	Sequence 317, App	307	158.5	8.8	4943	4	US-09-677-046A-7	Sequence 7, Appli
235	163.5	9.1	4235	4	US-09-671-325-317	Sequence 317, App	308	158.5	8.8	5220	4	US-09-677-046A-1	Sequence 1, Appli
236	163.5	9.1	4235	4	US-09-589-184-317	Sequence 317, App	309	158	8.7	2208	5	PCT-US93-00031-14	Sequence 14, Appli
237	163.5	9.1	4235	4	US-09-658-824-317	Sequence 317, App	310	157.5	8.7	1140	3	US-09-462-270-1	Sequence 1, Appli
238	163.5	9.1	5720	4	US-08-800-729-18	Sequence 18, Appl	311	157.5	8.7	5170	4	US-09-677-046A-5	Sequence 5, Appli
239	163	9.0	2775	1	US-08-481-130-25	Sequence 25, Appl	312	157	8.7	1421	3	US-09-188-930-254	Sequence 254, App
240	163	9.0	2775	1	US-08-656-984A-25	Sequence 25, Appl	313	157	8.7	1421	3	US-09-312-283C-254	Sequence 254, App
241	163	9.0	2775	1	US-08-485-604-25	Sequence 25, Appl	314	157	8.7	1822	4	US-09-397-243D-1	Sequence 1, Appli
242	163	9.0	2775	2	US-08-487-595-25	Sequence 25, Appl	315	157	8.7	1857	4	US-09-907-794A-118	Sequence 118, App
243	163	9.0	2927	1	US-08-481-130-27	Sequence 27, Appl	316	157	8.7	1857	4	US-09-905-125A-118	Sequence 118, App
244	163	9.0	2927	1	US-08-656-984A-27	Sequence 27, Appl	317	157	8.7	1857	4	US-09-902-775A-118	Sequence 118, App
245	163	9.0	2927	1	US-08-485-604-27	Sequence 27, Appl	318	157	8.7	1857	4	US-09-906-700-118	Sequence 118, App
246	163	9.0	2927	2	US-08-487-595-27	Sequence 27, Appl	319	157	8.7	1857	4	US-09-903-603A-118	Sequence 118, App
247	162	9.0	1024	6	5169835-16	Patent No. 5169835	320	157	8.7	1857	4	US-09-904-920A-118	Sequence 118, App
248	162	9.0	1024	6	5169835-16	Patent No. 5169835	321	157	8.7	1857	4	US-09-909-064-118	Sequence 118, App
249	162	9.0	3503	1	US-07-631-717A-1	Sequence 1, Appli	322	157	8.7	1857	4	US-09-905-381A-118	Sequence 118, App
250	162	9.0	3503	1	US-08-166-717D-1	Sequence 1, Appli	323	157	8.7	1857	4	US-09-906-618-118	Sequence 118, App
251	161	8.9	1869	4	US-09-499-846-1	Sequence 1, Appli	324	156.5	8.7	1426	4	US-09-638-649-2	Sequence 2, Appli
252	161	8.9	3554	4	US-09-907-794A-422	Sequence 422, App	325	156.5	8.7	1426	4	US-09-638-648-2	Sequence 2, Appli
253	161	8.9	3554	4	US-09-905-125A-422	Sequence 422, App	326	156	8.6	1940	1	US-08-429-742-3	Sequence 3, Appli
254	161	8.9	3554	4	US-09-902-775A-422	Sequence 422, App	327	155.5	8.6	1421	3	US-09-188-930-70	Sequence 70, Appl
255	161	8.9	3554	4	US-09-906-700-422	Sequence 422, App	328	155.5	8.6	1421	4	US-09-312-283C-70	Sequence 70, Appl
256	161	8.9	3554	4	US-09-603A-422	Sequence 422, App	329	155.5	8.6	2184	3	US-09-484-370B-161	Sequence 161, App
257	161	8.9	3554	4	US-09-904-920A-422	Sequence 422, App	330	155.5	8.6	3307	1	US-08-456-647B-5	Sequence 5, Appli
258	161	8.9	3554	4	US-09-909-064-422	Sequence 422, App	331	155.5	8.6	3307	2	US-08-237-401A-5	Sequence 5, Appli
259	161	8.9	3554	4	US-09-905-381A-422	Sequence 422, App	332	155.5	8.6	3785	1	US-08-445-640-9	Sequence 9, Appli
260	161	8.9	3554	4	US-09-906-618-422	Sequence 422, App	333	155.5	8.6	3785	3	US-08-170-558-9	Sequence 9, Appli
261	161	8.9	5470	2	US-08-443-861-1	Sequence 1, Appli	334	155.5	8.6	3785	3	US-08-447-314-9	Sequence 9, Appli
262	161	8.9	5470	3	US-08-193-829B-1	Sequence 1, Appli	335	155.5	8.6	3785	3	US-08-445-461-9	Sequence 9, Appli
263	161	8.9	5470	3	US-09-967-655-10	Sequence 10, Appl	336	155.5	8.6	3785	4	US-09-223-490-9	Sequence 9, Appli
264	160.5	8.9	3159	3	US-08-986-485-3	Sequence 3, Appli	337	155	8.6	2431	3	US-08-985-526-35	Sequence 35, Appl
265	160.5	8.9	4111	4	US-09-375-248-1	Sequence 1, Appli	338	155	8.6	4006	4	US-09-949-016-4724	Sequence 4724, Ap
266	160.5	8.9	4195	1	US-08-340-011-1	Sequence 1, Appli	339	155	8.6	4006	1	US-09-949-016-4725	Sequence 4725, Ap
267	160.5	8.9	4195	3	US-08-901-710-1	Sequence 1, Appli	340	155	8.6	5406	1	US-07-813-593-3	Sequence 3, Appli
268	160.5	8.9	4195	4	US-09-169-079-1	Sequence 1, Appli	341	155	8.6	5406	1	US-07-977-451-5	Sequence 5, Appli
269	160.5	8.9	4416	3	US-08-795-430-1	Sequence 1, Appli	342	155	8.6	5406	1	US-07-946-507-3	Sequence 3, Appli
270	160.5	8.9	4416	3	US-09-355-700-1	Sequence 1, Appli	343	155	8.6	5406	1	US-08-252-517-5	Sequence 5, Appli
271	160.5	8.9	4416	3	US-08-601-132-36	Sequence 36, Appl	344	155	8.6	5406	1	US-07-906-397A-5	Sequence 5, Appli
272	160.5	8.9	4416	4	US-08-671-573B-36	Sequence 36, Appl	345	155	8.6	5406	1	US-08-601-891-5	Sequence 5, Appli
273	160.5	8.9	4416	4	US-09-631-092B-36	Sequence 36, Appl	346	155	8.6	5406	2	US-09-021-324-5	Sequence 5, Appli
274	160.5	8.9	4416	4	US-09-534-376A-1	Sequence 1, Appli	347	155	8.6	5406	4	US-09-872-136B-5	Sequence 5, Appli
275	160.5	8.9	4425	1	US-08-222-616-31	Sequence 31, Appl	348	155	8.6	5406	5	PCT-US92-03750-7	Sequence 7, Appli
276	160.5	8.9	4425	3	US-08-446-648-31	Sequence 31, Appl	349	155	8.6	5406	5	PCT-US92-05401-5	Sequence 5, Appli
277	160.5	8.9	4425	4	US-09-023-655-889	Sequence 889, App	350	155	8.6	5406	5	PCT-US92-09893-5	Sequence 5, Appli
278	160.5	8.9	4425	4	US-09-982-610-31	Sequence 31, Appl	351	154.5	8.6	1493	2	US-08-752-307B-6	Sequence 6, Appli
279	160.5	8.9	4425	5	PCT-US95-04228-31	Sequence 31, Appl	352	154.5	8.6	1493	3	US-09-707-802-6	Sequence 6, Appli
280	160.5	8.9	4795	1	US-08-340-011-3	Sequence 3, Appli	353	154.5	8.6	1493	3	US-09-991-326-6	Sequence 6, Appli
281	160.5	8.9	4795	3	US-08-901-710-3	Sequence 3, Appli	354	154.5	8.6	2600	2	US-08-427-497B-4	Sequence 4, Appli
282	160.5	8.9	4795	4	US-09-169-079-3	Sequence 3, Appli	355	154.5	8.6	2685	4	US-09-949-016-4734	Sequence 4734, Ap
283	160.5	8.9	9108	3	US-08-446-648-45	Sequence 45, Appl	356	154.5	8.6	7702	4	US-09-023-655-1336	Sequence 1336, Ap
284	160.5	8.9	9108	4	US-09-982-610-45	Sequence 45, Appl	357	154.5	8.6	7702	4	US-09-743-492A-3	Sequence 3, Appli
285	160.5	8.9	9108	5	PCT-US95-04228-45	Sequence 45, Appl	358	154	8.5	1009	3	US-09-462-270-3	Sequence 3, Appli
286	160	8.9	960	3	US-08-597-495B-23	Sequence 23, Appl	359	154	8.5	1737	3	US-09-173-151A-1	Sequence 1, Appli
287	160	8.9	960	3	US-09-068-051A-23	Sequence 23, Appl	360	154	8.5	2061	3	US-09-173-151A-3	Sequence 3, Appli
288	160	8.9	2469	1	US-07-997-133-2	Sequence 2, Appli	361	153.5	8.5	1964	3	US-08-468-856B-7	Sequence 7, Appli
289	160	8.9	2469	1	US-08-459-296-1	Sequence 1, Appli	362	153.5	8.5	1964	3	US-08-468-859A-7	Sequence 7, Appli
290	160	8.9	2469	5	US-07-997-133-2	Sequence 2, Appli	363	153	8.5	571	4	US-09-270-767-1097	Sequence 1097, Ap
291	160	8.9	2662	2	US-08-451-822A-14	Sequence 14, Appl	364	153	8.5	571	4	US-09-270-767-16379	Sequence 16379, A
292	160	8.9	2662	3	US-08-323-430-14	Sequence 14, Appl	365	153	8.5	1574	4	US-09-270-767-12428	Sequence 12428, A
293	160	8.9	2733	5	PCT-US96-00331-14	Sequence 14, Appl	366	153	8.5	6263	4	US-09-023-655-1473	Sequence 1473, Ap
294	160	8.9	2733	5	US-09-949-016-1876	Sequence 1876, Ap	367	152	8.4	3173	3	US-08-468-856B-1	Sequence 1, Appli
295	160	8.9	3944	4	US-09-949-016-1876	Sequence 1876, Ap	368	152	8.4	3173	3	US-08-468-859A-1	Sequence 1, Appli
296	160	8.9	3944	4	US-09-949-016-1877	Sequence 1877, Ap	369	152	8.4	3766	4	US-09-949-016-1651	Sequence 359, App
297	160	8.9	3944	4	US-09-949-016-1878	Sequence 1878, Ap	370	152	8.4	3766	4	US-09-949-016-359	Sequence 359, App
298	160	8.9	3944	4	US-09-949-016-1879	Sequence 1879, Ap	371	151.5	8.4	1190	4	US-09-949-016-1720	Sequence 1720, Ap
299	160	8.9	3944	4	US-09-949-016-1880	Sequence 1880, Ap	372	151.5	8.4	2003	1	US-08-036-555B-21	Sequence 21, Appl
300	160	8.9	3944	4	US-09-949-016-1881	Sequence 1881, Ap	373	151.5	8.4	2003	1	US-08-469-569-21	Sequence 21, Appl
301	160	8.9	3944	4	US-09-949-016-1882	Sequence 1882, Ap	374	151.5	8.4	2003	1	US-08-249-322A-21	Sequence 21, Appl
302	160	8.9	3944	4	US-09-949-016-1883	Sequence 1883, Ap	375	151.5	8.4	2003	1	US-08-469-526A-21	Sequence 21, Appl
303	159	8.8	462	4	US-09-270-767-2319	Sequence 2319, Ap	376	151.5	8.4	2003	2	US-08-734-591A-21	Sequence 21, Appl
304	159	8.8	462	4	US-09-270-767-17601	Sequence 17601, A	377	151.5	8.4	2003	2	US-08-469-660-21	Sequence 21, Appl

378	151.5	8.4	2003	3	US-08-341-018-71	Sequence 71, Appl	451	141.5	7.8	1140	3	US-08-470-339-149	Sequence 149, App
379	151.5	8.4	2003	3	US-08-470-335-21	Sequence 21, Appl	452	141.5	7.8	1140	3	US-08-467-602-149	Sequence 149, App
380	151.5	8.4	2003	3	US-08-735-021-21	Sequence 21, Appl	453	141.5	7.8	1140	4	US-08-411-295F-48	Sequence 48, Appl
381	151.5	8.4	2003	3	US-08-734-664A-21	Sequence 21, Appl	454	141.5	7.8	1140	5	PCT-US94-05083C-145	Sequence 145, App
382	151.5	8.4	2003	3	US-08-470-339-21	Sequence 21, Appl	455	141.5	7.8	1140	5	PCT-US95-06846A-149	Sequence 149, App
383	151.5	8.4	2003	3	US-08-467-602-21	Sequence 21, Appl	456	141.5	7.8	1164	1	US-08-445-640-11	Sequence 11, Appl
384	151.5	8.4	2003	4	US-08-411-295F-64	Sequence 64, Appl	457	141.5	7.8	1164	3	US-08-170-558-11	Sequence 11, Appl
385	151.5	8.4	2003	5	PCT-US94-05083C-21	Sequence 21, Appl	458	141.5	7.8	1164	3	US-08-447-314-11	Sequence 11, Appl
386	151.5	8.4	2003	5	PCT-US95-06846A-21	Sequence 21, Appl	459	141.5	7.8	1164	3	US-08-445-461-11	Sequence 11, Appl
387	150.5	8.3	1364	4	US-09-924-103-3	Sequence 3, Appl	460	141.5	7.8	1164	4	US-09-223-490-11	Sequence 11, Appl
388	150.5	8.3	2287	4	US-09-023-655-1216	Sequence 1216, Ap	461	141.5	7.8	1193	1	US-08-036-355B-134	Sequence 134, App
389	150	8.3	1079	1	US-08-471-570-13	Sequence 13, Appl	462	141.5	7.8	1193	1	US-08-469-569-134	Sequence 134, App
390	150	8.3	1954	1	US-08-471-570-5	Sequence 5, Appl	463	141.5	7.8	1193	1	US-08-249-322A-134	Sequence 134, App
391	150	8.3	2676	1	US-08-471-570-7	Sequence 7, Appl	464	141.5	7.8	1193	2	US-08-469-660-134	Sequence 134, App
392	149.5	8.3	5690	2	US-08-447-464-2	Sequence 2, Appl	465	141.5	7.8	1193	5	PCT-US94-05083C-130	Sequence 130, App
393	149.5	8.3	5690	2	US-08-716-679-2	Sequence 2, Appl	466	141.5	7.8	1193	5	PCT-US95-06846A-134	Sequence 134, App
394	148.5	8.2	4078	4	US-09-016-434-1132	Sequence 1132, Ap	467	141.5	7.8	1194	4	US-08-411-295F-3	Sequence 3, Appl
395	148.5	8.2	6000	1	US-08-348-006B-6	Sequence 6, Appl	468	141	7.8	2079	4	US-09-949-016-3171	Sequence 3171, Ap
396	148.5	8.2	6000	2	US-08-800-825A-6	Sequence 6, Appl	469	141	7.8	2079	4	US-09-949-016-3172	Sequence 3172, Ap
397	148.5	8.2	6000	3	US-09-158-657-6	Sequence 6, Appl	470	141	7.8	2079	4	US-09-949-016-3173	Sequence 3173, Ap
398	148.5	8.2	6000	5	PCT-US94-10166-6	Sequence 6, Appl	471	141	7.8	2079	4	US-09-949-016-3174	Sequence 3174, Ap
399	148	8.2	2351	1	US-08-168-091A-1	Sequence 1, Appl	472	141	7.8	2079	4	US-09-949-016-3175	Sequence 3175, Ap
400	147.5	8.2	1347	4	US-09-638-648-6	Sequence 6, Appl	473	141	7.8	2079	4	US-09-949-016-3176	Sequence 3176, Ap
401	147.5	8.2	1348	4	US-09-638-649-6	Sequence 6, Appl	474	141	7.8	2079	4	US-09-949-016-3177	Sequence 3177, Ap
402	147	8.1	2430	4	US-09-620-312D-176	Sequence 176, App	475	141	7.8	2079	4	US-09-949-016-3178	Sequence 3178, Ap
403	145.5	8.1	1199	4	US-09-270-767-13050	Sequence 13050, A	476	141	7.8	2079	4	US-09-949-016-3179	Sequence 3179, Ap
404	145	8.0	726	3	US-09-254-465A-4	Sequence 4, Appl	477	141	7.8	2079	4	US-09-949-016-3180	Sequence 3180, Ap
405	145	8.0	726	4	US-09-953-459-4	Sequence 4, Appl	478	141	7.8	6172	4	US-09-774-528-89	Sequence 89, Appl
406	144	8.0	3992	4	US-09-944-807-9	Sequence 9, Appl	479	140.5	7.8	1659	4	US-09-969-532-7	Sequence 7, Appl
407	143.5	7.9	1103	2	US-08-602-725-33	Sequence 33, Appl	480	140.5	7.8	1692	4	US-09-969-532-5	Sequence 5, Appl
408	143.5	7.9	1896	3	US-09-412-554A-8	Sequence 8, Appl	481	140.5	7.8	1701	4	US-09-969-532-3	Sequence 3, Appl
409	143.5	7.9	3416	2	US-08-451-822A-15	Sequence 15, Appl	482	140.5	7.8	1734	4	US-09-969-532-1	Sequence 1, Appl
410	143.5	7.9	3416	3	US-08-323-430-15	Sequence 15, Appl	483	140.5	7.8	1767	4	US-09-866-510-11	Sequence 11, Appl
411	143	7.9	2313	1	US-08-232-538-5	Sequence 5, Appl	484	140.5	7.8	2661	4	US-09-969-532-15	Sequence 15, Appl
412	143	7.9	2313	3	US-09-427-353-1	Sequence 1, Appl	485	140.5	7.8	2694	4	US-09-969-532-13	Sequence 13, Appl
413	143	7.9	2651	2	US-08-786-164-5	Sequence 5, Appl	486	140.5	7.8	2703	4	US-09-969-532-11	Sequence 11, Appl
414	143	7.9	2651	4	US-09-953-318-19	Sequence 19, Appl	487	140.5	7.8	2736	4	US-09-969-532-9	Sequence 9, Appl
415	143	7.9	3394	4	US-09-953-318-100	Sequence 100, App	488	140.5	7.8	2742	1	US-08-286-305A-2	Sequence 2, Appl
416	142.5	7.9	3394	4	US-09-592-998C-8	Sequence 8, Appl	489	140.5	7.8	2742	2	US-08-441-104A-2	Sequence 2, Appl
417	142.5	7.9	1958	6	5169835-1	Patent No. 5169835	490	140.5	7.8	2742	3	US-08-440-816A-2	Sequence 2, Appl
418	142.5	7.9	1958	6	5169835-1	Patent No. 5169835	491	140.5	7.8	2742	3	US-09-417-381A-2	Sequence 2, Appl
419	142.5	7.9	2205	5	PCT-US93-00031-12	Sequence 12, Appl	492	140.5	7.8	2768	4	US-09-949-016-1697	Sequence 1697, Ap
420	142.5	7.9	2217	5	PCT-US93-00031-8	Sequence 8, Appl	493	140.5	7.8	3270	4	US-09-866-510-1	Sequence 1, Appl
421	142.5	7.9	3080	1	US-08-482-073-4	Sequence 4, Appl	494	140.5	7.8	3270	4	US-09-866-510-3	Sequence 3, Appl
422	142	7.9	992	1	US-08-481-130-24	Sequence 24, Appl	495	140.5	7.8	3270	4	US-09-866-510-5	Sequence 5, Appl
423	142	7.9	992	1	US-08-656-984A-24	Sequence 24, Appl	496	140.5	7.8	3270	4	US-09-866-510-7	Sequence 7, Appl
424	142	7.9	992	1	US-08-485-604-24	Sequence 24, Appl	497	140.5	7.8	3270	4	US-09-866-510-9	Sequence 9, Appl
425	142	7.9	992	2	US-08-487-595-24	Sequence 24, Appl	498	140.5	7.8	3411	4	US-09-969-532-33	Sequence 33, Appl
426	141.5	7.8	1108	1	US-08-036-555B-135	Sequence 135, App	499	140.5	7.8	3611	1	US-08-445-640-1	Sequence 1, Appl
427	141.5	7.8	1108	1	US-08-469-569-135	Sequence 135, App	500	140.5	7.8	3611	3	US-08-170-558-1	Sequence 1, Appl
428	141.5	7.8	1108	1	US-08-249-322A-135	Sequence 135, App	501	140.5	7.8	3611	3	US-08-447-314-1	Sequence 1, Appl
429	141.5	7.8	1108	1	US-08-469-526A-135	Sequence 135, App	502	140.5	7.8	3611	3	US-08-445-461-1	Sequence 1, Appl
430	141.5	7.8	1108	2	US-08-734-591A-135	Sequence 135, App	503	140.5	7.8	3611	4	US-09-223-490-1	Sequence 1, Appl
431	141.5	7.8	1108	2	US-08-469-660-135	Sequence 135, App	504	140.5	7.8	4054	1	US-08-180-195-35	Sequence 35, Appl
432	141.5	7.8	1108	3	US-08-341-018-5	Sequence 5, Appl	505	140.5	7.8	4054	1	US-08-477-329-35	Sequence 35, Appl
433	141.5	7.8	1108	3	US-08-470-335-135	Sequence 135, App	506	140.5	7.8	4054	2	US-08-475-458-35	Sequence 35, Appl
434	141.5	7.8	1108	3	US-08-735-021-135	Sequence 135, App	507	140.5	7.8	4054	3	US-08-980-400-35	Sequence 35, Appl
435	141.5	7.8	1108	3	US-08-734-664A-135	Sequence 135, App	508	140.5	7.8	4054	3	US-09-583-459A-35	Sequence 35, Appl
436	141.5	7.8	1108	3	US-08-470-339-135	Sequence 135, App	509	140.5	7.8	4054	3	US-09-583-210-35	Sequence 35, Appl
437	141.5	7.8	1108	4	US-08-467-602-135	Sequence 135, App	510	140.5	7.8	4054	3	US-09-583-449A-35	Sequence 35, Appl
438	141.5	7.8	1108	4	US-08-411-295F-5	Sequence 5, Appl	511	140.5	7.8	4054	3	US-09-435-059-35	Sequence 35, Appl
439	141.5	7.8	1108	5	PCT-US94-05083C-131	Sequence 131, App	512	140.5	7.8	4100	1	US-08-168-917-3	Sequence 3, Appl
440	141.5	7.8	1140	1	US-08-036-555B-149	Sequence 149, App	513	140.5	7.8	4100	2	US-08-460-510-3	Sequence 3, Appl
441	141.5	7.8	1140	1	US-08-469-569-149	Sequence 149, App	514	140.5	7.8	4100	2	US-08-460-490-3	Sequence 3, Appl
442	141.5	7.8	1140	1	US-08-249-322A-149	Sequence 149, App	515	140.5	7.8	4100	5	PCT-US92-00730-3	Sequence 3, Appl
443	141.5	7.8	1140	1	US-08-469-526A-149	Sequence 149, App	516	140.5	7.8	4100	5	PCT-US92-00862-3	Sequence 3, Appl
444	141.5	7.8	1140	2	US-08-734-591A-149	Sequence 149, App	517	140.5	7.8	6373	3	US-08-462-728-1	Sequence 1, Appl
445	141.5	7.8	1140	2	US-08-469-660-149	Sequence 149, App	518	140.5	7.8	6373	3	US-08-461-917-1	Sequence 1, Appl
446	141.5	7.8	1140	2	US-08-469-660-149	Sequence 149, App	519	140.5	7.8	6373	4	US-08-464-436-1	Sequence 1, Appl
447	141.5	7.8	1140	3	US-08-341-018-55	Sequence 55, Appl	520	140.5	7.8	6375	1	US-08-168-917-5	Sequence 5, Appl
448	141.5	7.8	1140	3	US-08-470-335-149	Sequence 149, App	521	140.5	7.8	6375	1	US-08-460-510-5	Sequence 5, Appl
449	141.5	7.8	1140	3	US-08-735-021-149	Sequence 149, App	522	140.5	7.8	6375	2	US-08-460-490-5	Sequence 5, Appl
450	141.5	7.8	1140	3	US-08-734-664A-149	Sequence 149, App	523	140.5	7.8	6375	2	US-08-460-490-5	Sequence 5, Appl

524	140.5	7.8	6375	5	PCT-US92-00730-5	Sequence 5, Appli	597	134.5	7.4	1602	3	US-09-651-200-11	Sequence 11, Appli
525	140.5	7.8	6375	5	PCT-US92-00862-5	Sequence 5, Appli	598	134.5	7.4	1929	5	PCT-US93-00031-18	Sequence 10, Appli
526	140.5	7.8	6378	4	US-09-023-655-1194	Sequence 1194, Ap	599	134.5	7.4	1941	5	PCT-US93-00031-10	Sequence 18, Appli
527	140.5	7.8	6378	4	US-09-919-497-40	Sequence 40, Appli	600	134.5	7.4	1941	5	PCT-US93-00031-22	Sequence 22, Appli
528	140.5	7.8	6378	4	US-09-949-016-832	Sequence 832, App	601	134.5	7.4	2220	5	PCT-US93-00031-16	Sequence 16, Appli
529	140.5	7.8	6412	4	US-09-769-987-1	Sequence 1, Appli	602	134.5	7.4	2229	3	US-09-651-200-5	Sequence 5, Appli
530	140	7.8	610	4	US-09-270-767-39243	Sequence 29243, A	603	134.5	7.4	2811	3	US-08-482-073-3	Sequence 3, Appli
531	140	7.8	753	4	US-09-270-767-11521	Sequence 11521, A	604	134.5	7.4	2813	2	US-08-344-155C-99	Sequence 99, Appli
532	140	7.8	5084	1	US-09-306-691B-21	Sequence 21, Appli	605	134.5	7.4	2813	3	US-09-009-490A-90	Sequence 90, Appli
533	140	7.8	5084	4	US-09-023-655-1335	Sequence 1335, Ap	606	134.5	7.4	3063	3	US-09-620-312D-844	Sequence 844, App
534	140	7.8	5084	5	PCT-US93-06251-25	Sequence 25, Appli	607	134	7.4	1573	6	5169835-5	Patent No. 5169835
535	140	7.8	8083	3	US-09-383-630-4	Sequence 4, Appli	608	134	7.4	1573	6	5169835-5	Patent No. 5169835
536	140	7.8	8083	3	US-09-383-630-5	Sequence 5, Appli	609	133.5	7.4	1467	4	US-09-499-846-11	Sequence 11, Appli
537	139.5	7.7	2110	4	US-09-907-794A-319	Sequence 319, App	610	133	7.4	952	4	US-09-684-708A-22	Sequence 22, Appli
538	139.5	7.7	2110	4	US-09-905-125A-319	Sequence 319, App	611	133	7.4	1004	4	US-09-684-708A-24	Sequence 24, Appli
539	139.5	7.7	2110	4	US-09-902-775A-319	Sequence 319, App	612	133	7.4	1858	2	US-08-359-705B-7	Sequence 7, Appli
540	139.5	7.7	2110	4	US-09-906-700-319	Sequence 319, App	613	133	7.4	1858	2	US-08-286-846A-7	Sequence 7, Appli
541	139.5	7.7	2110	4	US-09-903-603A-319	Sequence 319, App	614	133	7.4	1858	2	US-08-457-880A-7	Sequence 7, Appli
542	139.5	7.7	2110	4	US-09-904-920A-319	Sequence 319, App	615	133	7.4	1858	3	US-08-444-622A-7	Sequence 7, Appli
543	139.5	7.7	2110	4	US-09-909-064-319	Sequence 319, App	616	133	7.4	1858	3	US-08-942-562-7	Sequence 7, Appli
544	139.5	7.7	2110	4	US-09-905-381A-319	Sequence 319, App	617	133	7.4	1858	3	US-09-156-923-7	Sequence 7, Appli
545	139.5	7.7	2110	4	US-09-906-618-319	Sequence 319, App	618	133	7.4	2715	2	US-08-359-705B-5	Sequence 5, Appli
546	139	7.7	989	1	US-08-282-951-5	Sequence 5, Appli	619	133	7.4	2715	2	US-08-286-846A-5	Sequence 5, Appli
547	139	7.7	1438	4	US-08-755-235-1	Sequence 1, Appli	620	133	7.4	2715	2	US-08-457-880A-5	Sequence 5, Appli
548	139	7.7	2477	1	US-08-429-742-1	Sequence 1, Appli	621	133	7.4	2715	3	US-08-444-622A-5	Sequence 5, Appli
549	139	7.7	25633	4	US-09-949-016-12084	Sequence 12084, A	622	133	7.4	2715	3	US-08-942-562-5	Sequence 5, Appli
550	139	7.7	25633	4	US-09-949-016-13721	Sequence 13721, A	623	133	7.4	2715	3	US-09-156-923-5	Sequence 5, Appli
551	138.5	7.7	1193	1	US-08-469-526A-134	Sequence 134, App	624	133	7.4	2903	4	US-09-949-016-5033	Sequence 5033, Ap
552	138.5	7.7	1193	2	US-08-734-591A-134	Sequence 134, App	625	133	7.4	2940	1	US-08-286-305A-8	Sequence 8, Appli
553	138.5	7.7	1193	3	US-08-341-018-3	Sequence 3, Appli	626	133	7.4	2940	2	US-08-441-104A-8	Sequence 8, Appli
554	138.5	7.7	1193	3	US-08-470-335-134	Sequence 134, App	627	133	7.4	2940	2	US-08-440-816A-8	Sequence 8, Appli
555	138.5	7.7	1193	3	US-08-735-021-134	Sequence 134, App	628	133	7.4	2940	2	US-09-417-381A-8	Sequence 8, Appli
556	138.5	7.7	1193	3	US-08-734-664A-134	Sequence 134, App	629	133	7.4	7476	4	US-09-949-016-17005	Sequence 17005, A
557	138.5	7.7	1193	3	US-08-470-339-134	Sequence 134, App	630	132.5	7.3	2009	3	US-08-468-856B-8	Sequence 8, Appli
558	138.5	7.7	1193	3	US-08-467-602-134	Sequence 134, App	631	132.5	7.3	2009	3	US-08-468-859A-8	Sequence 8, Appli
559	138.5	7.7	1545	4	US-09-949-016-5509	Sequence 5509, Ap	632	132	7.3	2166	3	US-09-175-928-1	Sequence 1, Appli
560	138.5	7.7	1710	4	US-09-723-368-3	Sequence 3, Appli	633	132	7.3	2434	3	US-09-272-496-1	Sequence 1, Appli
561	138.5	7.7	3199	4	US-09-628-188A-2	Sequence 2, Appli	634	132	7.3	2434	4	US-09-949-016-193	Sequence 193, App
562	137	7.6	1164	1	US-08-445-640-5	Sequence 5, Appli	635	132	7.3	2866	3	US-09-724-864-30	Sequence 30, Appli
563	137	7.6	1164	3	US-08-170-558-5	Sequence 5, Appli	636	131.5	7.3	1182	3	US-09-336-536-38	Sequence 38, Appli
564	137	7.6	1164	3	US-08-447-314-5	Sequence 5, Appli	637	131.5	7.3	1295	3	US-09-254-465A-8	Sequence 8, Appli
565	137	7.6	1164	3	US-08-445-461-5	Sequence 5, Appli	638	131.5	7.3	1295	4	US-09-907-794A-63	Sequence 63, Appli
566	137	7.6	1164	3	US-09-223-490-5	Sequence 5, Appli	639	131.5	7.3	1295	4	US-09-905-125A-63	Sequence 63, Appli
567	137	7.6	1591	3	US-08-468-856B-9	Sequence 9, Appli	640	131.5	7.3	1295	4	US-09-902-775A-63	Sequence 63, Appli
568	137	7.6	1591	3	US-08-468-859A-9	Sequence 9, Appli	641	131.5	7.3	1295	4	US-09-906-700-63	Sequence 63, Appli
569	137	7.6	2598	4	US-09-949-016-3414	Sequence 3414, Ap	642	131.5	7.3	1295	4	US-09-903-603A-63	Sequence 63, Appli
570	137	7.6	3111	3	US-08-891-845-1	Sequence 1, Appli	643	131.5	7.3	1295	4	US-09-904-920A-63	Sequence 63, Appli
571	137	7.6	3111	4	US-09-514-573-1	Sequence 1, Appli	644	131.5	7.3	1295	4	US-09-909-064-63	Sequence 63, Appli
572	136.5	7.6	1004	3	US-09-383-586-24	Sequence 24, Appli	645	131.5	7.3	1295	4	US-09-905-381A-63	Sequence 63, Appli
573	136.5	7.6	1004	3	US-09-823-038A-24	Sequence 24, Appli	646	131.5	7.3	1295	4	US-09-906-618-63	Sequence 63, Appli
574	136.5	7.6	2244	3	US-09-354-151-1	Sequence 1, Appli	647	131.5	7.3	1295	4	US-09-953-499-8	Sequence 8, Appli
575	136.5	7.6	2426	4	US-09-023-655-1156	Sequence 1156, Ap	648	131.5	7.3	1846	3	US-09-336-536-37	Sequence 37, Appli
576	136.5	7.6	2557	2	US-09-044-506A-1	Sequence 1, Appli	649	131	7.3	734	1	US-08-471-570-11	Sequence 11, Appli
577	136.5	7.6	2557	3	US-08-478-208-31	Sequence 31, Appli	650	131	7.3	1027	4	US-09-684-708A-26	Sequence 26, Appli
578	136.5	7.6	2557	3	US-09-336-536-72	Sequence 72, Appli	651	131	7.3	1423	4	US-09-823-038A-46	Sequence 46, Appli
579	136.5	7.6	2557	6	5264554-1	Patent No. 5264554	652	131	7.3	1584	3	US-08-928-383B-1	Sequence 1, Appli
580	136.5	7.6	2557	6	5264554-1	Patent No. 5264554	653	131	7.3	1604	4	US-09-419-788-18	Sequence 18, Appli
581	136	7.5	1326	4	US-09-799-451-382	Sequence 382, App	654	131	7.3	1683	4	US-09-866-510-23	Sequence 23, Appli
582	136	7.5	1377	3	US-09-435-956A-2	Sequence 2, Appli	655	131	7.3	3086	4	US-09-684-708A-20	Sequence 20, Appli
583	136	7.5	1603	1	US-08-471-570-3	Sequence 3, Appli	656	131	7.3	3321	4	US-09-866-510-13	Sequence 13, Appli
584	136	7.5	1932	5	PCT-US93-00031-20	Sequence 20, Appli	657	131	7.3	3321	4	US-09-866-510-15	Sequence 15, Appli
585	136	7.5	2310	1	US-08-471-570-9	Sequence 9, Appli	658	131	7.3	3321	4	US-09-866-510-17	Sequence 17, Appli
586	135	7.5	1042	2	US-08-427-497E-6	Sequence 6, Appli	659	131	7.3	3321	4	US-09-866-510-19	Sequence 19, Appli
587	135	7.5	1494	4	US-09-499-846-6	Sequence 5, Appli	660	131	7.3	3321	4	US-09-866-510-21	Sequence 21, Appli
588	135	7.5	1494	4	US-09-499-846-9	Sequence 9, Appli	661	131	7.3	4465	1	US-08-180-195-1	Sequence 1, Appli
589	135	7.5	1578	4	US-09-499-846-3	Sequence 3, Appli	662	131	7.3	4465	1	US-08-477-329-1	Sequence 1, Appli
590	135	7.5	1578	4	US-09-499-846-7	Sequence 7, Appli	663	131	7.3	4465	2	US-08-475-458-1	Sequence 1, Appli
591	135	7.5	2214	1	US-08-245-295-7	Sequence 7, Appli	664	131	7.3	4465	3	US-08-980-400-1	Sequence 1, Appli
592	135	7.5	2214	1	US-08-481-130-7	Sequence 7, Appli	665	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
593	135	7.5	2214	1	US-08-656-984A-7	Sequence 7, Appli	666	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
594	135	7.5	2214	1	US-08-485-604-7	Sequence 7, Appli	667	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
595	135	7.5	2214	1	US-08-487-595-7	Sequence 7, Appli	668	131	7.3	4465	3	US-09-583-459A-1	Sequence 1, Appli
596	135	7.5	2768	4	US-09-774-528-426	Sequence 426, App	669	131	7.3	5427	1	US-08-168-917-1	Sequence 1, Appli

670	131	7.3	5427	2	US-08-460-510-1	Sequence 1, Appli	743	127.5	7.1	1554	4	US-09-949-016-3333	Sequence 3333, Ap
671	131	7.3	5427	2	US-08-460-490-1	Sequence 1, Appli	744	127.5	7.1	1554	4	US-09-949-016-3334	Sequence 3334, Ap
672	131	7.3	5427	3	US-08-462-728-3	Sequence 3, Appli	745	127.5	7.1	1554	4	US-09-949-016-3335	Sequence 3335, Ap
673	131	7.3	5427	3	US-08-461-917-3	Sequence 3, Appli	746	127.5	7.1	1652	1	US-08-036-555B-148	Sequence 148, App
674	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	747	127.5	7.1	1652	1	US-08-469-569-148	Sequence 148, App
675	131	7.3	5427	4	US-08-464-436-3	Sequence 3, Appli	748	127.5	7.1	1652	1	US-08-249-322A-148	Sequence 148, App
676	131	7.3	5427	5	PCT-US92-00730-1	Sequence 1, Appli	749	127.5	7.1	1652	1	US-08-469-526A-148	Sequence 148, App
677	131	7.3	5427	5	PCT-US92-00862-1	Sequence 1, Appli	750	127.5	7.1	1652	1	US-08-734-591A-148	Sequence 148, App
678	131	7.3	5570	4	US-09-023-655-1193	Sequence 1193, Ap	751	127.5	7.1	1652	2	US-08-469-660-148	Sequence 148, App
679	130.5	7.2	1022	3	US-09-152-060-35	Sequence 35, Appli	752	127.5	7.1	1652	3	US-08-341-018-53	Sequence 53, Appli
680	130.5	7.2	1401	4	US-09-604-107A-7	Sequence 7, Appli	753	127.5	7.1	1652	3	US-08-470-335-148	Sequence 148, App
681	130.5	7.2	1452	4	US-09-949-016-5250	Sequence 5250, Ap	754	127.5	7.1	1652	3	US-08-735-021-148	Sequence 148, App
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686	130	7.2	744	1	US-08-249-322A-133	Sequence 133, App	759	127.5	7.1	1652	5	PCT-US94-05083C-144	Sequence 144, App
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688	130	7.2	744	2	US-08-734-591A-133	Sequence 133, App	761	127.5	7.1	1831	3	US-09-484-970B-84	Sequence 84, Appli
689	130	7.2	744	2	US-08-469-660-133	Sequence 133, App	762	127.5	7.1	32207	2	US-08-770-379-20	Sequence 20, Appli
690	130	7.2	744	3	US-08-341-018-1	Sequence 1, Appli	763	127.5	7.1	32207	3	US-08-757-669A-20	Sequence 20, Appli
691	130	7.2	744	3	US-08-470-335-133	Sequence 133, App	764	127.5	7.1	32207	3	US-09-230-371A-20	Sequence 20, Appli
692	130	7.2	744	3	US-08-735-021-133	Sequence 133, App	765	127	7.0	1046	4	US-09-419-788-163	Sequence 163, App
693	130	7.2	744	3	US-08-734-664A-133	Sequence 133, App	766	127	7.0	1730	4	US-09-919-172-19	Sequence 19, Appli
694	130	7.2	744	3	US-08-470-339-133	Sequence 133, App	767	127	7.0	2430	4	US-09-949-016-5179	Sequence 5179, Ap
695	130	7.2	744	3	US-08-467-602-133	Sequence 133, App	768	127	7.0	2885	4	US-09-949-016-5773	Sequence 5773, Ap
696	130	7.2	744	5	PCT-US94-05083C-129	Sequence 129, App	769	127	7.0	2901	4	US-09-949-016-251	Sequence 251, App
697	130	7.2	744	5	PCT-US95-06846A-133	Sequence 133, App	770	127	7.0	2949	3	US-09-412-554A-3	Sequence 3, Appli
698	130	7.2	2534	2	US-09-044-506A-30	Sequence 30, Appli	771	126.5	7.0	377	4	US-09-270-767-6506	Sequence 6506, Ap
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701	129.5	7.2	1884	3	US-09-398-496-5	Sequence 5, Appli	774	126	7.0	1870	2	US-08-286-846A-3	Sequence 3, Appli
702	129.5	7.2	2376	1	US-07-913-952-3	Sequence 3, Appli	775	126	7.0	1870	2	US-08-457-880A-3	Sequence 3, Appli
703	129.5	7.2	2453	1	US-07-813-593-1	Sequence 1, Appli	776	126	7.0	1870	3	US-08-444-622A-3	Sequence 3, Appli
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705	129.5	7.2	3453	1	US-07-946-507-1	Sequence 1, Appli	778	126	7.0	1870	3	US-09-156-923-3	Sequence 3, Appli
706	129.5	7.2	3453	1	US-08-252-517-1	Sequence 1, Appli	779	126	7.0	3060	2	US-08-286-305A-6	Sequence 6, Appli
707	129.5	7.2	3453	1	US-07-906-397A-1	Sequence 1, Appli	780	126	7.0	3060	2	US-08-441-104A-6	Sequence 6, Appli
708	129.5	7.2	3453	1	US-08-601-891-1	Sequence 1, Appli	781	126	7.0	3060	2	US-08-440-816A-6	Sequence 6, Appli
709	129.5	7.2	3453	2	US-09-021-324-1	Sequence 1, Appli	782	126	7.0	3060	3	US-09-417-381A-6	Sequence 6, Appli
710	129.5	7.2	3453	4	US-09-872-136B-1	Sequence 1, Appli	783	126	7.0	3194	2	US-08-359-705B-1	Sequence 1, Appli
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712	129.5	7.2	3453	5	PCT-US92-05401-1	Sequence 1, Appli	785	126	7.0	3194	2	US-08-457-880A-1	Sequence 1, Appli
713	129.5	7.2	3453	5	PCT-US92-09893-1	Sequence 1, Appli	786	126	7.0	3194	3	US-08-444-622A-1	Sequence 1, Appli
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715	129	7.1	1459	4	US-09-949-016-658	Sequence 858, App	788	126	7.0	3194	3	US-09-156-923-1	Sequence 1, Appli
716	129	7.1	1597	3	US-09-038-832-3	Sequence 3, Appli	789	125.5	6.9	1095	3	US-08-942-383B-3	Sequence 3, Appli
717	129	7.1	2449	4	US-09-949-016-1248	Sequence 1248, Ap	790	125	6.9	1176	5	PCT-US95-15696-1	Sequence 1, Appli
718	129	7.1	2866	4	US-09-949-016-2340	Sequence 2340, Ap	791	125	6.9	1472	1	US-08-245-295-9	Sequence 9, Appli
719	129	7.1	2900	3	US-09-038-832-1	Sequence 1, Appli	792	125	6.9	1472	1	US-08-481-130-9	Sequence 9, Appli
720	129	7.1	3008	3	US-09-188-930-65	Sequence 65, Appli	793	125	6.9	1472	1	US-08-656-984A-9	Sequence 9, Appli
721	129	7.1	3008	4	US-09-312-283C-65	Sequence 65, Appli	794	125	6.9	1472	1	US-08-485-604-9	Sequence 9, Appli
722	128.5	7.1	3521	1	US-08-222-299-1	Sequence 11, Appli	795	125	6.9	1472	2	US-08-487-595-9	Sequence 9, Appli
723	128.5	7.1	3521	2	US-08-434-878-1	Sequence 1, Appli	796	125	6.9	1715	1	US-07-847-743B-24	Sequence 24, Appli
724	128.5	7.1	3521	5	PCT-US95-03718-1	Sequence 1, Appli	797	125	6.9	1715	1	US-08-456-201-24	Sequence 24, Appli
725	128	7.1	1110	3	US-09-336-536-27	Sequence 27, Appli	798	125	6.9	1715	2	US-08-456-241-24	Sequence 24, Appli
726	128	7.1	1460	2	US-08-392-338A-18	Sequence 18, Appli	799	125	6.9	1715	5	PCT-US92-04295A-24	Sequence 24, Appli
727	128	7.1	1460	3	US-09-166-750-18	Sequence 18, Appli	800	125	6.9	2199	1	US-07-847-743B-7	Sequence 7, Appli
728	128	7.1	1460	3	US-09-166-093-18	Sequence 18, Appli	801	125	6.9	2199	1	US-08-086-277-7	Sequence 7, Appli
729	128	7.1	1460	3	US-09-172-019-18	Sequence 18, Appli	802	125	6.9	2199	2	US-08-456-201-7	Sequence 7, Appli
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732	128	7.1	1869	3	US-09-336-536-26	Sequence 26, Appli	805	125	6.9	2199	3	US-08-703-089-7	Sequence 7, Appli
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735	128	7.1	3707	4	US-09-949-016-827	Sequence 827, App	808	125	6.9	2431	1	US-08-456-201-25	Sequence 25, Appli
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740	127.5	7.1	1554	4	US-09-949-016-3330	Sequence 3330, Ap	813	125	6.9	2490	2	US-08-456-241-23	Sequence 23, Appli
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816	124.5	6.9	2681	1	US-08-070-165F-9	Sequence 9, Appli	889	121.5	6.7	390	3	US-09-254-465A-3	Sequence 3, Appli
c 817	124.5	6.9	2681	2	US-08-885-418-9	Sequence 9, Appli	890	121.5	6.7	390	4	US-09-953-499-3	Sequence 3, Appli
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871	122.5	6.8	1813	4	US-09-905-361A-38	Sequence 38, Appli	944	119	6.6	3397	4	US-09-949-016-2188	Sequence 2188, Ap
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962	117.5	6.5	3011	4	US-08-406-824A-5	Sequence 5, Appli	1035	115	6.4	820	4	US-09-270-767-1214	Sequence 1214, Ap
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1007	116	6.4	2909	1	US-08-554-612C-11	Sequence 11, Appl	1080	113.5	6.3	975	3	US-08-996-338-11	Sequence 11, Appl
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1013	115.5	6.4	755	1	US-08-515-903A-5	Sequence 5, Appli	1086	113.5	6.3	1817	1	US-08-473-981A-5	Sequence 5, Appli
1014	115.5	6.4	755	5	PCT-US95-12840-5	Sequence 5, Appli	1087	113.5	6.3	1817	2	US-08-474-087-5	Sequence 5, Appli
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1016	115.5	6.4	1693	2	US-08-487-113D-118	Sequence 118, App	1089	113.5	6.3	2830	3	US-09-110-618-3	Sequence 3, Appli
1017	115.5	6.4	1693	2	US-08-720-420A-118	Sequence 118, App	1090	113.5	6.3	2830	3	US-09-578-178-3	Sequence 3, Appli
1018	115.5	6.4	2675	1	US-08-070-165F-5	Sequence 5, Appli	1091	113.5	6.3	2830	4	US-09-577-806-3	Sequence 3, Appli
1019	115.5	6.4	2675	2	US-08-885-418-5	Sequence 5, Appli	1092	113.5	6.3	2830	4	US-09-621-502-7	Sequence 7, Appli
c1020	115	6.4	344	4	US-09-702-705-964	Sequence 964, App	1093	113.5	6.3	3095	3	US-08-434-000A-7	Sequence 7, Appli
1021	115	6.4	344	4	US-09-702-705-1148	Sequence 1148, Ap	1094	113.5	6.3	3095	4	US-09-312-157-7	Sequence 7, Appli
1022	115	6.4	344	4	US-09-702-705-1321	Sequence 1321, Ap	1095	113.5	6.3	3095	4	US-09-717-888-7	Sequence 7, Appli
c1023	115	6.4	344	4	US-09-736-457-964	Sequence 964, App	1096	113.5	6.3	3556	4	US-09-270-767-10439	Sequence 10439, A
1024	115	6.4	344	4	US-09-736-457-1148	Sequence 1148, Ap	c1097	113	6.3	536	4	US-09-736-457-1461	Sequence 1461, Ap
1025	115	6.4	344	4	US-09-736-457-1321	Sequence 1321, Ap	c1098	113	6.3	536	4	US-09-614-124B-1461	Sequence 1461, Ap
c1026	115	6.4	344	4	US-09-614-124B-964	Sequence 964, App	c1099	113	6.3	536	4	US-09-671-325-1461	Sequence 1461, Ap
1027	115	6.4	344	4	US-09-614-124B-1148	Sequence 1148, Ap	c1100	113	6.3	536	4	US-09-671-325-1461	Sequence 1461, Ap
1028	115	6.4	344	4	US-09-614-124B-1321	Sequence 1321, Ap	c1101	113	6.3	536	4	US-09-658-824-1461	Sequence 1461, Ap
c1029	115	6.4	344	4	US-09-671-325-964	Sequence 964, App	1102	112.5	6.2	1106	3	US-09-361-434-16	Sequence 16, Appl
1030	115	6.4	344	4	US-09-671-325-1148	Sequence 1148, Ap	c1103	112.5	6.2	1106	3	US-09-361-434-18	Sequence 18, Appl
1031	115	6.4	344	4	US-09-671-325-1321	Sequence 1321, Ap	1104	112.5	6.2	1106	3	US-09-635-025-16	Sequence 16, Appl
c1032	115	6.4	344	4	US-09-658-824-964	Sequence 964, App	c1105	112.5	6.2	1106	3	US-09-635-025-18	Sequence 18, Appl
1033	115	6.4	344	4	US-09-658-824-1148	Sequence 1148, Ap	1106	112.5	6.2	1331	3	US-08-463-903-7	Sequence 7, Appli
1034	115	6.4	344	4	US-09-658-824-1321	Sequence 1321, Ap	1107	112.5	6.2	1331	3	US-07-935-695-7	Sequence 7, Appli

1108	112.5	6.2	1515	3	US-08-928-383B-25	Sequence 25, Appl	1181	110	6.1	1456	4	US-09-828-995B-16	Sequence 16, Appl
1109	112.5	6.2	1557	1	US-08-481-130-26	Sequence 26, Appl	c1182	110	6.1	1456	4	US-09-828-995B-18	Sequence 18, Appl
1110	112.5	6.2	1557	1	US-08-656-984A-26	Sequence 26, Appl	1183	110	6.1	1742	3	US-09-517-605-7	Sequence 7, Appl
1111	112.5	6.2	1557	1	US-08-485-604-26	Sequence 26, Appl	1184	110	6.1	1742	3	US-09-023-655-1013	Sequence 1013, Ap
1112	112.5	6.2	1557	2	US-08-487-595-26	Sequence 26, Appl	c1185	110	6.1	1742	3	US-09-453-702B-243	Sequence 243, App
1113	112.5	6.2	2433	4	US-08-999-689A-2	Sequence 2, Appl	1186	109.5	6.1	1213	1	US-08-554-612C-14	Sequence 14, Appl
1114	112.5	6.2	2433	4	US-09-944-807-3	Sequence 3, Appl	1187	109.5	6.1	1443	1	US-08-443-965B-10	Sequence 10, Appl
1115	112	6.2	1330	3	US-08-463-903-5	Sequence 5, Appl	1188	109.5	6.1	1443	2	US-08-425-989B-10	Sequence 10, Appl
1116	112	6.2	1330	3	US-07-935-695-5	Sequence 5, Appl	1189	109.5	6.1	1443	2	US-08-443-966B-10	Sequence 10, Appl
1117	112	6.2	2309	3	US-09-075-215A-16	Sequence 16, Appl	1190	109.5	6.1	1452	3	US-09-039-982A-36	Sequence 36, Appl
1118	111.5	6.2	989	3	US-09-361-434-21	Sequence 21, Appl	1191	109.5	6.1	1452	3	US-09-039-641-36	Sequence 36, Appl
1119	111.5	6.2	989	3	US-09-361-434-23	Sequence 23, Appl	1192	109.5	6.1	1452	3	US-09-039-762A-36	Sequence 36, Appl
1120	111.5	6.2	989	3	US-09-635-025-21	Sequence 21, Appl	1193	109.5	6.1	1452	3	US-09-042-92D-36	Sequence 36, Appl
1121	111.5	6.2	989	3	US-09-635-025-23	Sequence 23, Appl	1194	109.5	6.1	1452	3	US-08-913-612A-36	Sequence 36, Appl
1122	111.5	6.2	1359	4	US-08-961-309-69	Sequence 69, Appl	1195	109.5	6.1	1452	4	US-10-266-463A-36	Sequence 36, Appl
1123	111.5	6.2	1377	4	US-09-732-877B-25	Sequence 25, Appl	1196	109.5	6.1	1518	3	US-09-240-915-1	Sequence 1, Appl
1124	111.5	6.2	1704	3	US-09-032-337-38	Sequence 38, Appl	1197	109.5	6.1	1518	3	US-09-591-435-1	Sequence 1, Appl
1125	111.5	6.2	1907	4	US-09-949-016-1692	Sequence 1692, Ap	1198	109.5	6.1	1599	2	US-08-689-870-1	Sequence 1, Appl
1126	111.5	6.2	1928	4	US-09-723-368-1	Sequence 1, Appl	1199	109.5	6.1	1599	2	US-08-689-873-1	Sequence 1, Appl
1127	111.5	6.2	1928	4	US-09-949-016-407	Sequence 407, App	1200	109.5	6.1	1611	3	US-09-039-982A-35	Sequence 35, Appl
1128	111.5	6.2	3120	1	US-08-222-616-22	Sequence 22, Appl	1201	109.5	6.1	1611	3	US-09-039-641-35	Sequence 35, Appl
1129	111.5	6.2	3120	3	US-08-446-648-22	Sequence 22, Appl	1202	109.5	6.1	1611	3	US-09-039-762A-35	Sequence 35, Appl
1130	111.5	6.2	3120	4	US-09-982-610-22	Sequence 22, Appl	1203	109.5	6.1	1611	3	US-08-042-492D-35	Sequence 35, Appl
1131	111.5	6.2	3120	5	PCT-US93-04228-22	Sequence 22, Appl	1204	109.5	6.1	1611	3	US-08-913-612A-35	Sequence 35, Appl
1132	111.5	6.2	4989	3	US-09-560-639-3	Sequence 3, Appl	1205	109.5	6.1	1611	4	US-10-266-463A-35	Sequence 35, Appl
1133	111	6.1	966	3	US-09-361-434-19	Sequence 19, Appl	1206	109.5	6.1	1656	3	US-08-318-039A-2	Sequence 2, Appl
1134	111	6.1	966	3	US-09-361-434-20	Sequence 20, Appl	1207	109.5	6.1	1656	3	US-08-318-038D-16	Sequence 16, Appl
1135	111	6.1	966	3	US-09-635-025-19	Sequence 19, Appl	1208	109.5	6.1	1656	3	US-08-227-496C-20	Sequence 20, Appl
1136	111	6.1	966	3	US-09-635-025-20	Sequence 20, Appl	1209	109.5	6.1	1656	3	US-08-435-568A-2	Sequence 2, Appl
1137	111	6.1	1264	4	US-09-579-845-5	Sequence 5, Appl	1210	109.5	6.1	1784	1	US-08-554-612C-13	Sequence 13, Appl
1138	111	6.1	1286	4	US-09-949-016-3587	Sequence 3587, Ap	1211	109.5	6.1	1846	1	US-08-483-389-117	Sequence 117, App
1139	111	6.1	1357	1	US-08-091-519-1	Sequence 1, Appl	1212	109.5	6.1	2986	3	US-09-062-416-1	Sequence 1, Appl
1140	111	6.1	1357	1	US-08-442-043A-1	Sequence 1, Appl	1213	109.5	6.1	3003	4	US-09-023-655-1115	Sequence 1115, Ap
1141	111	6.1	1357	4	US-09-461-908-1	Sequence 1, Appl	1214	109.5	6.1	3016	2	US-08-344-155C-97	Sequence 97, Appl
1142	111	6.1	1357	4	US-08-441-893A-1	Sequence 1, Appl	1215	109.5	6.1	3017	3	US-09-009-490A-86	Sequence 86, Appl
1143	111	6.1	1357	4	US-08-406-824A-7	Sequence 7, Appl	1216	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1144	111	6.1	1357	4	US-09-921-667-7	Sequence 7, Appl	1217	109.5	6.1	3024	6	5284931-1	Patent No. 5284931
1145	111	6.1	1357	5	PCT-US91-03478-1	Sequence 1, Appl	1218	109	6.0	2142	4	US-09-774-528-100	Sequence 100, App
1146	111	6.1	1458	4	US-08-030-175-6	Sequence 6, Appl	1219	109	6.0	2163	4	US-09-774-528-99	Sequence 99, Appl
1147	111	6.1	1458	4	US-08-030-175-7	Sequence 7, Appl	1220	109	6.0	3734	3	US-09-579-692B-7	Sequence 7, Appl
1148	110.5	6.1	534	4	US-09-702-705-1325	Sequence 1325, Ap	1221	108.5	6.0	1255	3	US-09-412-554A-7	Sequence 7, Appl
1149	110.5	6.1	534	4	US-09-736-457-1325	Sequence 1325, Ap	1222	108.5	6.0	1320	2	US-08-125-462-3	Sequence 3, Appl
1150	110.5	6.1	534	4	US-09-614-124B-1325	Sequence 1325, Ap	1223	108.5	6.0	1320	2	US-08-891-848-3	Sequence 3, Appl
1151	110.5	6.1	534	4	US-09-671-325-1325	Sequence 1325, Ap	1224	108.5	6.0	2818	4	US-09-620-312D-92	Sequence 92, Appl
1152	110.5	6.1	534	4	US-09-658-824-1325	Sequence 1325, Ap	1225	108.5	6.0	2820	4	US-09-799-451-370	Sequence 370, App
1153	110.5	6.1	2614	2	US-08-795-868-15	Sequence 15, Appl	1226	108.5	6.0	4900	1	US-08-245-295-5	Sequence 5, Appl
1154	110.5	6.1	2614	3	US-09-303-089-15	Sequence 15, Appl	1227	108.5	6.0	4900	1	US-08-481-130-5	Sequence 5, Appl
1155	110.5	6.1	2614	3	US-09-134-250-15	Sequence 15, Appl	1228	108.5	6.0	4900	1	US-08-656-984A-5	Sequence 5, Appl
1156	110.5	6.1	2906	4	US-09-907-794A-291	Sequence 291, App	1229	108.5	6.0	4900	2	US-08-485-604-5	Sequence 5, Appl
1157	110.5	6.1	2906	4	US-09-905-125A-291	Sequence 291, App	1230	108.5	6.0	4900	2	US-08-487-595-5	Sequence 5, Appl
1158	110.5	6.1	2906	4	US-09-902-775A-291	Sequence 291, App	1231	108.5	6.0	4900	3	US-08-863-790-26	Sequence 26, Appl
1159	110.5	6.1	2906	4	US-09-906-700-291	Sequence 291, App	1232	108.5	6.0	4900	3	US-08-296-749-26	Sequence 26, Appl
1160	110.5	6.1	2906	4	US-09-903-603A-291	Sequence 291, App	1233	108.5	6.0	5077	1	US-08-245-295-8	Sequence 8, Appl
1161	110.5	6.1	2906	4	US-09-904-920A-291	Sequence 291, App	1234	108.5	6.0	5077	1	US-08-481-130-8	Sequence 8, Appl
1162	110.5	6.1	2906	4	US-09-909-064-291	Sequence 291, App	1235	108.5	6.0	5077	1	US-08-656-984A-8	Sequence 8, Appl
1163	110.5	6.1	2906	4	US-09-905-381A-291	Sequence 291, App	1236	108.5	6.0	5077	1	US-08-485-604-8	Sequence 8, Appl
1164	110.5	6.1	2906	4	US-09-906-618-291	Sequence 291, App	1237	108.5	6.0	5077	2	US-08-487-595-8	Sequence 8, Appl
1165	110.5	6.1	2926	2	US-08-724-394A-13	Sequence 13, Appl	1238	108	6.0	836	3	US-08-463-903-1	Sequence 1, Appl
1166	110.5	6.1	2970	4	US-09-566-921-105	Sequence 105, App	1239	108	6.0	836	3	US-07-935-695-1	Sequence 1, Appl
1167	110.5	6.1	7100	4	US-09-949-016-16418	Sequence 16418, A	1240	108	6.0	856	3	US-08-463-903-16	Sequence 16, Appl
1168	110	6.1	738	2	US-08-224-591-13	Sequence 13, Appl	1241	108	6.0	856	3	US-07-935-695-16	Sequence 16, Appl
1169	110	6.1	738	2	US-08-392-338A-22	Sequence 22, Appl	1242	108	6.0	1642	4	US-10-000-489-77	Sequence 77, Appl
1170	110	6.1	738	2	US-08-926-789-13	Sequence 13, Appl	1243	108	6.0	1645	2	US-08-724-394A-14	Sequence 14, Appl
1171	110	6.1	738	3	US-09-166-750-22	Sequence 22, Appl	1244	108	6.0	4626	4	US-09-566-921-4	Sequence 4, Appl
1172	110	6.1	738	3	US-09-166-093-22	Sequence 22, Appl	1245	108	6.0	24154	4	US-09-949-016-16374	Sequence 16374, A
1173	110	6.1	738	3	US-09-172-019-22	Sequence 22, Appl	1246	107.5	6.0	597	2	US-08-768-964-11	Sequence 11, Appl
1174	110	6.1	738	3	US-09-166-094-22	Sequence 22, Appl	c1247	107.5	6.0	597	2	US-08-768-964-16	Sequence 16, Appl
1175	110	6.1	738	4	US-09-443-213-22	Sequence 22, Appl	1248	107.5	6.0	597	3	US-09-005-299-11	Sequence 11, Appl
1176	110	6.1	738	5	PCT-US93-11138-13	Sequence 13, Appl	c1249	107.5	6.0	597	3	US-09-005-299-16	Sequence 16, Appl
1177	110	6.1	1213	6	5223418-1	Patent No. 5223418	1250	107.5	6.0	597	3	US-09-515-431-11	Sequence 11, Appl
1178	110	6.1	1213	6	5223418-1	Patent No. 5223418	c1251	107.5	6.0	597	3	US-09-515-431-16	Sequence 16, Appl
1179	110	6.1	1352	3	US-08-463-903-11	Sequence 11, Appl	1252	107.5	6.0	789	2	US-08-768-964-4	Sequence 4, Appl
1180	110	6.1	1352	3	US-07-935-695-11	Sequence 11, Appl	c1253	107.5	6.0	789	2	US-08-768-964-5	Sequence 5, Appl

1254	107.5	6.0	789	3	US-09-005-299-4	Sequence 4, Appli	1327	103.5	5.7	409	4	US-09-702-705-1328	Sequence 1328, Ap
c1255	107.5	6.0	789	3	US-09-005-299-5	Sequence 5, Appli	1328	103.5	5.7	409	4	US-09-736-457-1328	Sequence 1328, Ap
1256	107.5	6.0	789	3	US-09-515-431-4	Sequence 4, Appli	1329	103.5	5.7	409	4	US-09-614-124B-1328	Sequence 1328, Ap
c1257	107.5	6.0	789	3	US-09-515-431-5	Sequence 5, Appli	1330	103.5	5.7	409	4	US-09-671-325-1328	Sequence 1328, Ap
1258	107.5	6.0	803	1	US-08-323-445A-7	Sequence 7, Appli	1331	103.5	5.7	409	4	US-09-658-824-1328	Sequence 1328, Ap
1259	107.5	6.0	803	1	US-08-515-903A-7	Sequence 7, Appli	1332	103.5	5.7	522	2	US-08-768-964-14	Sequence 14, Appl
1260	107.5	6.0	803	5	PCT-US95-12840-7	Sequence 7, Appli	c1333	103.5	5.7	522	2	US-08-768-964-14	Sequence 14, Appl
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c1262	107.5	6.0	1069	2	US-08-768-964-3	Sequence 3, Appli	c1335	103.5	5.7	522	3	US-09-005-299-15	Sequence 15, Appl
1263	107.5	6.0	1069	3	US-09-005-299-1	Sequence 1, Appli	1336	103.5	5.7	522	3	US-09-515-431-14	Sequence 14, Appl
c1264	107.5	6.0	1069	3	US-09-005-299-3	Sequence 3, Appli	c1337	103.5	5.7	522	3	US-09-515-431-15	Sequence 15, Appl
1265	107.5	6.0	1069	3	US-09-515-431-1	Sequence 1, Appli	1338	103.5	5.7	714	2	US-08-768-964-6	Sequence 6, Appli
c1266	107.5	6.0	1069	3	US-09-515-431-3	Sequence 3, Appli	c1339	103.5	5.7	714	2	US-08-768-964-8	Sequence 8, Appli
c1267	107.5	6.0	63183	4	US-09-949-016-13047	Sequence 13047, A	1340	103.5	5.7	714	3	US-09-005-299-6	Sequence 6, Appli
c1268	107.5	6.0	63183	4	US-09-949-016-13048	Sequence 13048, A	c1341	103.5	5.7	714	3	US-09-005-299-8	Sequence 8, Appli
1269	107	5.9	752	6	5455030-12	Patent No. 5455030	1342	103.5	5.7	714	3	US-09-515-431-6	Sequence 6, Appli
1270	107	5.9	752	6	5455030-12	Patent No. 5455030	c1343	103.5	5.7	714	3	US-09-515-431-8	Sequence 8, Appli
1271	107	5.9	1149	3	US-08-477-460B-5	Sequence 5, Appli	1344	103.5	5.7	819	4	US-09-910-174B-20	Sequence 20, Appl
1272	107	5.9	1149	3	US-08-379-516-5	Sequence 5, Appli	1345	103.5	5.7	819	4	US-09-620-461-20	Sequence 20, Appl
1273	107	5.9	1149	3	US-09-329-916-5	Sequence 5, Appli	1346	103.5	5.7	1223	4	US-09-949-016-2283	Sequence 2283, Ap
1274	107	5.9	1149	3	US-08-485-372A-5	Sequence 5, Appli	1347	103.5	5.7	2200	4	US-09-774-528-309	Sequence 309, App
1275	107	5.9	1149	3	US-09-409-006A-5	Sequence 5, Appli	1348	103.5	5.7	2229	4	US-09-910-174B-1	Sequence 1, Appli
1276	107	5.9	1149	3	US-08-484-681-5	Sequence 5, Appli	1349	103.5	5.7	2229	4	US-09-620-461-1	Sequence 1, Appli
1277	107	5.9	1149	4	US-09-766-995-5	Sequence 5, Appli	1350	103.5	5.7	2831	2	US-08-808-982-3	Sequence 3, Appli
1278	107	5.9	1149	5	PCT-US93-07422-5	Sequence 5, Appli	1351	103.5	5.7	2831	2	US-09-306-902A-3	Sequence 3, Appli
1279	107	5.9	1561	3	US-09-656-952-18	Sequence 18, Appl	1352	103.5	5.7	7783	4	US-09-495-880A-3	Sequence 3, Appli
1280	107	5.9	1591	3	US-09-656-952-17	Sequence 17, Appl	1353	103.5	5.7	19272	4	US-09-949-016-13462	Sequence 13462, A
1281	107	5.9	1592	3	US-09-656-952-1	Sequence 1, Appli	c1354	103.5	5.7	20662	4	US-09-949-016-15156	Sequence 15156, A
1282	106.5	5.9	879	2	US-08-400-115-3	Sequence 3, Appli	1355	103	5.7	538	3	US-09-221-298-3	Sequence 3, Appli
1283	106.5	5.9	879	2	US-08-463-903-14	Sequence 14, Appl	1356	103	5.7	538	3	US-09-401-064-3	Sequence 3, Appli
1284	106.5	5.9	877	3	US-07-935-695-14	Sequence 14, Appl	1357	103	5.7	723	4	US-09-791-540-5	Sequence 5, Appli
1285	106.5	5.9	744	2	US-08-392-338A-12	Sequence 12, Appl	1358	103	5.7	744	4	US-09-910-174B-30	Sequence 30, Appl
1286	106	5.9	744	3	US-09-166-750-12	Sequence 12, Appl	1359	103	5.7	836	4	US-08-961-309-63	Sequence 63, Appl
1287	106	5.9	744	3	US-09-166-093-12	Sequence 12, Appl	1360	103	5.7	1020	3	US-09-651-200-7	Sequence 7, Appli
1288	106	5.9	744	3	US-09-172-019-12	Sequence 12, Appl	1361	103	5.7	1273	3	US-08-466-368-1	Sequence 1, Appli
1289	106	5.9	744	3	US-09-166-094-12	Sequence 12, Appl	1362	103	5.7	1273	3	US-08-328-500-1	Sequence 1, Appli
1290	106	5.9	744	4	US-09-443-213-12	Sequence 12, Appl	1363	103	5.7	2691	3	US-09-651-200-1	Sequence 1, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 1, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of t
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1032
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-1
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: 4
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RESULT 2

US-09-700-397-2

03-05-700-337-2
; Sequence 2, Application US/09700397

; Patent No. 6664383

GENERAL INFORMATION:

APPLICANT: Ono Pharmaceutical Co., Ltd

TITLE OF INVENTION: No. 6664383e1 Polypeptides, cDNA encoding the same, and use of

; FILE REFERENCE: Q61459

; CURRENT APPLICATION NUMBER: US/09/700,397

; CURRENT FILING DATE: 2001-01-05

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; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1693
; TYPE: DNA
; ORGANISM: Homo sapiens
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; OTHER INFORMATION: Clone OC001 derived from human brain
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Alignment Scores:		
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Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
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Qy	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
Db	310	AACCGGTCACCCGGGTGGCTGGCTAAACGCGACGACCATCTCTATGCTGGGAATGAC	369
Qy	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
Db	370	AAGTGTGTCCTGGATCTCGCGTGGTCCCTCTGAGCAACGCCAAACGCGATACAGCATC	429
Qy	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
Db	430	GAGATCCAGAACGTTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	489
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	490	AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTGTAGAG	549
Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	550	ATTTCTTTCAGATATCTCATTAATGAAGGGAAACAATATTAGCCTCACCTGCGATAGCACT	609
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	610	GGTAGACCAGACGCTACGGTTACTTGGAGACACATCTCTCCCAACCGGTTGGCTTTGTG	669
Qy	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerClyAspTyrGlu	200
Db	670	AGTGAAGACGGAATACTTTGGAATTTCAGGGCATCACCCGGGAGCAGTTCAGGGGACTACGAG	729
Qy	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220

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Db 730 TGCAGTCCCAATGAGTGGCGCGCGCGTGTGTACGGAGAGTAAGGTACCGTGAAC 789
Qy 221 TyrProPofrileSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 790 TATCCACCATACATTTTCAGAGGCAAGGGGTACAGGTGTCCCGGTGGGACAAAAGGGGACA 849
Qy 241 LeuGlnCysGluAlaSerAlaValProSerLagluPheGlnTfrrLysAspAspLys 260
Db 850 CTGCAGTGTGAAGGCTCAGCAGTCCCTCAGCAGAAATTCACAGTGTGTAACAGGATGACAAA 909
Qy 261 ArgLeuLysGlyLysLysGlyValLysValGluAenArgProPheLeuSerLysLeu 280
Db 910 AGACTGATTGAGAGAAAGGGGTGAAGTGAAGAAACAGACCTTCTCTCAAAATC 969
Qy 281 IlePhePheAnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 970 ATCTTCTCAATGCTCTGACATGACTATATGGAACTACACTTTCGGTGGCTCCACCAAG 1029
Qy 301 LeuGlyHisThrAnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1030 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCGCGTCCAGCGAGGTGAGC 1089
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLysLeu 340
Db 1090 AACGGCAGTCGAGAGGGGAGGCTGGCTGTGGCTGTGGCTCTTCTGGTCTTGACCTG 1149
Qy 341 LeuLeuLysPhe 344
Db 1150 CTTCTCAAAATTT 1161

RESULT 3
US-09-700-397-5
; Sequence 5, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: NO. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-700-397-5

Alignment Scores:
Pred. No.: 1,41e-200 Length: 939
Score: 1642.00 Matches: 313
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.92% Indels: 0
DB: 4 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-700-397-5 (1-939)

Qy 32 ArgSerGlyAspAlaThrPheProLysAlaMetAspAenValThrValArgGlnGlyGlu 51
Db 1 CGCAGCGAGATGCCACCTTCCCAAGCTATGACACAGTGACGGTCCGGCAGGGGAG 60
Qy 52 SerAlaThrLeuArgCysThrIleAspAenArgValThrArgValAlaTrpLeuAsnArg 71
Db 61 AGCGCACCTTCAGGTGCACTATTGACAAACCGGGTCAACCGGTGGCTGCTAAACCGC 120
Qy 72 SerThrIleLeuTyrAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeu 91
Db 121 AGCCACCATCTTATGTCTGGGAATGACAAAGTGGTGGCTGGATCTCTCGCGTGTCTTCTG 180
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Qy 92 SerAsnThrGlnThrGlnTyrSerIleGluIleAenValAspValTyrAspGluGly 111
Db 181 AGCAACACCCAAACCGCAGTACAGCATCGAGATCCAGAACCGTGGATGTGTATGACAGGGC 240
Qy 112 ProTyrThrCysSerValGlnThrAspAenHisProLysThrSerArgValHisLeuLeu 131
Db 241 CTTTACACCTGCTCGGTGCGAGACAGAACCCCAAGACCTCTAGGGTCCACCTCATTT 300
Qy 132 ValGlnValSerProLysIleValGluIleSerSerAspIleSerIleAsnGluGlyAsn 151
Db 301 GTGCAGTATCTCCCAAAATTTAGAGATTTCTTCAGATATCTCCATTAATGAGGGGAC 360
Qy 152 AsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTrpArgHis 171
Db 361 AATATTAGCCTCACCTGATAGCAACTGGTAGACAGAGCCTACGGTTACTTTGGAGACAC 420
Qy 172 IleSerProLysAlaValGlyPheValSerGluAspGlnTyrLeuGluIleGlnGlyLeu 191
Db 421 ATCTCTCCCAAGCGGTGGCTTTGTGAGTGAAGACGAATACTTTGGAATTTTCAGGGCATC 480
Qy 192 ThrArgGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaProVal 211
Db 481 ACCGGGAGCAGTCAGGGGACTACGAGTGCAGTGCCTCCATGACGTGGCGCGCCCGTG 540
Qy 212 ValArgArgValLysValThrValAsnTyrProProTyrIleSerGluAlaLysGlyThr 231
Db 541 GTACGGAGAGTAAAGGTCCCGTGAACCTATCCACCATACATTTTCAGAAAGCCAGGGTACA 600
Qy 232 GlyValProValGlnLysGlyThrLeuGlnCysGluAlaSerAlaValProSerAla 251
Db 601 GGTGTCCCGTGGGACAAAAGGGGACACTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCA 660
Qy 252 GluPheGlnTrpTyrLysAspAspLysArgLeuIleGluGlyLysLysGlyValLysVal 271
Db 661 GAATTCAGTGTGTACAGGATGACAAAGACTGATTAAGGAAGAAGGGGTGAAGATG 720
Qy 272 GluAsnArgProPheLeuSerLysLeuIlePhePheAsnValSerGluHisAspTyrGly 291
Db 721 GAAACACAGACCTTTCTCTCTCAAACTCATCTTCTCAATGTCTCTGAACATGACTATGG 780
Qy 292 AsnTyrThrCysValAlaSerAsnLysLeuGlyHisThrAnAlaSerIleMetLeuPhe 311
Db 781 AACTACACTTTCGTGGCTCCCAACAGCTGGGCGCACCAATGCGCAGCATCATCTATTT 840
Qy 312 GlyProGlyAlaValSerGluValSerAsnGlyThrSerArgArgAlaGlyCysValTrp 331
Db 841 GGTCCAGCGCGCTCAGCGAGGTGAGCAACGGCACGTCGAGGAGGGCAGGCTGCTCTGG 900
Qy 332 LeuLeuProLeuLeuValLeuHisLeuLeuLysPhe 344
Db 901 CTGCTGCTCTTCTGTGCTTTGCACCTGCTTCTCAAAATTT 939

RESULT 4
US-09-976-594-403
; Sequence 403, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 403
; LENGTH: 1195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
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Qy	39	ProLysAlaMetAspAsnValThrValArgGlnGlyGluserAlaThrLeuArgCysThr	58
Db	103	AACCGAGGACGGACAACATCACCGTGAGCGAGGGGACACGCGCCATCCTCAGGTGTGTG	162
Qy	59	IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly	78
Db	163	GTGAAGACAGAAGCTCGAAAGTGGCCCTGGTTGAACCGCTCTGGCATCATCTCTCGCTGGA	222
Qy	79	AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr	98
Db	223	CACGACAACTGGTCTCTCGACCCCTCGGTTGAGCTGGAGAAACGCATGCTCTGGANATC	282
Qy	99	SerTleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln	118
Db	283	AGCCTCCGAATCCAGAAGTGGATGCTCTATGATGAAGGATCTTACATCATGCTCAGTTCAG	342
Qy	119	ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle	138
Db	343	ACACAGCATGATGCCCAACAGCTCTCAAGTTTACTTTGATTGTACAAGTTCCACCAAGATC	402
Qy	139	ValGluIleSerSerAspIleSerTleAsnGluGlyAsnAsnIleSerLeuThrCysIle	158
Db	403	TCCAACATCTCTCGATGTCACTGTAATGAGGCAGCAATGTAACCTGTGTCTGCATG	462
Qy	159	AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly	178
Db	463	GCCAAATGGCGCCCTGAACCTCTTATCATCTGGAGACACCTTACACCATTTGGAAGAGNA	522
Qy	179	PheValSerGluAspGluTyrIleuGluTleGlnGlyIleThrArgGluGlnSerGlyAsp	198
Db	523	TTTCAAGGAGAAGAATAATCTGGAGATCTCTAGGATCCTCAGGCAATCACCAGGGAACAGTCAGGCAAA	582
Qy	199	TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgValIysValThr	218
Db	583	TATCAGTGCAAAGCTGCCCAACGAGGTCTCTCCGCGGATGTCAAAACAAGTCAAGGTCACT	642
Qy	219	ValAsnTyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys	238
Db	643	GTGAACATATCCACCACCATCACAGAGCTTAGAGCAATGAAGCACCCACAGCAGACANA	702
Qy	239	GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp	258
Db	703	GCTTCCCTCAAATGTGAAGCCTCAGCGTGCCTGCACCTGACTTTGAGTGGTACCGGAT	762
Qy	259	AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer	278
Db	763	GACACACAGG--ATAAACAGTGCMAACGCGCTTGAGATTAGAGCACTGAGGCGCCAGTCC	819
Qy	279	LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer	298
Db	820	TCCCTGACGGTGACCAACGTCATCAGGAGAACACTACGGCAACTATACCTGTGTGGCTGCC	879
Qy	299	AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu	318
Db	880	AACAAGCTCGGGCTCACCATAAGCCAGACCTAGTCCCTTTTCAGACCCCGGTGCGGTGAGAGA	939
Qy	319	ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu	338
Db	940	ATC---AACGGATCCATCAGTCTGSCCGTACCACCTGTGGCTCTCTGGCAGCGCTCTGTTTC	996
Qy	339	HisLeuLeuLeuLys	343
Db	997	TGCTTCTTCAGCANA	1011

RESULT 6

RESULT 6
IIS-09-135-080-7

US-09-135-080-7
; Sequence 7, Application US/09135080
; Patent No. 6423827

: GENERAL INFORMATION:

GENERAL INFORMATION: APPLICANT: Levitt. pat. R.

APPLICANT: Levitt, Pat R.
APPLICANT: Pimenta, Aurea

APPLICANT: Pimenta, Aurea
APPLICANT: Fischer, Tizhak

```

; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:

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Alignment Scores:	
Pred. No.:	1014
Score:	926.50
Percent Similarity:	73.54%
Best Local Similarity:	55.08%
Query Match:	51.30%
DB:	3
	Gaps: 4
	Indels: 5
	Mismatches: 81
	Conservative: 60
	Matches: 179

US-10-017-084A-523 (1-344) X US-09-135-080-7 (1-1014)

Qy	20	LeuAlaIaLeuCysLeuPhe---	GlnGlyValProValArgSerGlyAspAlaThrPhe	38
Db	49	CTGAGACTGTCTCGCTTCTTCCACACAGCACTGC	CGCGTTCCGACGCTGGAT-----TTT	102
Qy	39	ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr	58	
		:::		
Db	103	AACCGAGCGCAGCAACATCACCGTAGCGACGGGGACCGGCATCTCTAGGTGTGTG	162	
Qy	59	IleAspAsnArgValThrArgValAlaIlePLeuAsnArgSerThrIleLeuTyrAlaGly	78	
		:::		
Db	163	GTAGAACAAGAACTCGAAAGTCGCCTGTGTGAACCGCTCTGGCATCATCTTCGTGCGA	222	
Qy	79	AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr	98	
		:::		
Db	223	CACGACAAAGTGTCTCTGGACCCCTCGGGTGGAGTGGAGAAACGCCATGCTCTGGAAATAC	282	
Qy	99	SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln	118	
Db	283	AGCCTCCGAATCCCAAGAAGGTGCATGTCTATCATGAAGCATCTCAACATGCTCAGTTCAG	342	


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Qy 119 ThrAspAenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 343 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGTATGATGTTACAAAGTTCCACCAAGATC 402
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAenIleSerLeuThrCysIle 158
Db 403 TCCAAACATCTCTCGGATGTCACGTGTAATGAGGCGAGCAATGTAACCCCTGCTCGCATG 462
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 463 GCCAATGGCGCCCTGAACTGTTATACCTTGGAGACACCTTACACACTTGGAGAGAA 522
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAsp 198
Db 523 TTTGAAGGAGAAGAATAATCTGGAGATCTCGAGATCTAGGCATCACCAGGAAACAGTCAGGCAA 582
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValIleValThr 218
Db 583 TATGAGTCAAGGCTGCCAAGGAGTCTCTCCGGGATGTCAAACAAAGTCAAGGTCACT 642
Qy 219 ValAenTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 643 GTGAACATTCACCCACCATCACAGAGTCTAAGACCAATGAAGCCACACAGGACGAA 702
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAsp 258
Db 703 GCTTCCTCAAAATGTGAAGCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACCGGAT 762
Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 763 GACACACAGG---ATAAACAGATGCAACAGCGCTTGAGATTAAGAGCAGCTAGGCGCCAGTCC 819
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 820 TCCCTGACGGTGACCACTGCTGAGGAACACTACGCAACTATACCTGTGTGGCTGCC 879
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 880 AACAGCTCGCGTGACCAATGCCAGCTAGTCTCTTTTCAGACCCGCGTCCGTGAGAGGA 939
Qy 319 ValSerAenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeu 338
Db 940 ATC---AACCGATCCATCAGTCTGCGCGTACCACTGTGGCTGTGGTCCCTGCTGTCCTGTC 996
Qy 339 HisLeuLeuLys 343
Db 997 TGCCTTCTCAGCAA 1011
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RESULT 7

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US-08-414-657D-3
; Sequence 3, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56...1069
; OTHER INFORMATION:
; US-08-414-657D-3
Alignment Scores:
Pred. No.: 1-78e-108 Length: 1238
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 2 Gaps: 4
US-10-017-084a-523 (1-344) x US-08-414-657D-3 (1-1238)
Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 104 CTGAGACTGCTCTGCCCTTCTCCACAGGACTGCGCTTCGACGCTGGAT-----TTT 157
Qy 39 ProLysAlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 158 AACCGAGCGACGGAAACATCACCGTGAGGCGAGGCGGACACGGCCATCTCTCAGGTGTGTG 217
Qy 59 IleAspAenArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGly 78
Db 218 GTAGAACACAGAACTCGAAAGTGGCTGTGTGAACCGCTCTGCATCATCTTCGCTGGA 277
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnThrGlnTyr 98
Db 278 CACGACAAGTGGTCTCTGGACCCCTCGGTTGAGCTGGAGAAACGCCATGCTCTGGAATAC 337
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 338 AGCTCCGAAATCCAGAAAGGTGGATGCTATGATGAAGGATCCTACACATGCTCGATTCCAG 397
Qy 119 ThrAspAenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTGTATGATGTTACAAAGATC 457
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAenIleSerLeuThrCysIle 158
Db 458 TCCAAACATCTCTCGGATGTCACGTGTAATGAGGCGAGCAATGTAACCCCTGCTGTCATG 517
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 518 GCCAATGGCGCCCTGAACTGTTATCACCTTGGAGACACCTTACACCACTTGGAGAGAA 577
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyLeuThrArgGluGlnSerGlyAsp 198
Db 578 TTTGAAGGAGAAGAATAATCTGGAGATCTTAGCATCCTACGAGGAAACAGTCAGGCGAA 637
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValIleValThr 218
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Db 638 TATGAGTGAAGGTCGCAACGAGGTCCTCCCGGATGTCAAACAGTCAAGGTCACT 697
Qy 219 ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 698 GTGAACATATCACCCACCATCACAGAGTCTAAGAGCAATGAAGCACCACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp 258
Db 758 GCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACGGGAT 817
Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACCCAGG---ATAAACAGTGCAAACGCGCTTGAGATTAAAGAGCACTGAGGGCCAGTCC 874
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
Db 875 TCCCTGAGCGGTGACCAACGTCACGTGAGGAAACACTACGCGCACTATACCTGTGTGGTGGC 934
Qy 299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 935 AACAAAGTCGGCGTCACCAATGCCAGCCTAGTCTCTTTTCAGACCCGGGTGCGTGAGAGGA 994
Qy 319 ValSerAsnGlyThrSerArgAlaGlyCysValTyrPheLeuProLeuLeuValLeu 338
Db 995 ATC---AACGGATCCATCAGTCTGGCCGCTACCATGCTGTGGTGTGCTGGCAGCGTCCCTGTTC 1051
Qy 339 HisLeuLeuLeuLys 343
Db 1052 TGCCTTCTCAGCAAA 1066

RESULT 8
US-09-135-080-3
; Sequence 3, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESS: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 31743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1238 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 56..1069
; OTHER INFORMATION:
; US-09-135-080-3

Alignment Scores:
Pred. No.: 1.78e-108 Length: 1238
Score: 926.50 Matches: 179
Percent Similarity: 73.54% Conservative: 60
Best Local Similarity: 55.08% Mismatches: 81
Query Match: 51.30% Indels: 5
DB: 3 Gaps: 4

US-10-017-084a-523 (1-344) x US-09-135-080-3 (1-1238)

Qy 20 LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 104 CTGAGACTGTCTTCCCGTCTTCCACAGGACTGCCCGTTCGACGCTGGAT-----TTT 157
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 158 AACCGAGCGCAGGACAAACATCACCGTCAGCGCAGGGGACACGGCCATCTCTCAGGTGTG 217
Qy 59 IleAspAsnArgValThrArgValAlaTyrPheAsnArgSerThrIleLeuTyrAlaGly 78
Db 218 GTAGAACAGAACTCGAAAGTGGCTTGGTGGACCGCTCTGGCATCATCTCTTCGCTGGA 277
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnTyr 98
Db 278 CACGACAAGTGGTCTCTGGACCCCTCGGGTTGAGTCGGAGAAACGCCATGCTCTGGAATAC 337
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln 118
Db 338 AGCCTCCGAATCCAGAAAGGTGGATGTCTATGATGAAGGATCCTACATGCTCTCAGTTCAG 397
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 398 ACACAGCATGAGCCCAAGACCTCTCAAGTTTACTTTGATTGTACAAAGTCCACCAAGATC 457
Qy 139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIle 158
Db 458 TCCAAACATCTCTCGGATGTCACTGTAATGAGGCGAGCAATGTAACCCCTGCTCTGCATG 517
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 518 GCCAATGGCGCCCTGAACCTGTTATCACCTGGAGACACCTTACACCACCTTGGAGAGAA 577
Qy 179 PheValSerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAsp 198
Db 578 TTTGAAGAGAAAGAAATATCTGGAGATCTTAGGCATCACCAGGAAACAGTCAAGGCAAA 637
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThr 218
Db 638 TATGAGTGAAGGCTGCCAACGAGGTCTCTCCCGCGGATGTCAAAACAGTCAAGGTCACT 697
Qy 219 ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlnLys 238
Db 698 GTGAACATATCCACCCACCATCACAGAGTCTAAGAGCAATGAAGCACCACAGGACGACAA 757
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp 258
Db 758 GCTTCCCTCAAAATGTGAAGCCTCAGCGGTGCTGCACCTGACTTTGAGTGTGTACGGGAT 817
Qy 259 AspLysArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSer 278
Db 818 GACACCCAGG---ATAAACAGTGCAAACGCGCTTGAGATTAAAGAGCACTGAGGGCCAGTCC 874
Qy 279 LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer 298
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Db 875 TCCTGACGGTGACCAACGTCACCTGAGGAACACTACGCGCAACTATACCTGTGTGCTGCC 934
Qy 299 AenlyseLeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 935 AACAGCTCGGCGTCACCAATGCCAGCTAGTCCTTTTCAGACCGGGTCGGTGAGAGGA 994
Qy 319 ValSerAenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
Db 995 ATC---AACGGATCCATCAGCTGCGCTACCACTGTGTGCTGCTGGCAGCGCTCCCTGTC 1051
Qy 339 HisLeuLeuLeuLys 343
Db 1052 TGCCTTCTCAGCAA 1066

RESULT 9

US-08-414-657D-1
; Sequence 1, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Lmbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 977 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 2...976
; OTHER INFORMATION:
US-08-414-657D-1

Alignment Scores:
Pred. No.: 2,896-108 Length: 977
Score: 923.50 Matches: 177
Percent Similarity: 74.06% Conservative: 60
Best Local Similarity: 55.31% Mismatches: 78
Query Match: 51.14% Indels: 5
DB: 2 Gaps: 4

US-10-017-084A-523 (1-344) x US-08-414-657D-1 (1-977)
Qy 20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 29 CTGAGATTGCTCTGCCCTTCTTCCACAGGACTGCTGTTCGACGGTGAT-----TTT 82
Qy 39 ProlyseAlaMetAspAenValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 83 AACCGGACGACGACACATCACCCTGAGCGAGGCGGACACAGCATCTCTCAGGTGGT 142
Qy 59 IleAspAenArgValThrArgValAlaTrpLeuAenArgSerThrIleLeuTyAlaGly 78
Db 143 CTAGACACAAGAACTCAAAGGTGGCTGTGTAACCGTTCTCGCATCATATTTTGTCTGA 202
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAenThrGlnTyr 98
Db 203 CATGACAAGTGGTCTCTGGACCCACGGGTGAGCTGGAGAAACGCCATTCTCTGGAATAC 262
Qy 99 SerIleGluIleGlnAenValAspValTyAspGluGlyProTyThrCysSerValGln 118
Db 263 AGCTCTCCGAATCCAGAGGTGGATGCTATGATGAGGGTTCCTACACTTGTCTCAGTTCCAG 322
Qy 119 ThrAspAenHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAAAGTCCCAACCAAGATC 382
Qy 139 ValGluIleSerSerAspIleSerIleAenGluGlyAenAenIleSerLeuThrCysIle 158
Db 383 TCCNATATCTCTCGGATGTCATGTAAGGGGACAGACGACTCTGCTGTGCAIG 442
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 443 GCCAATGGCGCTCTCGAACCTGTTATCACCTGGAGACACCTTACCAACCTGGAAGGAA 502
Qy 179 PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
Db 503 TTTGAAGGAGAAGAAGATATCTGGAGATCTTGGCATCTTGGCATCACAGGAGCAGTCAGGCAAA 562
Qy 199 TyrGluCysSerAlaSerAenAspValAlaAlaProValValArgValValValThr 218
Db 563 TATGAGTGCAAAAGCTGCCAACGAGGTCTCTCGCGGAGTGTCAAAACAAAGTCAAGGTCACT 622
Qy 219 ValAenTyProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
Db 623 GTGAACCTATCTCCCACTATCACAGATCCAAGACATGAAGCAATGAAGCCACACAGGACAA 682
Qy 239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp 258
Db 683 GCTTCACTCAAATGTGAGGCTCGGCAGTGCCTGCACCTGACTTTGAGTGGTACCGGAT 742
Qy 259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAenArgProPheLeuSer 278
Db 743 GACACTAGG---ATAAATAGTGCCTTGGATGGCTTGGATTAAGACACGAGGGCCAGTCT 799
Qy 279 LysLeuIlePhePheAenValSerGluHisAspTyTrpGlyAenTyThrCysValAlaSer 298
Db 800 TCCCTGACGGTGACCAACGTCACCTGAGGAGCAGTACGCGCACTACACCTGTGTGCTGCC 859
Qy 299 AsnLysLeuGlyHisThrAenAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
Db 860 AACAAAGCTGGGGTCAACCAATGCCAGCTAGTCCTTTTCAGACCTGGGTGCGGTGAGAGGA 919
Qy 319 ValSerAenGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeu 338
Db 920 ATA---AATGGATCCATCAGTCTGCGCGGTACCACTGTGTGCTGCGCAGCATCTCTGCTC 976

RESULT 10

US-09-135-080-1
; Sequence 1, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak
APPLICANT: Zhukareva, Victoria
TITLE OF INVENTION: Limbic System-Associated Membrane
TITLE OF INVENTION: Protein and DNA
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/135,080
FILING DATE: 17-AUG-1998

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/414,657

FILING DATE: 31-MAR-1995

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102A

TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-620-3214

TELEFAX: 609-620-3259

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 977 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 2...976

OTHER INFORMATION:

US-09-135-080-1

Alignment Scores:

Pred. No.: 2,89e-108 Length: 977

Score: 923.50 Matches: 177

Percent Similarity: 74.06% Conservative: 60

Best Local Similarity: 55.31% Mismatches: 78

Query Match: 51.14% Indels: 5

DB: 3 Gaps: 4

US-10-017-084A-523 (1-344) x US-09-135-080-1 (1-977)

20 LeuAlaAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38

29 CTGAGATTGCTCTGCTTCTCCACAGACTGCTGTTGCGAGCGTGGAT-----TTT 82

39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58

83 AACCGAGGACGACGACACATCAGCGTCGAGCGGAGGGGACACAGCCATCTCAGGTGGGTT 142

59 IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly 78

143 CTAGAAGACAGAACTCAAAAGTGCGCTGTGAACCGTTCTGGCATCATTTTTCGTGGA 202

79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrp 98

203 CATGACAGTGGTCTCTGGACCCACCGGTTGAGTGGAGAACGCCATTCTCTGGAATAC 262

99 SerIleGluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGln 118

263 AGCCTCCGAATCCAGAGGTGGATGTTCTATGATGAGGGTTCTTACACTTGTCTCAGTTT 322

119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
323 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTGTATCGTACAGTCCCAAGATC 382
139 ValGluIleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle 158
383 TCCAATATCTCTCGGATGTCTGTAATGAGGGCAGCAACGTCAGTCTGCTGTCATG 442
159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
443 GCCAATGGCCGCTCTGAACCTGTATCCTGAGACACCTTACCACTGAGAGGAA 502
179 PheValSerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp 198
503 TTTGAAGGAGAGAAGAAATATCTGGAGATCTTGGCATCACCGAGGAGCAGTCAGGCAA 562
199 TyrGluCysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThr 218
563 TATGAGTGCAGGCTGCCAAGAGGTCTCTCGCGGATGTCAAAACAAAGTCAAGGTCACT 622
219 ValAsnTyrProProTyIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys 238
623 GTGAACATATCTCCACTATCACAGATCCCAAGAGCAATGAAGCCACACAGAGCAAA 682
239 GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyLysAsp 258
683 GCTTCACTCAATGTGAGGCTCGGCAGTGCCTGCACCTGACTTGTAGTGGTACCGGAT 742
259 AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer 278
743 GACACTAGG---ATAAATAGTGCAATGGCTTGAAGTAAAGACGAGGAGGCGCAGTCT 799
279 LysLeuIlePhePheAsnValSerGluHisAspTyGlyAsnTrpThrCysValAlaSer 298
800 TCCCTGACGTGACCAACGTCACCTGAGGAGCAGTACGCGCACTACACTGTGTGGCTGCC 859
299 AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu 318
860 AACAGCTGGGGTCAACCATGCCAGCTAGTCTTTTCAGACCTGGTGGTGGAGGA 919
319 ValSerAsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeu 338
920 ATA---AATGATCCATCAGTCTGGCGGTACCACTGTGGCTGTGGCAGCATCTCTGCTC 976

RESULT 11

US-08-414-657D-7

Sequence 7, Application US/08414657D

Patent No. 5861283

GENERAL INFORMATION:

APPLICANT: Levitt, Pat

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

APPLICANT: Zhukareva, Victoria

TITLE OF INVENTION: Limbic System-Associated Membrane

TITLE OF INVENTION: Protein and DNA

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,657D

FILING DATE: 31-MAR-1995

CLASSIFICATION: 435

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 924 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..924
; OTHER INFORMATION:
;
US-08-414-657D-7

Alignment Scores:
Pred. No.: 2,57e-106 Length: 924
Score: 908.00 Matches: 170
Percent Similarity: 75.50% Conservative: 58
Best Local Similarity: 56.29% Mismatches: 70
Query Match: 50.28% Indels: 4
DB: 2 Gaps: 3

US-10-017-084a-523 (1-344) x US-08-414-657D-7 (1-924)

Qy 20 LeuAlaLeuLysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe 38
Db 28 CTGAGATTGCTCGCTCTTCCACAGGACTGCTGTTCGACGCTGGAT-----TTT 81
Qy 39 ProLysAlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThr 58
Db 82 AACCGAGCGCAGGACACATCACCGTGAGCGAGGGGACAGCATCTCCTCAGGTGGTT 141
Qy 59 IleAspAsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGly 78
Db 142 CTAGAAGACAAGAACTCAAAGCTGGCTGGTTGAACCGTTCTGGCATCATTTTGTCTGA 201
Qy 79 AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr 98
Db 202 CATGACAAAGTGGTCTCTGGACCCACGGGTTGAGCTGGAGAAACGCCATTCTCTGGAATAC 261
Qy 99 SerIleGluIleGlnAsnValAspValTyrAspGlyProTyrThrCysSerValGln 118
Db 262 AGCTCCGAATCCAGAGGTGGATGCTATGATGAGGGTTCTACACTTGTCTAGTTGAG 321
Qy 119 ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle 138
Db 322 ACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTTGATCGTACAAAGTCCCAACCAAGATC 381
Qy 139 ValGluIleSerSerAspIleSerIleAsnGlnGlyAsnAniIleSerLeuThrCysIle 158
Db 382 TCCAATATCTCTCGGATGTCACTGTGAATGAGGCGACCAACGTAAGTCTGCTCGCATG 441
Qy 159 AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly 178
Db 442 GCCAATGGCCGCTCTGAACCTGTTATCACCTGGAGACACCTTACCACTGGAGGAA 501
Qy 179 PheValSerGluAspGlyLeuGluIleGlnGlyThrArgGluGlnSerGlyAsp 198
Db 502 TTGAAGGAGAAGAATAATCTGGAGATCTTGGCATCACCGAGGAGCAGTCAGGCAAA 561
Qy 199 TyrGluCysSerAlaSerAsnAspValAlaProValValArgArgValIleValThr 218
Db 562 TATGAGTCAAAGCTGCCAACAGAGGTCTCTCTGGCGGATGTCAAACCAAGTCAAGGTCACT
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US-08-414-657D-8		US-10-017-084A-523 (1-344) x US-08-414-657D-8 (1-945)	
Alignment Scores:			
Pred. No.:	3-59e-106	Length:	945
Score:	907.00	Matches:	170
Percent Similarity:	75.50%	Conservative:	58
Best Local Similarity:	56.29%	Mismatches:	70
Query Match:	50.22%	Indels:	4
DB:	2	Gaps:	3
US-10-017-084A-523 (1-344) x US-08-414-657D-8 (1-945)			
Qy	20	LeuAlaLeuCysLeuPhe---GlnGlyValProValArgSerGlyAspAlaThrPhe	38
Db	49	CTGAGACTGCTGCTCTCTCCACAGGACTGCGCGTTCGACGGTGGAT-----TTT	102
Qy	39	ProLysAlaMetAspAsnValThrValArgGlnGlyCysSerAlaThrLeuArgCysThr	58
Db	103	AACGGAGCGGACCAACATCACCGTGAGCGGAGGGGACACGCCCATCTCTCAGGTGTG	162
Qy	59	IleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGly	78
Db	163	GTAGAAGCAAGAACTCGAAGTGGCTGTGTGACCGCTCTGGCATCATCTTCGCTGA	222
Qy	79	AsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyr	98
Db	223	CACGACAAGTGGTCTCTGGACCTCGCGTTGAGCTGGAGAAACGCCATGCTCTGGAATC	282
Qy	99	SerIleGluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGln	118
Db	283	AGCTCCGAATCCAGAAGGTGGATGCTATGATGAAGGATCCTACATGCTCTGATTCAG	342
Qy	119	ThrAspAsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIle	138
Db	343	ACACAGATGAGCCCAAGACTCTCAAGTTTACTTGTACDAGTTCCACCAAGATC	402
Qy	139	ValGluSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIle	158
Db	403	TCCAACATCTCTCGGATGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGTGTCTGAGT	462
Qy	159	AlaThrGlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGly	178
Db	463	GCCAATGGCGGCGCTGAACTGTTTATCACCTGGAGACACCTTACACCACTTGGAAAGAA	522
Qy	179	PheValSerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAsp	198
Db	523	TTTGAAGGAGAGAGATATCTGGAGATCTTAGGATCACCAGGAAACAGTCAAGGAAA	582
Qy	199	TyrGluCysSerAlaSerAsnAspAlaAlaProValValArgArgValLysValThr	218
Db	583	TATGAGTGAAGGTGCGCAACGAGGTCTCTCCCGCGATGTCAAAACAAGTCAAGGTCACT	642
Qy	219	ValAsnTyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLys	238
Db	643	GTGAACATATCCACCACCATCACAGAGTCTAAGAGCAATGAAGCCACACAGGACGAA	702
Qy	239	GlyThrLeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAsp	258
Db	703	GCTTCCCTCAATGTGAAGCCTCAGCGGTGCTGCACCTGACTGTGAGTGTACGGGAT	762
Qy	259	AspLysArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSer	278
Db	763	GACACCCAGG---ATAAAGAGTGCAACCGGCTTGAAGATTAAGAGCACTGAGGGCCAGTCC	819
Qy	279	LysLeuIlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSer	298
Db	820	TCCCTGAGCGGTGACCAACGTCACCTGAGGAAACACTACCGCAACTATCTGTGTGCTGCC	879
Qy	299	AsnLysLeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGlu	318
Db	880	AACAAAGCTCGCGGTGACCAATGCGCAGCTAGTCTCTTTTCAGACCCCGGTGCGTGAGGA	939
Qy	319	ValSer	320

Db

940 ATCAAC 945

RESULT 13

US-08-414-657D-6

Sequence 6, Application US/08414657D

Patent No. 5861283

GENERAL INFORMATION:

APPLICANT: Levitt, Pat

APPLICANT: Pimenta, Aurea

APPLICANT: Fischer, Itzhak

APPLICANT: Zhukareva, Victoria

TITLE OF INVENTION: Limbic System-Associated Membrane

TITLE OF INVENTION: Protein and DNA

NUMBER OF SEQUENCES: 60

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dechert Price & Rhoads

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

STATE: NJ

COUNTRY: USA

ZIP: 08543

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/414,657D

FILING DATE: 31-MAR-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Bloom, Allen

REGISTRATION NUMBER: 29,135

REFERENCE/DOCKET NUMBER: 317743-102

TELECOMMUNICATION INFORMATION:

TELEPHONE: 609-520-3214

TELEFAX: 609-520-3259

TELEX:

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 912 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: Coding Sequence

LOCATION: 1...912

OTHER INFORMATION:

US-08-414-657D-6

Alignment Scores:

Pred. No.: 1.48e-105

Score: 902.00

Percent Similarity: 74.68%

Best Local Similarity: 55.52%

Query Match: 49.94%

DB: 2

Gaps: 3

US-10-017-084A-523 (1-344) x US-08-414-657D-6 (1-912)

Qy 31 ValArgSerGlyAspAlaThrPheProLysAlaMetAspAsnValThrValArgGlnGly 50

Db 1 GTTCGACGCTGGAT-----TTTACCGAGGCGACGACCAACATCACCGTGAGCGAGGG 54

Qy 51 GluSerAlaThrLeuArgCysThrIleAspAsnArgValThrArgValAlaTrpLeuAsn 70

Db 55 GACACGCCATCTCTCAGTGGTCTTAGAAGACAAAGAACTCAAAGGTGGCTGTGTTGAAC 114

Qy 71 ArgSerThrIleLeuTyAlaGlyAsnAspLysTrpCysLeuAspProArgValValLeu 90

Db 115 CGTTCTGGCATCATTTTGTGGACATGACAAGTGGTCTCTGGACCCAGCGGTTGAGCTG 174
Qy 91 LeuSerAsnThrGlnThrGlnThrSerIleGluLeuGlnAsnValAspValTyrAspGlu 110
Db 175 GAGAAACGCCATTCTCTGGATACAGCTCCGAATCCAGAAAGGTGGATGTCTATGATGAG 234
Qy 111 GlyProTyrThrCysSerValGlnThrAspAsnHisProLysThrSerArgValHisLeu 130
Db 235 GGTTCCTACATCTGCTAGTTCAACACAGCATGAGCCCAAGACCTCCCAAGTTTACTTG 294
Qy 131 IleValGlnValSerProLysIleValGluLeuSerSerAspIleSerIleAsnGluGly 150
Db 295 ATCGTACAAGTCCCAACAGATCTCCAATATCTCTCGGATGTCACCTGTGAATGAGGCG 354
Qy 151 AsnAsnIleSerLeuThrCysIleAlaThrGlyArgProGluProThrValThrTyrArg 170
Db 355 AGCAACGTGACTCTGGTGTGATGGCCCAATGCGCGTCTGAACTATCTCCACCTGGAGA 414
Qy 171 HisIleSerProLysAlaValGlyPheValSerGluAspGluTyrLeuGluIleGlnGly 190
Db 415 CACCTTACACCACTGGNAGGAATTTGAAGGAGAGAGAGATATCTGGAGATCCTTGGC 474
Qy 191 IleThrArgGluGlnSerGlyAspTyrGluCysSerAlaSerAsnAspValAlaAlaPro 210
Db 475 ATCACCAGGAGCAGTCAGGCAATATGAGTGCAAGCTGCCACGAGGTCTCTCTCGCGC 534
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RESULT 14

US-08-414-657D-9
; Sequence 9, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA

; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..861
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; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 861 base pairs
; TYPE: nucleic acid
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; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...861
; OTHER INFORMATION:
; US-08-414-657D-10
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Pred. No.: 1.77e-103 Length: 861
Score: 885.50 Matches: 164
Percent Similarity: 76.21% Conservative: 57
Best Local Similarity: 56.55% Mismatches: 66
Query Match: 49.03% Indels: 3
DB: 2 Gaps: 2
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SUMMARIES

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812	815	45.1	2840	18	US-10-210-028-611	Sequence 611, App	1084	268.5	14.9	5510	17	US-10-021-660-60	Sequence 60, Appl
813	815	45.1	2840	18	US-10-162-521A-611	Sequence 611, App	1085	268.5	14.9	5510	18	US-10-331-496A-8	Sequence 8, Appli
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816	815	45.1	2840	22	US-10-897-359-611	Sequence 611, App	1088	268.5	14.9	5530	19	US-10-243-552-737	Sequence 737, App
817	815	45.1	2840	22	US-10-893-802-611	Sequence 611, App	1089	268.5	14.9	5530	19	US-10-276-774-607	Sequence 607, App
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1195	229.5	12.7	7329	19	US-10-435-751-165	Sequence 165, App							
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1208	229.5	12.7	7650	19	US-10-435-751-164	Sequence 164, App							
1209	229.5	12.7	7650	19	US-10-435-751-170	Sequence 170, App							
1210	229.5	12.7	7650	19	US-10-435-751-176	Sequence 176, App							
1211	229.5	12.7	7650	19	US-10-435-751-182	Sequence 182, App							
1212	229.5	12.7	7650	19	US-10-435-751-188	Sequence 188, App							

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